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OM nucleic - nucleic search, using sw model

Run on: May 23, 2004, 11:33:59 ; Search time 258 Seconds  
(without alignments)  
12241.184 Million cell updates/sec

Title: US-09-964-956-12  
Perfect score: 5691  
Sequence: 1 atgaagcgcacgtccctggaa.....gcttagacagctgaaataaa 5691

Scoring table: OLIGO NUC  
Gapop 60.0 , Gapext 60.0

Searched: 682709 seqs, 277475446 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents NA:\*  
1: /cgn2\_6/ptodata/2/ina/5A COMB.seq:\*  
2: /cgn2\_6/ptodata/2/ina/5B COMB.seq:\*  
3: /cgn2\_6/ptodata/2/ina/5A COMB.seq:\*  
4: /cgn2\_6/ptodata/2/ina/5B COMB.seq:\*  
5: /cgn2\_6/ptodata/2/ina/5A COMB.seq:\*  
6: /cgn2\_6/ptodata/2/ina/5B COMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	ID	Description
C 1	20	0.4	249	4	US-09-252-991A-3017
C 2	20	0.4	311	4	US-09-313-294A-7021
C 3	20	0.4	462	4	US-09-401-084-165
C 4	20	0.4	616	3	US-09-385-982-238
5	20	0.4	894	4	US-09-252-991A-2754
6	20	0.4	1029	4	US-09-252-991A-2651
C 7	20	0.4	1455	4	US-09-252-991A-3212
C 8	20	0.4	1456	4	US-09-976-594-779
C 9	20	0.4	1636	4	US-08-630-915A-31
C 10	20	0.4	2522	4	US-09-620-312D-702
C 11	20	0.4	13842	3	US-09-105-537-30
C 12	20	0.4	36778	3	US-09-105-537-5
C 13	20	0.4	38506	3	US-09-320-878-19
C 14	20	0.4	38506	4	US-09-141-908-1
C 15	20	0.4	38506	4	US-09-657-440-19
C 16	19	0.3	531	5	PCT-US95-04583-1
C 17	19	0.3	588	2	US-08-924-695A-3
C 18	19	0.3	791	4	US-09-657-346A-10
C 19	19	0.3	900	1	US-07-955-041-1
20	19	0.3	900	1	US-08-227-455-1
21	19	0.3	900	1	US-08-472-482-1
22	19	0.3	900	1	US-08-487-069-1
C 23	19	0.3	1236	4	US-09-328-352-326
C 24	19	0.3	1407	4	US-09-894-844-35
C 25	19	0.3	2238	1	US-07-841-651-1
C 26	19	0.3	2477	4	US-09-907-794A-169
27	19	0.3	2477	4	US-09-905-125A-169

28	19	0.3	2477	4	US-09-902-775A-169	Sequence 169, Ap
29	19	0.3	2965	4	US-09-833-381-1216	Sequence 1216, Ap
30	19	0.3	4474	1	US-08-480-547A-9	Sequence 9, Appl
31	19	0.3	4474	1	US-08-250-847B-9	Sequence 9, Appl
32	19	0.3	4474	2	US-08-463-949A-9	Sequence 9, Appl
33	19	0.3	4474	3	US-08-464-410A-9	Sequence 9, Appl
34	19	0.3	4474	5	PCT-US94-06066-9	Sequence 9, Appl
C 35	19	0.3	30310	4	US-09-657-346A-96	Sequence 96, Appl
C 36	19	0.3	536165	4	US-09-214-808-1	Sequence 1, Appl
37	19	0.3	4403765	3	US-09-103-840A-2	Sequence 2, Appl
38	19	0.3	4411529	3	US-09-103-840A-1	Sequence 1, Appl
C 39	18	0.3	71	2	US-08-465-591A-29	Sequence 29, Appl
C 40	18	0.3	71	2	US-08-465-594A-29	Sequence 29, Appl
C 41	18	0.3	71	3	US-08-973-124-214	Sequence 214, App
C 42	18	0.3	71	5	PCT-US96-08014-214	Sequence 214, App
C 43	18	0.3	288	4	US-09-313-294A-6281	Sequence 6281, Ap
44	18	0.3	532	4	US-09-621-976-1479	Sequence 1479, Ap
45	18	0.3	792	4	US-09-252-991A-7444	Sequence 7444, Ap

ALIGNMENTS

RESULT 1  
US-09-252-991A-3017/c  
; Sequence 3017, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 3017  
; LENGTH: 249  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-3017

Query Match 0.4%; Score 20; DB 4; Length 249;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1920 GGAGACCGGCATGACCTTCG 1939  
DB 108 GGAGACCGGCATGACCTTCG 89

RESULT 2  
US-09-313-294A-7021/c  
; Sequence 7021, Application US/09313294A  
; Patent No. 6476212  
; GENERAL INFORMATION:  
; APPLICANT: Ito, Laura Y.  
; APPLICANT: Sherman, Bradley K.  
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR  
; FILE REFERENCE: PL-0017 US  
; CURRENT APPLICATION NUMBER: US/09/313,294A  
; CURRENT FILING DATE: 1999-05-14  
; NUMBER OF SEQ ID NOS: 7600  
; SOFTWARE: PERL Program  
; SEQ ID NO 7021  
; LENGTH: 311  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:

FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(616)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-385-982-238

Query Match 0.4%; Score 20; DB 3; Length 616;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4827 CAACTCCACCGTCTCCAGGA 4846  
DB 71 CAACTCCACCGTCTCCAGGA 52

RESULT 5  
US-09-252-991A-2754  
; Sequence 2754, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 2754  
; LENGTH: 894  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-2754

Query Match 0.4%; Score 20; DB 4; Length 894;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1920 GGAGACCGCATGACCTTCG 1939  
DB 687 GGAGACCGCATGACCTTCG 706

RESULT 6  
US-09-252-991A-2651  
; Sequence 2651, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 2651  
; LENGTH: 1029  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-2651

Query Match 0.4%; Score 20; DB 4; Length 1029;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1920 GGAGACCGCATGACCTTCG 1939

NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No. 6476212 700381005H1  
; NAME/KEY: unsure  
; LOCATION: 87, 254, 276, 286  
; OTHER INFORMATION: a, t, c, g, or other  
US-09-313-294A-7021

Query Match 0.4%; Score 20; DB 4; Length 311;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4827 CAACTCCACCGTCTCCAGGA 4846  
DB 115 CAACTCCACCGTCTCCAGGA 96

RESULT 3  
US-09-401-064-165/c  
; Sequence 165, Application US/09401064  
; Patent No. 6623923  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Lodes, Michael J.  
; APPLICANT: Secret, Heather  
; APPLICANT: Benson, Darin R.  
; APPLICANT: Mesgher, Madeline Joy  
; APPLICANT: Stolk, John A.  
; APPLICANT: Wang, Tongtong  
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND  
; FILE REFERENCE: 210121.47102  
; CURRENT APPLICATION NUMBER: US/09/401,064  
; CURRENT FILING DATE: 1999-09-22  
; NUMBER OF SEQ ID NOS: 371  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 165  
; LENGTH: 462  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-09-401-064-165

Query Match 0.4%; Score 20; DB 4; Length 462;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4827 CAACTCCACCGTCTCCAGGA 4846  
DB 116 CAACTCCACCGTCTCCAGGA 97

RESULT 4  
US-09-385-982-238/c  
; Sequence 238, Application US/09385982  
; Patent No. 6262334  
; GENERAL INFORMATION:  
; APPLICANT: ENDEGE, WILSON O., ET AL.  
; TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION  
; TITLE OF INVENTION: PRODUCTS: II  
; FILE REFERENCE: CCDA-260XX  
; CURRENT APPLICATION NUMBER: US/09/385,982  
; CURRENT FILING DATE: 1999-08-30  
; EARLIER APPLICATION NUMBER: 09/328,111  
; EARLIER FILING DATE: 1999-06-08  
; EARLIER APPLICATION NUMBER: 60/117,393  
; EARLIER FILING DATE: 1999-01-27  
; EARLIER APPLICATION NUMBER: 60/098,639  
; EARLIER FILING DATE: 1998-08-31  
; NUMBER OF SEQ ID NOS: 544  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 238  
; LENGTH: 616  
; TYPE: DNA  
; ORGANISM: Homo sapiens

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Db      361 GGAGACCGGATGACCTTCG 380
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RESULT 7
US-09-252-991A-3212/c
; Sequence 3212, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 3212
; LENGTH: 1455
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-3212
Query Match      0.4%; Score 20; DB 4; Length 1455;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1920 GGAGACCGGATGACCTTCG 1939
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Db      322 GGAGACCGGATGACCTTCG 303
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RESULT 8
US-09-976-594-779/c
; Sequence 779, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
; APPLICANT: Furness, Michael
; APPLICANT: Buchbinder, Jenny
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
; FILE REFERENCE: PA-0041 US
; CURRENT APPLICATION NUMBER: US/09/976,594
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,409
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program
; SEQ ID NO 779
; LENGTH: 1456
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673549 1384715.4
; NAME/KEY: unsure
; LOCATION: 1453
; OTHER INFORMATION: a, t, c, g, or other
US-09-976-594-779
Query Match      0.4%; Score 20; DB 4; Length 1456;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4827 CAACTCCACCGTCTCCAGGA 4845
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Db      425 CAACTCCACCGTCTCCAGGA 406
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RESULT 9
US-08-630-915A-31

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; Sequence 31, Application US/08630915A
; Patent No. 6309820
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: HOFFMAN, No. 6309820h
; APPLICANT: KAY, Brian K.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: MCCONNELL, Stephen J.
; TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
; TITLE OF INVENTION: DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
; NUMBER OF SEQUENCES: 227
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/630,915A
; FILING DATE: 03-APR-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-174
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1636 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-630-915A-31
Query Match      0.4%; Score 20; DB 4; Length 1636;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4179 GCTGCAGAGCAAGCTGGAGT 4198
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Db      863 GCTGCAGAGCAAGCTGGAGT 882
|||||

RESULT 10
US-09-620-312D-702/c
; Sequence 702, Application US/09620312D
; Patent No. 6569662
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yungqing
; APPLICANT: Wang, Dunrui

```

; APPLICANT: Wang, Zhiwei  
; APPLICANT: John Tillingshast  
; APPLICANT: Drmanac, Radoje T.  
; TITLE OF INVENTION: No. 6569662el Nucleic Acids and  
; TITLE OF INVENTION: Polypeptides  
; FILE REFERENCE: 784CIP28  
; CURRENT APPLICATION NUMBER: US/09/620,312D  
; CURRENT FILING DATE: 2000-07-19  
; PRIOR APPLICATION NUMBER: 09/552,317  
; PRIOR FILING DATE: 2000-04-25  
; PRIOR APPLICATION NUMBER: 09/488,725  
; PRIOR FILING DATE: 2000-01-21  
; NUMBER OF SEQ ID NOS: 1105  
; SOFTWARE: pt\_FL\_genes Version 1.0  
; SEQ ID NO 702  
; LENGTH: 2522  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (179)..(1606)  
US-09-620-312D-702

Query Match 0.4%; Score 20; DB 4; Length 2522;  
Best Local Similarity 100.0%; Pred. No. 15;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1888 CACCATGTCGTACAGCTTCA 1907  
Db 517 CACCATGTCGTACAGCTTCA 498

RESULT 11  
US-09-105-537-30/c  
; Sequence 30, Application US/09105537A  
; Patent No. 6265202  
; GENERAL INFORMATION:  
; APPLICANT: Sherman, D.H.  
; APPLICANT: Liu, H.  
; APPLICANT: Xue, Y.  
; APPLICANT: Zhao, L.  
; TITLE OF INVENTION: DNA encoding methymycin and pikromycin  
; FILE REFERENCE: 600.438US1  
; CURRENT APPLICATION NUMBER: US/09/105,537A  
; CURRENT FILING DATE: 1998-06-26  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 30  
; LENGTH: 13842  
; TYPE: DNA  
; ORGANISM: Streptomyces venezuelae  
US-09-105-537-30

Query Match 0.4%; Score 20; DB 3; Length 13842;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4828 AACTCCACCGTCTCCAGGAC 4847  
Db 10196 AACTCCACCGTCTCCAGGAC 10177

RESULT 12  
US-09-105-537-5/c  
; Sequence 5, Application US/09105537A  
; Patent No. 6265202  
; GENERAL INFORMATION:  
; APPLICANT: Sherman, D.H.  
; APPLICANT: Liu, H.  
; APPLICANT: Xue, Y.  
; APPLICANT: Zhao, L.  
; TITLE OF INVENTION: DNA encoding methymycin and pikromycin  
; FILE REFERENCE: 600.438US1

; CURRENT APPLICATION NUMBER: US/09/105,537A  
; CURRENT FILING DATE: 1998-06-26  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 5  
; LENGTH: 36778  
; TYPE: DNA  
; ORGANISM: Streptomyces venezuelae  
US-09-105-537-5

Query Match 0.4%; Score 20; DB 3; Length 36778;  
Best Local Similarity 100.0%; Pred. No. 17;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4828 AACTCCACCGTCTCCAGGAC 4847  
Db 11937 AACTCCACCGTCTCCAGGAC 11918

RESULT 13  
US-09-320-878-19/c  
; Sequence 19, Application US/09320878A  
; Patent No. 6117659  
; GENERAL INFORMATION:  
; APPLICANT: ASHLEY, Gary  
; APPLICANT: BETLACH, Melanie C.  
; APPLICANT: BETLACH, Mary C.  
; APPLICANT: MCDANIEL, Robert  
; APPLICANT: TANG, Li  
; TITLE OF INVENTION: RECOMBINANT NARBONOLIDE POLYKETIDE SYNTHASE  
; FILE REFERENCE: 300622002120  
; CURRENT APPLICATION NUMBER: US/09/320,878A  
; CURRENT FILING DATE: 1998-05-27  
; EARLIER APPLICATION NUMBER: CIP OF 09/141,908  
; EARLIER FILING DATE: 1998-08-28  
; EARLIER APPLICATION NUMBER: CIP OF 09/073,538  
; EARLIER FILING DATE: 1998-05-06  
; EARLIER APPLICATION NUMBER: CIP OF 08/846,247  
; EARLIER FILING DATE: 1997-04-30  
; EARLIER APPLICATION NUMBER: 60/119,139  
; EARLIER FILING DATE: 1999-02-08  
; EARLIER APPLICATION NUMBER: 60/100,880  
; EARLIER FILING DATE: 1998-09-22  
; EARLIER APPLICATION NUMBER: 60/087,080  
; EARLIER FILING DATE: 1998-05-28  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 19  
; LENGTH: 38506  
; TYPE: DNA  
; ORGANISM: Streptomyces venezuelae  
US-09-320-878-19

Query Match 0.4%; Score 20; DB 3; Length 38506;  
Best Local Similarity 100.0%; Pred. No. 17;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4828 AACTCCACCGTCTCCAGGAC 4847  
Db 10079 AACTCCACCGTCTCCAGGAC 10060

RESULT 14  
US-09-141-908-1/c  
; Sequence 1, Application US/09141908  
; Patent No. 6503741  
; GENERAL INFORMATION:  
; APPLICANT: ASHLEY, Gary  
; APPLICANT: BETLACH, Melanie C.  
; APPLICANT: BETLACH, Mary  
; APPLICANT: MCDANIEL, Robert  
; APPLICANT: TANG, Li  
; TITLE OF INVENTION: Combinatorial Polyketide Libraries Produced Using a



; TITLE OF INVENTION: Modular PKS Gene Cluster as Scaffold  
; FILE REFERENCE: 300622002100  
; CURRENT APPLICATION NUMBER: US/09/141,908  
; CURRENT FILING DATE: 1998-08-28  
; EARLIER APPLICATION NUMBER: CIP OF 09/073,538  
; EARLIER FILING DATE: 1998-05-06  
; EARLIER APPLICATION NUMBER: CIP OF 08/846,247  
; EARLIER FILING DATE: 1997-04-30  
; EARLIER APPLICATION NUMBER: PROV. 60/076,919  
; EARLIER FILING DATE: 1998-03-05  
; EARLIER APPLICATION NUMBER: PROV. 60/087,080  
; EARLIER FILING DATE: 1998-05-28  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 38506  
; TYPE: DNA  
; ORGANISM: Streptomyces venezuelae  
US-09-141-908-1

Query Match 0.4%; Score 20; DB 4; Length 38506;  
Best Local Similarity 100.0%; Pred. No. 17;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4828 AACTCCACCGTCTCCAGGAC 4847  
Db 10079 AACTCCACCGTCTCCAGGAC 10060

RESULT 15  
US-09-657-440-19/c  
; Sequence 19, Application US/09657440  
; Patent No. 6509455  
; GENERAL INFORMATION:  
; APPLICANT: ASHLEY, Gary  
; APPLICANT: BETLACH, Melanie C.  
; APPLICANT: BETLACH, Mary C.  
; APPLICANT: MCDANIEL, Robert  
; APPLICANT: TANG, Li  
; TITLE OF INVENTION: RECOMBINANT NARBONOLIDE POLYKETIDE SYNTHASE  
; FILE REFERENCE: 300622002120  
; CURRENT APPLICATION NUMBER: US/09/657,440  
; CURRENT FILING DATE: 2000-09-07  
; PRIOR APPLICATION NUMBER: 09/320,878  
; PRIOR FILING DATE: 1999-05-27  
; PRIOR APPLICATION NUMBER: CIP OF 09/141,908  
; PRIOR FILING DATE: 1998-08-28  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 19  
; LENGTH: 38506  
; TYPE: DNA  
; ORGANISM: Streptomyces venezuelae  
US-09-657-440-19

Query Match 0.4%; Score 20; DB 4; Length 38506;  
Best Local Similarity 100.0%; Pred. No. 17;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4828 AACTCCACCGTCTCCAGGAC 4847  
Db 10079 AACTCCACCGTCTCCAGGAC 10060

Search completed: May 23, 2004, 12:40:27  
Job time : 265 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: May 23, 2004, 11:35:39 ; Search time 1466 Seconds  
(without alignments)  
17642.596 Million cell updates/sec

Title: US-09-964-956-12

Perfect score: 5691

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Scoring table: OLIGO NUC

Gapop\_60.0 , Gapext 60.0

Searched: 2953838 seqs, 2272363821 residues

Word size : 0

Total number of hits satisfying chosen parameters: 5907676

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications NA.\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	1108	19.5	3666	16	US-10-108-260A-802
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6	793	13.9	2597	13	US-10-245-103-91
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16	793	13.9	2597	15	US-10-245-055-91	Sequence 91, Appl
17	793	13.9	2597	15	US-10-245-147-91	Sequence 91, Appl
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ALIGNMENTS

RESULT 1

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; Sequence 12, Application US/09964956  
; Publication No. US20040043926A1  
; GENERAL INFORMATION:  
; APPLICANT: Gerlach, Valerie L  
; APPLICANT: MacDougall, John R  
; APPLICANT: Smithson, Glenda  
; APPLICANT: Millet, Isabelle  
; APPLICANT: Stone, David  
; APPLICANT: Gunther, Erik  
; APPLICANT: Ellerman, Karen  
; APPLICANT: Grosse, William M  
; APPLICANT: Alsobrook II, John P  
; APPLICANT: Lepley, Denise M  
; APPLICANT: Burgess, Catherine E  
; APPLICANT: Padigaru, Muralidhara  
; APPLICANT: Kekuda, Ramesh  
; APPLICANT: Spytek, Kimberly A  
; APPLICANT: Leach, Martin D  
; APPLICANT: Shinkets, Richard A  
; TITLE OF INVENTION: No. US20040043926A1el Proteins and Nucleic Acids Encoding Same  
; FILE REFERENCE: 21402-124  
; CURRENT APPLICATION NUMBER: US/09/964,956  
; CURRENT FILING DATE: 2001-09-26  
; PRIOR APPLICATION NUMBER: 60/235,631  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: 60/235,633  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: 60/235,808  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: 60/236,064  
; PRIOR FILING DATE: 2000-09-27  
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; PRIOR FILING DATE: 2000-09-27  
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; PRIOR FILING DATE: 2000-09-27

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; PRIOR APPLICATION NUMBER: 60/236,135
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 60/237,434
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/238,321
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: 60/238,399
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,396
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/276,667
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/294,823
; PRIOR FILING DATE: 2001-05-31
; PRIOR APPLICATION NUMBER: 60/304,868
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 5691
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; ORGANISM: Homo sapiens
US-09-964-956-12

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Best Local Similarity 100.0%; Pred. No. 0;
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Qy	2461	TTCCGATGTGGTGTGCGAGGCGCAGCCAGTGTGCACTTCCGACGACCTGCTGCC	2520
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Qy	3121	ACCATCGTGGGATTTGAGCCAGAAATGGAGCATTTGTCACTGGAACACACCCATCGCGTA	3180
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Db	3301	CTCGCTCTGGGTCCTGACCACTGACAGTCCGAGAGGCGCGAGGATTTGGCTTC	3360
Qy	3361	ATCCTGGACAGTCCAGTCCCTGCTCATCTCAACAGACCACTTCACTTACTATGCC	3420
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Qy	3421	AAACCCGGTGTGTTGAGCGCTTTGGTCCCTCAGGAATCTTGGAGCTCAAGCTTGGCACGCC	3480
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Qy	3481	ATCATCTTAAAGGCAAGACCTGATCCCGCTGGTGGGGCAACGTTGAAGTGTGAC	3540
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Qy	3601	TGCGAGTCCCGCAACCTCATCGGAGGCAAAAGTGTGCGCCGTGCTGGTGGCATGGAG	3660
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FILE REFERENCE: PF-0867 USN			Query Match		
CURRENT APPLICATION NUMBER: US/10/451.010			Best Local Similarity 97.2%; Score 5532; DB 17; Length 6367;		
PRIOR FILING DATE: 2003-06-17			Matches 5682; Conservative 0; Mismatches 3; Indels 0; Gaps 0;		
PRIOR APPLICATION NUMBER: PCT/US01/49206					
PRIOR FILING DATE: 2001-12-18					
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TYPE: DNA					
ORGANISM: Homo sapiens					
FEATURE:					
NAME/KEY: misc.feature					
OTHER INFORMATION: Incyte ID No: 7156379CB1					
FEATURE:					
NAME/KEY: unsure					
LOCATION: 166					
OTHER INFORMATION: a, t, c, g, or other					
US-10-451-010-19					
QY	1	ATGAAGCCATGCCCCCTGGAACTGGACCTGCTCTCCACCTCTCTCATGTGGGCATG	60		
DB	566	ATGAAGCCATGCCCCCTGGAACTGGACCTGCTCTCCACCTCTCTCATGTGGGCATG	625		
QY	61	GGCTCTCCACTTTGCTACCCCGCAGCCAGCCCGCTGTCCAGAGCAGCGGTCATTT	120		
DB	626	GGCTCTCCACTTTGCTACCCCGCAGCCAGCCCGCTGTCCAGAGCAGCGGTCATTT	685		
QY	121	GTCAATTCGAGAGAGCCCGCAGAGGTTTCAATCACTGGTGGTGGATGAGGACA	180		
DB	686	GTCAATTCGAGAGAGCCCGCAGAGGTTTCAATCACTGGTGGTGGATGAGGACA	745		
QY	181	GGACACATTTACTTTGGGGCGCTCAATCGGATTTACAAGCTCTCCAGCGACCTTGAAGTC	240		
DB	746	GGACACATTTACTTTGGGGCGCTCAATCGGATTTACAAGCTCTCCAGCGACCTTGAAGTC	805		
QY	241	TTGGTGACGATGAGACAGGGCGGAGAGCAACCCCAAGTTTACCACCCCGCATC	300		
DB	806	TTGGTGACGATGAGACAGGGCGGAGAGCAACCCCAAGTTTACCACCCCGCATC	865		
QY	301	GTCCAGACCTGCAATGAGCCCTGACCAACCAACAATGTCAACAGATGCTCTCTCATA	360		
DB	866	GTCCAGACCTGCAATGAGCCCTGACCAACCAACAATGTCAACAGATGCTCTCTCATA	925		
QY	361	GACTACAAGGAGAACAGGCTGATTTGCTGTGGAGCGCTGTACCAAGGCATCTGCAAGCTG	420		
DB	926	GACTACAAGGAGAACAGGCTGATTTGCTGTGGAGCGCTGTACCAAGGCATCTGCAAGCTG	985		
QY	421	CTGAGGCTGGAGGACCTTTCAAGCTGGGGAGCGCTTATCATTAAGAGGAGCACTATCTG	480		
DB	986	CTGAGGCTGGAGGACCTTTCAAGCTGGGGAGCGCTTATCATTAAGAGGAGCACTATCTG	1045		
QY	481	TCAGGTGTCAACGAGAGCGGCTCAGTCTTTGGAGTGTGCTCTCTACAGCAACCTGGAT	540		
DB	1046	TCAGGTGTCAACGAGAGCGGCTCAGTCTTTGGAGTGTGCTCTCTACAGCAACCTGGAT	1105		
QY	541	GACAAAGCTGTTTCATTCACCGGAGTGGAGGAGCGGAGTATTTTCCACCATCTCC	600		
DB	1106	GACAAAGCTGTTTCATTCACCGGAGTGGAGGAGCGGAGTATTTTCCACCATCTCC	1165		
QY	601	AGCCGGAACCTGACCAAGAACTCTGAGCGGATGGCATGTTTCGGGTACGCTTCCATGAT	660		
DB	1166	AGCCGGAACCTGACCAAGAACTCTGAGCGGATGGCATGTTTCGGGTACGCTTCCATGAT	1225		

QY	661	GAGTTCGTGGCTCGATGATTAAAGATCCCTTCGGACACCTTCACCATCATCCTGACTTT	720		
DB	1226	GAGTTCGTGGCTCGATGATTAAAGATCCCTTCGGACACCTTCACCATCATCCTGACTTT	1285		
QY	721	GATATCTACTATGTCTATGTTTACAGTGGCACTTTGTCTACTTTTGGACCTCCAA	780		
DB	1286	GATATCTACTATGTCTATGTTTACAGTGGCACTTTGTCTACTTTTGGACCTCCAA	1345		
QY	781	CTTGAGATGTTGTTCTCCACAGGCTCCACCAAGAGCAGGTGTATACATCAAGCTC	840		
DB	1346	CTTGAGATGTTGTTCTCCACAGGCTCCACCAAGAGCAGGTGTATACATCAAGCTC	1405		
QY	841	GTGAGGCTTTGAAAGAGGACACAGCTTCAACTCTATGTAGAGTGCCCATTTGGCTGT	900		
DB	1406	GTGAGGCTTTGAAAGAGGACACAGCTTCAACTCTATGTAGAGTGCCCATTTGGCTGT	1465		
QY	901	GAGCGCAGTGGGTGGAGTACCGCTCTGTCAGGCTGCCTTACCTGCTCCAAAGCGGGGCC	960		
DB	1466	GAGCGCAGTGGGTGGAGTACCGCTCTGTCAGGCTGCCTTACCTGCTCCAAAGCGGGGCC	1525		
QY	961	GTGCTTGGCAGGACCCCTTGGAGTCCATCCAGATGATGACCTGCTTTCACCGTCTCTCC	1020		
DB	1526	GTGCTTGGCAGGACCCCTTGGAGTCCATCCAGATGATGACCTGCTTTCACCGTCTCTCC	1585		
QY	1021	AAGGCCCAGAGCGGAAATGAAATCCCTGGATGAGTCGGCCCTGTGTCATCTTTCATCTTG	1080		
DB	1586	AAGGCCCAGAGCGGAAATGAAATCCCTGGATGAGTCGGCCCTGTGTCATCTTTCATCTTG	1645		
QY	1081	AAGCAGATAAATGACCCATTAAGAGCGGCTGAGTCTTGTTCACCGGCGAGGCGACG	1140		
DB	1646	AAGCAGATAAATGACCCATTAAGAGCGGCTGAGTCTTGTTCACCGGCGAGGCGACG	1705		
QY	1141	CTGAGACCTGGCTGGCTCAAGGTGAGGACATCCCTGTCAGCAGTGGCTCTTAAACCATTT	1200		
DB	1706	CTGAGACCTGGCTGGCTCAAGGTGAGGACATCCCTGTCAGCAGTGGCTCTTAAACCATTT	1765		
QY	1201	GACGATAAATTTCTGTGGCTGGACATGAATGCTCCCTGGAGGTGTCGACATGGTGGGT	1260		
DB	1766	GACGATAAATTTCTGTGGCTGGACATGAATGCTCCCTGGAGGTGTCGACATGGTGGGT	1825		
QY	1261	GGAAATCCCGTCTTTCAGGAGGACGGGACCGCATGACCTGTCTCATCGCATATGTCTAC	1320		
DB	1826	GGAAATCCCGTCTTTCAGGAGGACGGGACCGCATGACCTGTCTCATCGCATATGTCTAC	1885		
QY	1321	AAGAACCACTCTCTGGCCCTTTTGGGCACCAAAAGTGGCAAGCTGGAAGATCCGGGTG	1380		
DB	1886	AAGAACCACTCTCTGGCCCTTTTGGGCACCAAAAGTGGCAAGCTGGAAGATCCGGGTG	1945		
QY	1381	GATGACCCAGGAGGACCGCCCTCAGTATGAGAGCGGTGAGGTGGAGCCCGGCCCA	1440		
DB	1946	GATGACCCAGGAGGACCGCCCTCAGTATGAGAGCGGTGAGGTGGAGCCCGGCCCA	2005		
QY	1441	GTCTCTCCGGGATATGGCCCTTCTCCAAAGGACCAACAGCAACTCTACATCATGTCAAGAGG	1500		
DB	2006	GTCTCTCCGGGATATGGCCCTTCTCCAAAGGACCAACAGCAACTCTACATCATGTCAAGAGG	2065		
QY	1501	CAGCTCAACAGAGTCCCTGTGGAGTCTGTGGTCAAGTATCAGAGTGGCGGAGTGCCTT	1560		
DB	2066	CAGCTCAACAGAGTCCCTGTGGAGTCTGTGGTCAAGTATCAGAGTGGCGGAGTGCCTT	2125		
QY	1561	GGCTCAGGACCCCGCTCTGTGGTGGTGTGTGTCACAAACAGCTGACCCCGGAAGGAG	1620		
DB	2126	GGCTCAGGACCCCGCTCTGTGGTGGTGTGTGTCACAAACAGCTGACCCCGGAAGGAG	2185		
QY	1621	CGGTGTGAGCGGTCCAAGAGGACCCCGAGGTTTGGCTCGAGATGAAGCAGTGTCTCGG	1680		
DB	2186	CGGTGTGAGCGGTCCAAGAGGACCCCGAGGTTTGGCTCGAGATGAAGCAGTGTCTCGG	2245		
QY	1681	CTGAGCGTCCATCCCAATATCTCCGTCTCTCAGTACAACGCTGCTGTCTCTCTGGAG	1740		
DB	2246	CTGAGCGTCCATCCCAATATCTCCGTCTCTCAGTACAACGCTGCTGTCTCTCTGGAG	2305		

QY 1741 ACGTAAATGTCGCGAGCTGTACGCTGGCGTCAACTGACCTTTGAGGACCTGTGACAG 1800  
DB 2306 ACGTAAATGTCGCGAGCTGTACGCTGGCGTCAACTGACCTTTGAGGACCTGTGACAG 2365  
QY 1801 ATGGATGGGCTGGTCTGGGCAATCAGATCCAGTGTCTACTCCCTGACGCCAAGAGGTG 1860  
DB 2366 ATGGATGGGCTGGTCTGGGCAATCAGATCCAGTGTCTACTCCCTGACGCCAAGAGGTG 2425  
QY 1861 CCCCGGATCATCACAGAGATGGGACCAACATGTCGTACAGCTTCAGCTCAAAATCAAAG 1920  
DB 2426 CCCCGGATCATCACAGAGATGGGACCAACATGTCGTACAGCTTCAGCTCAAAATCAAAG 2485  
QY 1921 GAGACCGGATGACCTTTGGCCAGCACACAGCTTTGCTTTTACAAATGTCAGGCTGCACAA 1980  
DB 2486 GAGACCGGATGACCTTTGGCCAGCACACAGCTTTGCTTTTACAAATGTCAGGCTGCACAA 2545  
QY 1981 TCGTGCCTGCTGCTGGTGGAGAGTCCATACCGCTGCCACTGTGTAAATACCGGATGTC 2040  
DB 2546 TCGTGCCTGCTGCTGGTGGAGAGTCCATACCGCTGCCACTGTGTAAATACCGGATGTC 2605  
QY 2041 TGCACCCATGACCCCAAGACCTGCTCCTTCCAGGAAGCCGAGTGAAGCTCCCGGAGAC 2100  
DB 2606 TGCACCCATGACCCCAAGACCTGCTCCTTCCAGGAAGCCGAGTGAAGCTCCCGGAGAC 2665  
QY 2101 TGCACCCAGCTGCTGGAGTGACAGATCCTGTGTGCCGTGGAGGTGATCAAGCTATC 2160  
DB 2666 TGCACCCAGCTGCTGGAGTGACAGATCCTGTGTGCCGTGGAGGTGATCAAGCTATC 2725  
QY 2161 ACGCTGAAGGCCCAAGAACCTCCCGCAGCCCAAGTCTGGGACGCTGGGTACGAATGCATC 2220  
DB 2726 ACGCTGAAGGCCCAAGAACCTCCCGCAGCCCAAGTCTGGGACGCTGGGTACGAATGCATC 2785  
QY 2221 CTCACATTCAGGCGAGCAGCAGAGTGCCCGCCCTGCGCTTCAAAGCTTCCAGCGTA 2280  
DB 2786 CTCACATTCAGGCGAGCAGCAGAGTGCCCGCCCTGCGCTTCAAAGCTTCCAGCGTA 2845  
QY 2281 CAGTGCCAGAACACCTTTATTCTATGAAGGGATGGAGATCAACAACTGCGCCGTGGAG 2340  
DB 2846 CAGTGCCAGAACACCTTTATTCTATGAAGGGATGGAGATCAACAACTGCGCCGTGGAG 2905  
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QY 2401 CTCCTACAGTGTGGAGCCATGGTGTAGAGCTGCGGCTGTGCTCAAGGCTGACCCAGAC 2460  
DB 2966 CTCCTACAGTGTGGAGCCATGGTGTAGAGCTGCGGCTGTGCTCAAGGCTGACCCAGAC 3025  
QY 2461 TTGCGATGTGGTGTGCCAGGCCCCAGGCCAGTGACACCTTGCGCCAGCACTGCGCTGCC 2520  
DB 3026 TTGCGATGTGGTGTGCCAGGCCCCAGGCCAGTGACACCTTGCGCCAGCACTGCGCTGCC 3085  
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DB 3086 CAGGAGAGCAGTGGCTGGAGCTGTCTGTGCCAAAGCAAGTGACAAACCCCGCATC 3145  
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QY 2641 GAGAACTGGGCTGGATTTTCGCGACATCGCTCCCATGTCAAAGTTGCTGGCTGGAG 2700  
DB 3206 GAGAACTGGGCTGGATTTTCGCGACATCGCTCCCATGTCAAAGTTGCTGGCTGGAG 3265  
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DB 3446 CCCAGCCGGGGCCCATGTCCGAGGGACCCCAAGTGACCATCACAGGACCAACTGAT 3505  
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5641 TACAACTAGAACAAAGTATTAACCTCTGATGCTTGAAGCTTGAAGCTGTA 5685  
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RESULT 3

US-10-108-260A-802  
; Sequence 802, Application US/10108260A  
; Publication No. US20040005560A1  
; GENERAL INFORMATION:  
; APPLICANT: HELIX RESEARCH INSTITUTE  
; TITLE OF INVENTION: No. US20040005560A1el full length cDNA  
; FILE REFERENCE: H1-A0106  
; CURRENT APPLICATION NUMBER: US/10/108,260A  
; CURRENT FILING DATE: 2002-03-27  
; NUMBER OF SEQ ID NOS: 5458  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 802  
; LENGTH: 3666  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-108-260A-802

Query Match 19.5%; Score 1108; DB 16; Length 3666;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1158; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 4527 TGCACACAGCCCCGAGGTCCTGAGTAAAGATCTCAACTGTGACACATCACTCAGGTCAA 4586  
Db 1 TGCACACAGCCCCGAGGTCCTGAGTAAAGATCTCAACTGTGACACATCACTCAGGTCAA 60  
Qy 4587 GGAGAGAGATTCTGGATGCTCATCTTCAAGAATGTGCTTGTCTCCACCGGCCCAAGCTGC 4646



Db 61 GGAGAGAGATTCGGATGCCATCTTCAAGAAATGTGCTGCCACCGGCCCAAGCTGC 120  
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 Db 121 AGATATGGATTCGGATGCGCAAGAGAGTGGGCAAGGATGATCTTTCAGGATGAAGA 180  
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 Db 721 CAACATGATCAAGAACCCGAGTGTGTTGACATTCATTAAGACAGATCAAGAGCGC 780  
 QY 5307 CTGCTCTCTGTGGTGGCTCAGACCTTCATGACCTCTTCTGCTCAGCTCAGACCGGCT 5366  
 Db 781 CTGCTCTCTGTGGTGGCTCAGACCTTCATGACCTCTTCTGCTCAGCTCAGACCGGCT 840  
 QY 5367 GGGCAAGGACTCGCCCTCCAAACAGCTGTGTATGCCAAGGACATCCCGAGCTACAAGAA 5426  
 Db 841 GGGCAAGGACTCGCCCTCCAAACAGCTGTGTATGCCAAGGACATCCCGAGCTACAAGAA 900  
 QY 5427 TTGGTGGAGAGGTATTACTCAGACATAGGAGATGCCAGCATCAGGACCAAGCAT 5486  
 Db 901 TTGGTGGAGAGGTATTACTCAGACATAGGAGATGCCAGCATCAGGACCAAGCAT 960  
 QY 5487 GAACGCATACCTGGCTGAGCAGTCCCGGATGCACATGAATGATTTCAACACCATGAGTGC 5546  
 Db 961 GAACGCATACCTGGCTGAGCAGTCCCGGATGCACATGAATGATTTCAACACCATGAGTGC 1020  
 QY 5547 ACTCTCAGAGATCTTCTCTATGTGGCAATACAGCGAGGAGATCTTGGACCTTGA 5606  
 Db 1021 ACTCTCAGAGATCTTCTCTATGTGGCAATACAGCGAGGAGATCTTGGACCTTGA 1080  
 QY 5607 CCACGATGACAGTGTGGGAGCAGAACTGGGCTTACAACTAGAACAAAGTATTAACCT 5666  
 Db 1081 CCACGATGACAGTGTGGGAGCAGAACTGGGCTTACAACTAGAACAAAGTATTAACCT 1140  
 QY 5667 CATGAGCTTAGACAGCTGA 5685

Db 1141 CATGAGCTTAGACAGCTGA 1159  
 RESULT 4  
 US-10-245-752-91  
 ; Sequence 91, Application US/10245752  
 ; Publication No. US20030064473A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Baker, Kevin  
 ; APPLICANT: Baton, Dan  
 ; APPLICANT: Filvaroff, Ellen  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Grimaldi, J. Christopher  
 ; APPLICANT: Gurney, Austin  
 ; APPLICANT: Smith, Victoria  
 ; APPLICANT: Stephan, Jean-Phillippe  
 ; APPLICANT: Watanabe, Colin  
 ; APPLICANT: Wood, William  
 ; APPLICANT: Zhang, Zemin  
 ; APPLICANT: Fong, Sherman  
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
 ; FILE REFERENCE: P3630R1C66  
 ; CURRENT APPLICATION NUMBER: US/10/245,752  
 ; CURRENT FILING DATE: 2002-09-16  
 ; PRIOR APPLICATION NUMBER: 10/197942  
 ; PRIOR FILING DATE: 2002-07-18  
 ; PRIOR APPLICATION NUMBER: 60/059114  
 ; PRIOR FILING DATE: 1997-09-17  
 ; PRIOR APPLICATION NUMBER: 60/063046  
 ; PRIOR FILING DATE: 1997-10-24  
 ; PRIOR APPLICATION NUMBER: 60/065027  
 ; PRIOR FILING DATE: 1997-11-10  
 ; PRIOR APPLICATION NUMBER: 60/079689  
 ; PRIOR FILING DATE: 1998-03-27  
 ; PRIOR APPLICATION NUMBER: 60/086478  
 ; PRIOR FILING DATE: 1998-05-22  
 ; PRIOR APPLICATION NUMBER: 60/087607  
 ; PRIOR FILING DATE: 1998-06-02  
 ; PRIOR APPLICATION NUMBER: 60/089801  
 ; PRIOR FILING DATE: 1998-06-18  
 ; PRIOR APPLICATION NUMBER: 60/090557  
 ; PRIOR FILING DATE: 1998-06-24  
 ; PRIOR APPLICATION NUMBER: 60/090689  
 ; PRIOR FILING DATE: 1998-06-25  
 ; Remaining Prior Application data removed - See File Wrapper or PALM.  
 ; NUMBER OF SEQ ID NOS: 116  
 ; SEQ ID NO 91  
 ; LENGTH: 2597  
 ; TYPE: DNA  
 ; ORGANISM: Homo Sapien  
 ; US-10-245-752-91  
 Query Match 13.9%; Score 793; DB 13; Length 2597;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 793; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 579 CGAGTATTTCCCAACCATCTCCAGCCGGAATGACCAAGAACTCTGAGCGGATGGCAT 638  
 Db 1 CGAGTATTTCCCAACCATCTCCAGCCGGAATGACCAAGAACTCTGAGCGGATGGCAT 60  
 QY 639 GTTCGGCTAGCTCTTCCATGATGATTCGTGGCTCGATGATTAAGATCCCTTCGGACAC 698  
 Db 61 GTTCGGCTAGCTCTTCCATGATGATTCGTGGCTCGATGATTAAGATCCCTTCGGACAC 120  
 QY 699 CTTTCCATCATCCCTGACTTTGATATCTATGCTATGCTTGTGTTTACGAGTGGCACTT 758  
 Db 121 CTTTCCATCATCCCTGACTTTGATATCTATGCTATGCTTGTGTTTACGAGTGGCACTT 180  
 QY 759 TGTCTACTTTTGGACCTCCAACTGAGATGGTGTCTCCACCGAGGCTCCACCAAGGA 818  
 Db 181 TGTCTACTTTTGGACCTCCAACTGAGATGGTGTCTCCACCGAGGCTCCACCAAGGA 240





:	PRIOR FILING DATE:	1997-11-10			
:	PRIOR APPLICATION NUMBER:	60/079689			
:	PRIOR FILING DATE:	1998-03-27			
:	PRIOR APPLICATION NUMBER:	60/086478			
:	PRIOR FILING DATE:	1998-05-22			
:	PRIOR APPLICATION NUMBER:	60/087607			
:	PRIOR FILING DATE:	1998-06-02			
:	PRIOR APPLICATION NUMBER:	60/089801			
:	PRIOR FILING DATE:	1998-06-18			
:	PRIOR APPLICATION NUMBER:	60/090557			
:	PRIOR FILING DATE:	1998-06-24			
:	PRIOR APPLICATION NUMBER:	60/090689			
:	PRIOR FILING DATE:	1998-06-25			
:	Remaining Prior Application data removed - See File Wrapper or PALM.				
:	NUMBER OF SEQ ID NOS:	116			
:	SEQ ID NO 91				
:	LENGTH:	2597			
:	TYPE:	DNA			
:	ORGANISM:	Homo Sapien			
:	US-10-245-107-91				
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Query Match            13.9%; Score 793; DB 15; Length 2597;					
Best Local Similarity 100.0%; Pred.No. 0;					
Matches 793; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
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QY	579	CGAGTAATTTTCCCAACCATCTCCAGCGGAAACTGCACAAGAATCTGTGAGCGGATGGCAT	638		
DB	1	CGAGTAATTTTCCCAACCATCTCCAGCGGAAACTGCACAAGAATCTGTGAGCGGATGGCAT	60		
QY	639	GTTCCGTACGTCCTTCATCATGATGATGTCGTGGCTCGATGATTAGATCCCTTCGGAAC	698		
DB	61	GTTCCGTACGTCCTTCATCATGATGATGTCGTGGCTCGATGATTAGATCCCTTCGGAAC	120		
QY	699	CTTCACCATCATCCTCGACTTTTGATATCTACTATGCTATGCTTTTAGCAGTGGCAACTT	758		
DB	121	CTTCACCATCATCCTCGACTTTTGATATCTACTATGCTATGCTTTTAGCAGTGGCAACTT	180		
QY	759	TGCTACTTTTTTGACCTCCAACTCGATGGTGTCTCCACAGSGCTCCACCAAGGA	818		
DB	181	TGCTACTTTTTTGACCTCCAACTCGATGGTGTCTCCACAGSGCTCCACCAAGGA	240		
QY	819	CGAGTGATACATCCAAGCTCGTAGGCTTTGCAAGGAGGACACAGCCTTCAACTCCTA	878		
DB	241	CGAGTGATACATCCAAGCTCGTAGGCTTTGCAAGGAGGACACAGCCTTCAACTCCTA	300		
QY	879	TGTAGAGTGCCCATTCGCTGTGAGCGCAGTGGGTGGAGTAGCCGCTGCTGCAGGCTGC	938		
DB	301	TGTAGAGTGCCCATTCGCTGTGAGCGCAGTGGGTGGAGTAGCCGCTGCTGCAGGCTGC	360		
QY	939	CTACTGTGCCAAAAGCGGGGCGGTGCTGTGSCAGGAACCTTGGAGTCCATCCAGATGATGA	998		
DB	361	CTACTGTGCCAAAAGCGGGGCGGTGCTGTGSCAGGAACCTTGGAGTCCATCCAGATGATGA	420		
QY	999	CCTGCTCTTACCGCTCTTCTCCAAAGGCGCAGAGCGGAAAAATGAAATCCCTTGGATGAGTC	1058		
DB	421	CCTGCTCTTACCGCTCTTCTCCAAAGGCGCAGAGCGGAAAAATGAAATCCCTTGGATGAGTC	480		
QY	1059	GGCCCTGTGCATCTTTCATCTTTGAAGCAGATAAATGACCGCNTTAAGGACGGGCTGCAGTC	1118		
DB	481	GGCCCTGTGCATCTTTCATCTTTGAAGCAGATAAATGACCGCNTTAAGGACGGGCTGCAGTC	540		
QY	1119	TTGTTACCGGGGCGAGGCGCACGCTGGACCTGGGCTGGCTCAAAGGTGAAGGACATCCCCTG	1178		
DB	541	TTGTTACCGGGGCGAGGCGCACGCTGGACCTGGGCTGGCTCAAAGGTGAAGGACATCCCCTG	600		
QY	1179	CAGCAGTGCCTCTTACCATTCAGCATACTTCTGTGGCTCGGCACNTGAATGCTCCCT	1238		
DB	601	CAGCAGTGCCTCTTACCATTCAGCATACTTCTGTGGCTCGGCACNTGAATGCTCCCT	660		
QY	1239	GGGAGTGCCACATGGTGGTAATTCCTGCTTTTCAGGAGGACAGGACCGCATGAC	1298		
DB	661	GGGAGTGCCACATGGTGGTAATTCCTGCTTTTCAGGAGGACAGGACCGCATGAC	720		

Db 121 CTTACCATCATCCCTGACTTGTATATCTACTATGTCTATGGTTTACGAGTGGCAACTT 180  
Qy 759 TGTCTACTTTTGTACCTCCAACTGAGATGTTCTCCACAGGCTCCACCAAGGA 818  
Db 181 TGTCTACTTTTGTACCTCCAACTGAGATGTTCTCCACAGGCTCCACCAAGGA 240  
Qy 819 GCAGGTGTATACATCAAGCTCGTCAAGCTTGTCAAGGAGACACAGCTTCAACTCTTA 878  
Db 241 GCAGGTGTATACATCAAGCTCGTCAAGCTTGTCAAGGAGACACAGCTTCAACTCTTA 300  
Qy 879 TGTAGAGGTGCCATTTGGCTGTGAGCGAGTGGGTGAGTACCGCTGTGCAAGGTGC 938  
Db 301 TGTAGAGGTGCCATTTGGCTGTGAGCGAGTGGGTGAGTACCGCTGTGCAAGGTGC 360  
Qy 939 CTACCTGTCCAAAGCGGGCGCTGTTGGCAGGACCTTGGAGTCCATCCAGATGATGA 998  
Db 361 CTACCTGTCCAAAGCGGGCGCTGTTGGCAGGACCTTGGAGTCCATCCAGATGATGA 420  
Qy 999 CTTGCTCTTCAACCGTCTTCTCCAAAGCGGACAGGAGGAAATGAAATCCCTGGATGATC 1058  
Db 421 CTTGCTCTTCAACCGTCTTCTCCAAAGCGGACAGGAGGAAATGAAATCCCTGGATGATC 480  
Qy 1059 GGCCTGTGCATCTTCACTTTGAAGCAGTAAATGACCGCATTAAGAGGCGCTGCAGTC 1118  
Db 481 GGCCTGTGCATCTTCACTTTGAAGCAGTAAATGACCGCATTAAGAGGCGCTGCAGTC 540  
Qy 1119 TTGTTACCGGGCGAGGCGACGCTGGACCTGGCTGGCTCAAGGTGAAGGACATCCCTCG 1178  
Db 541 TTGTTACCGGGCGAGGCGACGCTGGACCTGGCTGGCTCAAGGTGAAGGACATCCCTCG 600  
Qy 1179 CAGCAGTGGCTCTTAAACATTCAGATAACTTCTGTGGCTGGACATGATGCTCCCT 1238  
Db 601 CAGCAGTGGCTCTTAAACATTCAGATAACTTCTGTGGCTGGACATGATGCTCCCT 660  
Qy 1239 GGGAGTGTCCGACATGGTGGTGGAAATTCCTTTCAGGAGGACAGGACCGCATGAC 1298  
Db 661 GGGAGTGTCCGACATGGTGGTGGAAATTCCTTTCAGGAGGACAGGACCGCATGAC 720  
Qy 1299 GTCTGTATCGCATATGTCTACAGAACCATCTCTGGCTTGTGGGACCAAAAGTGG 1358  
Db 721 GTCTGTATCGCATATGTCTACAGAACCATCTCTGGCTTGTGGGACCAAAAGTGG 780  
Qy 1359 CAAAGTGAAGAAG 1371  
Db 781 CAAAGTGAAGAAG 793

## RESULT 9

US-10-245-771-91  
; Sequence 91, Application US/10245771  
; Publication No. US20030068781A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin  
; APPLICANT: Eaton, Dan  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stephan, Jean-Philippe  
; APPLICANT: Watanabe, Colin  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; APPLICANT: Fong, Sherman  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE OF INVENTION: ACIDS ENCODING THE SAME  
; FILE REFERENCE: P3630R1C98  
; CURRENT APPLICATION NUMBER: US/10/245, 771  
; CURRENT FILING DATE: 2002-09-16  
; PRIOR APPLICATION NUMBER: 10/197942  
; PRIOR FILING DATE: 2002-07-18  
; PRIOR APPLICATION NUMBER: 60/059114  
; PRIOR FILING DATE: 1997-09-17

; PRIOR APPLICATION NUMBER: 60/063046  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/065027  
; PRIOR FILING DATE: 1997-11-10  
; PRIOR APPLICATION NUMBER: 60/079689  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: 60/086478  
; PRIOR FILING DATE: 1998-05-22  
; PRIOR APPLICATION NUMBER: 60/087607  
; PRIOR FILING DATE: 1998-06-02  
; PRIOR APPLICATION NUMBER: 60/089801  
; PRIOR FILING DATE: 1998-06-18  
; PRIOR APPLICATION NUMBER: 60/090557  
; PRIOR FILING DATE: 1998-06-24  
; PRIOR APPLICATION NUMBER: 60/090689  
; PRIOR FILING DATE: 1998-06-25  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 116  
; SEQ ID NO 91  
; LENGTH: 2597  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
US-10-245-771-91  
Query Match 13.9%; Score 793; DB 15; Length 2597;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 793; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 579 CGAGTATTTTCCACCACTCTCCAGCGGAAACTGACCAAGAACTCTGAGCGGATGGCAT 638  
Db 1 CGAGTATTTTCCACCACTCTCCAGCGGAAACTGACCAAGAACTCTGAGCGGATGGCAT 60  
Qy 639 GTTCGGGTAGCTTTCATGATGAGTGTGGCTCGATGATTAAGATCCCTTCGACAC 698  
Db 61 GTTCGGGTAGCTTTCATGATGAGTGTGGCTCGATGATTAAGATCCCTTCGACAC 120  
Qy 699 CTTACCATCATCCCTGACTTTTGTATCTACTATGTCTATGTTTGTAGCAGTGGCAACTT 758  
Db 121 CTTACCATCATCCCTGACTTTTGTATCTACTATGTCTATGTTTGTAGCAGTGGCAACTT 180  
Qy 759 TGTCTACTTTTGTACCTCCAACTGAGATGTTCTCCACAGGCTCCACCAAGGA 818  
Db 181 TGTCTACTTTTGTACCTCCAACTGAGATGTTCTCCACAGGCTCCACCAAGGA 240  
Qy 819 GCAGGTGTATACATCAAGCTCGTGGAGTTCCTCAAGGAGGACACAGCTTCAACTCTTA 878  
Db 241 GCAGGTGTATACATCAAGCTCGTGGAGTTCCTCAAGGAGGACACAGCTTCAACTCTTA 300  
Qy 879 TGTAGAGGTGCCATTTGGCTGTGAGCGAGTGGGTGGAGTACCGCTGTGTCAGGCTGC 938  
Db 301 TGTAGAGGTGCCATTTGGCTGTGAGCGAGTGGGTGGAGTACCGCTGTGTCAGGCTGC 360  
Qy 939 CTACCTGTCCAAAGCGGGCGCTGTTGGCAGGACCTTGGAGTCCATCCAGATGATGA 998  
Db 361 CTACCTGTCCAAAGCGGGCGCTGTTGGCAGGACCTTGGAGTCCATCCAGATGATGA 420  
Qy 999 CTTGCTCTTCAACCGTCTTCTCCAAAGGCGGAGGAGGAAATGAAATCCCTGGATGATC 1058  
Db 421 CTTGCTCTTCAACCGTCTTCTCCAAAGGCGGAGGAGGAAATGAAATCCCTGGATGATC 480  
Qy 1059 GGCCTGTGCATCTTCACTTTGAAGCAGTAAATGACCGCATTAAGAGGCGCTGCAGTC 1118  
Db 481 GGCCTGTGCATCTTCACTTTGAAGCAGTAAATGACCGCATTAAGAGGCGCTGCAGTC 540  
Qy 1119 TTGTTACCGGGCGAGGCGACGCTGGACCTGGCTGGCTCAAGGTGAAGGACATCCCTCG 1178  
Db 541 TTGTTACCGGGCGAGGCGACGCTGGACCTGGCTGGCTCAAGGTGAAGGACATCCCTCG 600  
Qy 1179 CAGCAGTGGCTCTTAAACATTCAGATAACTTCTGTGGCTGGACATGATGCTCCCT 1238  
Db 601 CAGCAGTGGCTCTTAAACATTCAGATAACTTCTGTGGCTGGACATGATGCTCCCT 660  
Qy 1239 GGGAGTGTCCGACATGGTGGTGGAAATTCCTTTCAGGAGGACAGGACCGCATGAC 1298

Db 661 GGGAGTCCGACATGTTGGTGGATTCCTGCTTCCAGGAGCAGGACCGCATGAC 720  
 Qy 1299 GTCTGTATCGCATATGTTACAAAGAACCACTCTCTGGCTTTTGTGGCCACCAAAAGTGG 1358  
 Db 721 GTCTGTATCGCATATGTTACAAAGAACCACTCTCTGGCTTTTGTGGCCACCAAAAGTGG 780  
 Qy 1359 CAGCTGAAGAAG 1371  
 Db 781 CAGCTGAAGAAG 793

RESULT 10  
 US-10-245-851-91  
 ; Sequence 91, Application US/10245851  
 ; Publication No. US20030068782A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Baker, Kevin  
 ; APPLICANT: Eaton, Dan  
 ; APPLICANT: Filvaroff, Ellen  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Grimaldi, J. Christopher  
 ; APPLICANT: Gurney, Austin  
 ; APPLICANT: Smith, Victoria  
 ; APPLICANT: Stephan, Jean-Phillippe  
 ; APPLICANT: Watanabe, Colin  
 ; APPLICANT: Wood, William  
 ; APPLICANT: Zhang, Zemin  
 ; APPLICANT: Fong, Sherman  
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
 ; TITLE OF INVENTION: ACIDS ENCODING THE SAME  
 ; FILE REFERENCE: P3630R1C93  
 ; CURRENT APPLICATION NUMBER: US/10/245,851  
 ; CURRENT FILING DATE: 2002-09-16  
 ; PRIOR APPLICATION NUMBER: 10/197942  
 ; PRIOR FILING DATE: 2002-07-18  
 ; PRIOR APPLICATION NUMBER: 60/059114  
 ; PRIOR FILING DATE: 1997-09-17  
 ; PRIOR APPLICATION NUMBER: 60/063046  
 ; PRIOR FILING DATE: 1997-10-24  
 ; PRIOR APPLICATION NUMBER: 60/065027  
 ; PRIOR FILING DATE: 1997-11-10  
 ; PRIOR APPLICATION NUMBER: 60/079689  
 ; PRIOR FILING DATE: 1998-03-27  
 ; PRIOR APPLICATION NUMBER: 60/086478  
 ; PRIOR FILING DATE: 1998-05-22  
 ; PRIOR APPLICATION NUMBER: 60/087607  
 ; PRIOR FILING DATE: 1998-06-02  
 ; PRIOR APPLICATION NUMBER: 60/089801  
 ; PRIOR FILING DATE: 1998-06-18  
 ; PRIOR APPLICATION NUMBER: 60/090557  
 ; PRIOR FILING DATE: 1998-06-24  
 ; PRIOR APPLICATION NUMBER: 60/090689  
 ; PRIOR FILING DATE: 1998-06-25  
 ; Remaining Prior Application data removed - See File Wrapper or PALM.  
 ; NUMBER OF SEQ ID NOS: 116  
 ; SEQ ID NO 91  
 ; LENGTH: 2597  
 ; TYPE: DNA  
 ; ORGANISM: Homo Sapien  
 US-10-245-851-91

Query Match 13.9%; Score 793; DB 15; Length 2597;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 793; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 579 CGAGTATTTCCACCATCTCCAGCGGGAATCCAGAACTCCAGAACTCTGAGGGGATGGCAT 638  
 Db 1 CGAGTATTTCCACCATCTCCAGCGGGAATCCAGAACTCTGAGGGGATGGCAT 60  
 Qy 639 GTTCGGGTACGCTTCCATGATGAGTTCGTGGCTCGATGATTAAGATCCCTTCGGACAC 698  
 Db 61 GTTCGGGTACGCTTCCATGATGAGTTCGTGGCTCGATGATTAAGATCCCTTCGGACAC 120

Qy 699 CTTACCATCATCCCTGACTTTGATATCTATCTATGTTTACAGTGGCACTT 758  
 Db 121 CTTACCATCATCCCTGACTTTGATATCTATCTATGTTTACAGTGGCACTT 180  
 Qy 759 TGTCTACTTTTGGACCTTCCAACTGAGATGTTCTCCACAGGCTCCACCAAGGA 818  
 Db 181 TGTCTACTTTTGGACCTTCCAACTGAGATGTTCTCCACAGGCTCCACCAAGGA 240  
 Qy 819 GCAGGTATATACATCCAACTGAGGCTTTGCAAGGAGGACACAGGCTTCACTCCTA 878  
 Db 241 GCAGGTATATACATCCAACTGAGGCTTTGCAAGGAGGACACAGGCTTCACTCCTA 300  
 Qy 879 TGTAGAGTGGCCCATTTGGCTGTGAGCGAGTGGGTGGAGTACCGCTGTCTCAGGCTGC 938  
 Db 301 TGTAGAGTGGCCCATTTGGCTGTGAGCGAGTGGGTGGAGTACCGCTGTCTCAGGCTGC 360  
 Qy 939 CTACCTGTCCAAAGCGGGGCGGTCTTGGCAGGACCTTGGAGTCCATCCAGATGATGA 998  
 Db 361 CTACCTGTCCAAAGCGGGGCGGTCTTGGCAGGACCTTGGAGTCCATCCAGATGATGA 420  
 Qy 999 CTGTCTCTTCCAGCGTCTTCTCCAAAGGCGGAGGAGGAAATGAAATCCCTGGATGATGC 1058  
 Db 421 CTGTCTCTTCCAGCGTCTTCTCCAAAGGCGGAGGAGGAAATGAAATCCCTGGATGATGC 480  
 Qy 1059 GGCCCTGTGCATCTTCACTTTGAAGAGATTAATGACCGCATTAAGAGCGGCTGCAGTC 1118  
 Db 481 GGCCCTGTGCATCTTCACTTTGAAGAGATTAATGACCGCATTAAGAGCGGCTGCAGTC 540  
 Qy 1119 TTGTTACCGGGGCGGAGCGCTGAGCTGAGCTGGCTGGCTCAAGGTGAAAGACATCCCTTG 1178  
 Db 541 TTGTTACCGGGGCGGAGCGCTGAGCTGAGCTGGCTGGCTCAAGGTGAAAGACATCCCTTG 600  
 Qy 1179 CAGCAGTGGCTCTTAACTTGAAGATTAATGACCGCATTAAGAGCGGCTGCAGTC 1238  
 Db 601 CAGCAGTGGCTCTTAACTTGAAGATTAATGACCGCATTAAGAGCGGCTGCAGTC 660  
 Qy 1239 GGGAGTGTCCGACATGTTGGTGGATTCCTGCTTCCAGGAGGACAGGAGCGCATGAC 1298  
 Db 661 GGGAGTGTCCGACATGTTGGTGGATTCCTGCTTCCAGGAGGACAGGAGCGCATGAC 720  
 Qy 1299 GTCTGTATCGCATATGTTACAAAGAACCACTCTCTGGCTTTTGTGGCCACCAAAAGTGG 1358  
 Db 721 GTCTGTATCGCATATGTTACAAAGAACCACTCTCTGGCTTTTGTGGCCACCAAAAGTGG 780  
 Qy 1359 CAGCTGAAGAAG 1371  
 Db 781 CAGCTGAAGAAG 793

RESULT 11  
 US-10-245-883-91  
 ; Sequence 91, Application US/10245883  
 ; Publication No. US20030068783A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Baker, Kevin  
 ; APPLICANT: Eaton, Dan  
 ; APPLICANT: Filvaroff, Ellen  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Grimaldi, J. Christopher  
 ; APPLICANT: Gurney, Austin  
 ; APPLICANT: Smith, Victoria  
 ; APPLICANT: Stephan, Jean-Phillippe  
 ; APPLICANT: Watanabe, Colin  
 ; APPLICANT: Wood, William  
 ; APPLICANT: Zhang, Zemin  
 ; APPLICANT: Fong, Sherman  
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
 ; TITLE OF INVENTION: ACIDS ENCODING THE SAME  
 ; FILE REFERENCE: P3630R1C70  
 ; CURRENT APPLICATION NUMBER: US/10/245,883  
 ; CURRENT FILING DATE: 2002-09-16  
 ; PRIOR APPLICATION NUMBER: 10/197942

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; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; SEQ ID NO 91
; LENGTH: 2597
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-245-883-91

Query Match      13.9%; Score 793; DB 15; Length 2597;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 793; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 579 CGAGTATTTCCACCATCTCCAGCGGAACTGACCAAGACTCTGAGCGGATGGCAT 638
DB 1 CGAGTATTTCCACCATCTCCAGCGGAACTGACCAAGACTCTGAGCGGATGGCAT 60
QY 639 GTTCGGGTAGCTTTCCATGATGATGCTGCGCTCGATTAAGATCCCTTCGACAC 698
DB 61 GTTCGGGTAGCTTTCCATGATGATGCTGCGCTCGATTAAGATCCCTTCGACAC 120
QY 699 CTTACCATCATCCCTGACTTGTATCTACTACTGCTAGTGTGTTAGCAGTGGCACTT 758
DB 121 CTTACCATCATCCCTGACTTGTATCTACTACTGCTAGTGTGTTAGCAGTGGCACTT 180
QY 759 TGTCTATTTTGGACCTCCAACTGAGATGGTGTCTCCACGAGGTCCACCAAGGA 818
DB 181 TGTCTATTTTGGACCTCCAACTGAGATGGTGTCTCCACGAGGTCCACCAAGGA 240
QY 819 GCAGGTGTATACATCCAGCTCTGAGGCTTTGCAAGGAGGACACAGCTTCACTCTA 878
DB 241 GCAGGTGTATACATCCAGCTCTGAGGCTTTGCAAGGAGGACACAGCTTCACTCTA 300
QY 879 TGTAGAGTGCCATTGGCTGTGAGCGCAGTGGGGTGGAGTACCGCTGCTGCAGGCTGC 938
DB 301 TGTAGAGTGCCATTGGCTGTGAGCGCAGTGGGGTGGAGTACCGCTGCTGCAGGCTGC 360
QY 939 CTACCTGTCCAAAGCGGGGGCGTCTTGGCAGACCTTGGAGTCCATCCAGATGATGA 998
DB 361 CTACCTGTCCAAAGCGGGGGCGTCTTGGCAGACCTTGGAGTCCATCCAGATGATGA 420
QY 999 CTTGCTCTTCCAGCTTCTTCCAAAGGCGCAGAGCGAAATGAAATCCCTTGGATGATC 1058
DB 421 CTTGCTCTTCCAGCTTCTTCCAAAGGCGCAGAGCGAAATGAAATCCCTTGGATGATC 480
QY 1059 GGCCCTGTGCATCTTCACTTTGAAGCGAGATTAATGACCGCATTAAGAGCGGCTGCAGTC 1118
DB 481 GGCCCTGTGCATCTTCACTTTGAAGCGAGATTAATGACCGCATTAAGAGCGGCTGCAGTC 540
QY 1119 TTGTATCCGGGGGAGGCGAGCTGGACCTGGCTTCAAGTGAAGGACATCCCTCTG 1178
DB 541 TTGTATCCGGGGGAGGCGAGCTGGACCTGGCTTCAAGTGAAGGACATCCCTCTG 600
QY 1179 CAGCAGTGGCTCTTAACTTACATGACATTAATCTTGTGGCTTGGACATGAATGCTCCCT 1238

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DB 601 CAGCAGTGGCTCTTAAACCATTTGACGATAACTTCTGTGGCTGGACATGAATGCTCCCT 660
QY 1239 GGGAGTGTCCGACATGTTGGTGGTGAATTCCTGCTTCAAGGAGGACAGGACCGCATGAC 1298
DB 661 GGGAGTGTCCGACATGTTGGTGGTGAATTCCTGCTTCAAGGAGGACAGGACCGCATGAC 720
QY 1299 GTCTGTCTATCGCATATGTTCTTACAGAACCACTCTCTGGCTTTTGTGGGACCAAAAGTGG 1358
DB 721 GTCTGTCTATCGCATATGTTCTTACAGAACCACTCTCTGGCTTTTGTGGGACCAAAAGTGG 780
QY 1359 CAAGCTGAAGAAG 1371
DB 781 CAAGCTGAAGAAG 793

RESULT 12
US-10-237-535-91
; Sequence 91, Application US/10237535
; Publication No. US20030073188A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Baton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Phillippe
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P630R1C3
; CURRENT APPLICATION NUMBER: US/10/237,535
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
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; PRIOR APPLICATION NUMBER: 60/063046
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; PRIOR APPLICATION NUMBER: 60/123957
; PRIOR FILING DATE: 1999-03-12
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; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 10/081056
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: 10/119480
; PRIOR FILING DATE: 2002-04-09

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Query Match

13.9%; Score 793; DB 15; Length 2597;



Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;  
 Matches 793; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 579 CGAGTATTTCCCAACCATCTCCAGCGGAACTGACCAAGAACTCTGAGCGGATGGCAT 638  
 Db 1 CGAGTATTTCCCAACCATCTCCAGCGGAACTGACCAAGAACTCTGAGCGGATGGCAT 60  
 QY 639 GTTCGGTACGCTTCCCATGATGAGTTCGTGSCCTCGATGATTAGATCCCTTCGGACAC 698  
 Db 61 GTTCGGTACGCTTCCCATGATGAGTTCGTGSCCTCGATGATTAGATCCCTTCGGACAC 120  
 QY 699 CTTCCACATCATCCCTGACTTTGATATCTATCTATCTATGTTTTAGAGTGGCAATT 758  
 Db 121 CTTCCACATCATCCCTGACTTTGATATCTATCTATCTATGTTTTAGAGTGGCAATT 180  
 QY 759 TGTCTACTTTTGGACCTCCACCTGAGATGAGTGTCTCCACGAGCTCCACCAAGGA 818  
 Db 181 TGTCTACTTTTGGACCTCCACCTGAGATGAGTGTCTCCACGAGCTCCACCAAGGA 240  
 QY 819 GCAGGTGTATATCAACCTCGTGAGGCTTTGCAAGGAGGACACAGGCTTCAATCTCTA 878  
 Db 241 GCAGGTGTATATCAACCTCGTGAGGCTTTGCAAGGAGGACACAGGCTTCAATCTCTA 300  
 QY 879 TGTAGAGTGGCCATTTGGCTGTGAGCGAGTGGGTGAGTACCGCTGCTGAGGCTCC 938  
 Db 301 TGTAGAGTGGCCATTTGGCTGTGAGCGAGTGGGTGAGTACCGCTGCTGAGGCTCC 360  
 QY 939 CTACCTGTCCAAAGCGGGGGCGGTGCTTGGCAGGACCCCTTGAGTCCATCCAGATGATGA 998  
 Db 361 CTACCTGTCCAAAGCGGGGGCGGTGCTTGGCAGGACCCCTTGAGTCCATCCAGATGATGA 420  
 QY 999 CTTGCTCTTCAACGCTTCTTCCAAAGCGGGGGCGGTGCTTGGCAGGACCCCTTGAGTCCATCCAGATGATGA 1058  
 Db 421 CTTGCTCTTCAACGCTTCTTCCAAAGCGGGGGCGGTGCTTGGCAGGACCCCTTGAGTCCATCCAGATGATGA 480  
 QY 1059 GGCCTGTGATCTTCAATCTTGAAGCAGATAATGATCCGCAATTAAGGAGCGCTCGAGTC 1118  
 Db 481 GGCCTGTGATCTTCAATCTTGAAGCAGATAATGATCCGCAATTAAGGAGCGCTCGAGTC 540  
 QY 1119 TTGTTACCGGGCGGAGGACGCTGACCTGGCTGGCTTCAAGGTGAAGGACATCCCTTG 1178  
 Db 541 TTGTTACCGGGCGGAGGACGCTGACCTGGCTGGCTTCAAGGTGAAGGACATCCCTTG 600  
 QY 1179 CAGCAGTGGCTTTAAACATTCACGATTAATCTTGGCTGGCTTCAAGGTGAAGGACATCCCTTG 1238  
 Db 601 CAGCAGTGGCTTTAAACATTCACGATTAATCTTGGCTGGCTTCAAGGTGAAGGACATCCCTTG 660  
 QY 1239 GGGAGTGTCCGACATGCTGCTGGAATTCCTGCTTTCACGGAGGACAGGACCGCATGAC 1298  
 Db 661 GGGAGTGTCCGACATGCTGCTGGAATTCCTGCTTTCACGGAGGACAGGACCGCATGAC 720  
 QY 1299 GTCTGTCATGCTATGCTTACAGAACCACTCTCTGGCTTTGTGGGACCAAAAGTGG 1358  
 Db 721 GTCTGTCATGCTATGCTTACAGAACCACTCTCTGGCTTTGTGGGACCAAAAGTGG 780  
 QY 1359 CAAGCTGAAGAAG 1371  
 Db 781 CAAGCTGAAGAAG 793

RESULT 13  
 US-10-238-183-91  
 ; Sequence 91, Application US/10238183  
 ; Publication No. US20030073189A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Baker, Kevin  
 ; APPLICANT: Eaton, Dan  
 ; APPLICANT: Filvaroff, Ellen  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Grimaldi, J. Christopher  
 ; APPLICANT: Gurney, Austin  
 ; APPLICANT: Smith, Victoria  
 ; APPLICANT: Stephan, Jean-Philippe

APPLICANT: Watanabe, Colin  
 APPLICANT: Wood, William  
 APPLICANT: Zhang, Zemin  
 APPLICANT: Fong, Sherman  
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
 TITLE OF INVENTION: ACIDS ENCODING THE SAME  
 FILE REFERENCE: P36301C11  
 CURRENT APPLICATION NUMBER: US/10/238,183  
 CURRENT FILING DATE: 2002-09-09  
 PRIOR APPLICATION NUMBER: 10/197942  
 PRIOR FILING DATE: 2002-07-18  
 PRIOR APPLICATION NUMBER: 60/059114  
 PRIOR FILING DATE: 1997-09-17  
 PRIOR APPLICATION NUMBER: 60/063046  
 PRIOR FILING DATE: 1997-10-24  
 PRIOR APPLICATION NUMBER: 60/065027  
 PRIOR FILING DATE: 1997-11-10  
 PRIOR APPLICATION NUMBER: 60/079689  
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 PRIOR APPLICATION NUMBER: 60/086478  
 PRIOR FILING DATE: 1998-05-22  
 PRIOR APPLICATION NUMBER: 60/087607  
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 PRIOR APPLICATION NUMBER: 60/089801  
 PRIOR FILING DATE: 1998-06-18  
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PRIOR APPLICATION NUMBER: 10/119480  
PRIOR FILING DATE: 2002-04-09

Query Match 13.9%; Score 793; DB 15; Length 2597;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 793; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	1	CGAGTATTTTCCACCATCTCCAGCGGAAACTGACCAAGAACTCTGAGGCGGATGGCAT	60
Qy	639	GTTCGGTACGTCCTCCATGATGATTCGTCGGCTCGATGATTAAAGATCCCTTCGGACAC	698
Db	61	GTTCGGTACGTCCTCCATGATGATTCGTCGGCTCGATGATTAAAGATCCCTTCGGACAC	120
Qy	699	CTTCACCATCATCCCTGACTTTTGATATCTACTATGTCTATGGTTTATGACGATGGCAACTT	758
Db	121	CTTCACCATCATCCCTGACTTTTGATATCTACTATGTCTATGGTTTATGACGATGGCAACTT	180
Qy	759	TGCTACTTTTGGACCTCCACCTGAGATGGTCTCTCCACGAGCTCCACCAAGGA	818
Db	181	TGCTACTTTTGGACCTCCACCTGAGATGGTCTCTCCACGAGCTCCACCAAGGA	240
Qy	819	GCAGGTGTATACATCCAAAGCTCGTGAGGCTTTGCAAGAGGACACAGCCTTCAACTCCTA	878
Db	241	GCAGGTGTATACATCCAAAGCTCGTGAGGCTTTGCAAGAGGACACAGCCTTCAACTCCTA	300
Qy	879	TGTAGAGGTGCCATTGGCTCTGAGCGCAGTGCGGTGGAGTACCCCTGCTGAGGCTGC	938
Db	301	TGTAGAGGTGCCATTGGCTCTGAGCGCAGTGCGGTGGAGTACCCCTGCTGAGGCTGC	360
Qy	939	CTACCTGTCCAAAGCGGGGCGCTGCTTTGGCAGGACCCCTTGGAGTCCATCCAGATGATGA	998

Db 361 CTACGTGTCACAAAGCGGGCGGTGCTTGGCAGGACCTTGGAGTCCATCCAGATGATGA 420  
 QY 999 CTTGCTCTTCAACCTCTTCTCCAGGCGCAGAGCGGAATGAATCCCTGGATGATGTC 1058  
 Db 421 CTTGCTCTTCAACCTCTTCTCCAGGCGCAGAGCGGAATGAATCCCTGGATGATGTC 480  
 QY 1059 GGCCTGTGCTATCTTCACTTTGAAGCAGATAAATGACCGCATTAAGGAGCGGCTGCAGTC 1118  
 Db 481 GGCCTGTGCTATCTTCACTTTGAAGCAGATAAATGACCGCATTAAGGAGCGGCTGCAGTC 540  
 QY 1119 TTGTTACGGGCGGAGGCGCAGCTGACCTGGCTGGCTGGCTCAAGGTGAAGGACATCCCTG 1178  
 Db 541 TTGTTACGGGCGGAGGCGCAGCTGACCTGGCTGGCTGGCTCAAGGTGAAGGACATCCCTG 600  
 QY 1179 CAGCAGTGGCTCTTAAACCAATTGACGATAAATCTTGTGGCTGGACATGAATGCTCCCT 1238  
 Db 601 CAGCAGTGGCTCTTAAACCAATTGACGATAAATCTTGTGGCTGGACATGAATGCTCCCT 660  
 QY 1239 GGGAGTGTCCGATGCTGCTGGGAAATCCCTCTTCAAGGAGGACAGGAGCGGATGAC 1298  
 Db 661 GGGAGTGTCCGATGCTGCTGGGAAATCCCTCTTCAAGGAGGACAGGAGCGGATGAC 720  
 QY 1299 GTCTGTCAATCGATATGCTCAAGAACCACTCTCTGGCTTTGTGGGACCAAAAGTGG 1358  
 Db 721 GTCTGTCAATCGATATGCTCAAGAACCACTCTCTGGCTTTGTGGGACCAAAAGTGG 780  
 QY 1359 CAAGCTGAAGAAG 1371  
 Db 781 CAAGCTGAAGAAG 793

RESULT 14

US-10-238-283-91  
 ; Sequence 91, Application US/10238283  
 ; Publication No. US20030073190A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Baker, Kevin  
 ; APPLICANT: Eaton, Dan  
 ; APPLICANT: Filvaroff, Ellen  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Grimaldi, J. Christopher  
 ; APPLICANT: Gurney, Austin  
 ; APPLICANT: Smith, Victoria  
 ; APPLICANT: Stephan, Jean-Phillippe  
 ; APPLICANT: Watanabe, Colin  
 ; APPLICANT: Wood, William  
 ; APPLICANT: Zhang, Zemin  
 ; APPLICANT: Fong, Sherman  
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
 ; FILE OF INVENTION: ACIDS ENCODING THE SAME  
 ; FILE REFERENCE: P3630R1C15  
 ; CURRENT APPLICATION NUMBER: US/10/238,283  
 ; CURRENT FILING DATE: 2002-09-09  
 ; PRIOR APPLICATION NUMBER: 10/197942  
 ; PRIOR FILING DATE: 2002-07-18  
 ; PRIOR APPLICATION NUMBER: 60/059114  
 ; PRIOR FILING DATE: 1997-09-17  
 ; PRIOR APPLICATION NUMBER: 60/063046  
 ; PRIOR FILING DATE: 1997-10-24  
 ; PRIOR APPLICATION NUMBER: 60/065027  
 ; PRIOR FILING DATE: 1997-11-10  
 ; PRIOR APPLICATION NUMBER: 60/079689  
 ; PRIOR FILING DATE: 1998-03-27  
 ; PRIOR APPLICATION NUMBER: 60/086478  
 ; PRIOR FILING DATE: 1998-05-22  
 ; PRIOR APPLICATION NUMBER: 60/087607  
 ; PRIOR FILING DATE: 1998-06-02  
 ; PRIOR APPLICATION NUMBER: 60/089801  
 ; PRIOR FILING DATE: 1998-06-18  
 ; PRIOR APPLICATION NUMBER: 60/090557  
 ; PRIOR FILING DATE: 1998-06-24  
 ; PRIOR APPLICATION NUMBER: 60/090689

; PRIOR FILING DATE: 1998-06-25  
 ; Remaining Prior Application data removed - See File Wrapper or PALM.  
 ; NUMBER OF SEQ ID NOS: 116  
 ; SEQ ID NO 91  
 ; LENGTH: 2597  
 ; TYPE: DNA  
 ; ORGANISM: Homo Sapien  
 ; US-10-238-283-91  
 Query Match 13.9%; Score 793; DB 15; Length 2597;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 793; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 579 CGAGTATTTTCCACCATCTCCAGCGGAACTGACCAAGAACTCTGAGCGGATGCGCAT 638  
 Db 1 CGAGTATTTTCCACCATCTCCAGCGGAACTGACCAAGAACTCTGAGCGGATGCGCAT 60  
 QY 639 GTTCGGGTACGTTCCATGATGAGTTCTGGGCTCGATGATTAAGATCCCTTCGACAC 698  
 Db 61 GTTCGGGTACGTTCCATGATGAGTTCTGGGCTCGATGATTAAGATCCCTTCGACAC 120  
 QY 699 CTTACCATCATCCCTGACCTTTGATATCTACTATGCTATGCTTTTACGAGTGGCACTT 758  
 Db 121 CTTACCATCATCCCTGACCTTTGATATCTACTATGCTATGCTTTTACGAGTGGCACTT 180  
 QY 759 TGTCTACTTTTTCACCCCTCCAACTCGAGATGCTCTCCACAGGCTCCACCAAGGA 818  
 Db 181 TGTCTACTTTTTCACCCCTCCAACTCGAGATGCTCTCCACAGGCTCCACCAAGGA 240  
 QY 819 GCAGGTGTATACATCCAAAGCTCTGAGCTCTTCCAAAGAGGACACAGCTTCACTCCTA 878  
 Db 241 GCAGGTGTATACATCCAAAGCTCTGAGCTCTTCCAAAGAGGACACAGCTTCACTCCTA 300  
 QY 879 TGTAGAGTGTCCCATTTGGCTGTGAGCGCAGTGGGTGGAGTACCGCTGTGCGAGGCTGC 938  
 Db 301 TGTAGAGTGTCCCATTTGGCTGTGAGCGCAGTGGGTGGAGTACCGCTGTGCGAGGCTGC 360  
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 Db 361 CTACCTGTCCAAAGCGGGGCGGTGCTTGGCAGGACCCCTTGGAGTCCATCCAGATGATGA 420  
 QY 999 CTTGCTCTTTCACCGCTCTTCTCCAAAGGCGCAGAGCGGAATGAATCCCTGGATGATGTC 1058  
 Db 421 CTTGCTCTTTCACCGCTCTTCTCCAAAGGCGCAGAGCGGAATGAATCCCTGGATGATGTC 480  
 QY 1059 GGCCTGTGCTATCTTCACTTTGAAGCAGATAAATGACCGCATTAAGGAGCGGCTGCAGTC 1118  
 Db 481 GGCCTGTGCTATCTTCACTTTGAAGCAGATAAATGACCGCATTAAGGAGCGGCTGCAGTC 540  
 QY 1119 TTGTTACGGGCGGAGGCGCAGCTGACCTGGCTGGCTCAAGGTGAAGGACATCCCTG 1178  
 Db 541 TTGTTACGGGCGGAGGCGCAGCTGACCTGGCTGGCTCAAGGTGAAGGACATCCCTG 600  
 QY 1179 CAGCAGTGGCTCTTAAACCAATTGACGATAAATCTTGTGGCTGGACATGAATGCTCCCT 1238  
 Db 601 CAGCAGTGGCTCTTAAACCAATTGACGATAAATCTTGTGGCTGGACATGAATGCTCCCT 660  
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 Db 661 GGGAGTGTCCGATGCTGCTGGGAAATCCCTCTTCAAGGAGGACAGGAGCGGATGAC 720  
 QY 1299 GTCTGTCAATCGATATGCTCAAGAACCACTCTCTGGCTTTGTGGGACCAAAAGTGG 1358  
 Db 721 GTCTGTCAATCGATATGCTCAAGAACCACTCTCTGGCTTTGTGGGACCAAAAGTGG 780  
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RESULT 15

US-10-238-370-91  
 ; Sequence 91, Application US/10238370

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; Publication No. US20030073191A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Baton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Phillippe
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3630R1C10
; CURRENT APPLICATION NUMBER: US/10/238,370
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
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; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 91
; LENGTH: 2597
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-238-370-91

Query Match      13.9%; Score 793; DB 15; Length 2597;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 793; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 579 CGAGTATTTTCCACCATCTCCAGCGGAAACTGACCAAGAACTCTGAGCGGATGCGAT 638
Db 1 CGAGTATTTTCCACCATCTCCAGCGGAAACTGACCAAGAACTCTGAGCGGATGCGAT 60

QY 639 GTTCGGTACGTCTTCCATGATGAGTTCGTGGCCTCGATGATTAAGATCCCTTCGGACAC 698
Db 61 GTTCGGTACGTCTTCCATGATGAGTTCGTGGCCTCGATGATTAAGATCCCTTCGGACAC 120

QY 699 CTTCCACCATCATCCCTGACTTTGATATCTACTATGCTATGCTATGCTTTAGCAGTGGCACTT 758
Db 121 CTTCCACCATCATCCCTGACTTTGATATCTACTATGCTATGCTATGCTTTAGCAGTGGCACTT 180

QY 759 TGTCTACTTTTTCACCTCCACCTGAGATGAGTGTCTCCACAGGCTCCACACCAAGGA 818
Db 181 TGTCTACTTTTTCACCTCCACCTGAGATGAGTGTCTCCACAGGCTCCACACCAAGGA 240

QY 819 GCAGGTGTATACATCCAAAGCTCGTGAGGCTTTGCAAGGAGGACACAGCCTTCAACTCCTA 878
Db 241 GCAGGTGTATACATCCAAAGCTCGTGAGGCTTTGCAAGGAGGACACAGCCTTCAACTCCTA 300

QY 879 TGTAGAGGTGCCCATTTGGCTGTGAGCGGACGTGGGTGGAGTACCGCCTGCTGCAGGCTGC 938

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Db 301 TGTAGAGGTGCCCATTTGGCTGTGAGCGGACGTGGGTGGAGTACCGCCTGCTGCAGGCTGC 360
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Db 361 CTACCTGTCCAAAGCGGGGGCGGTGCTTGGCAGGACCTTGGAGTCCATCCAGATGATGA 420
QY 999 CCTGTCTTTACCCGTCTTTCTCCAAAGGCGCAGAGCGGAAATGAAATCCCTTGGATGATC 1058.
Db 421 CCTGTCTTTACCCGTCTTTCTCCAAAGGCGCAGAGCGGAAATGAAATCCCTTGGATGATC 480
QY 1059 GGCCCTGTGCATCTTCATCTTTGAAGCAGATAAATGACCGCATTAAAGGAGCGGCTGCACTC 1118
Db 481 GGCCCTGTGCATCTTCATCTTTGAAGCAGATAAATGACCGCATTAAAGGAGCGGCTGCACTC 540
QY 1119 TTGTTTACCGGGGCGAGGCGACGCTGGACCTGGCTTCAAGGTGAAGGACATCCCTCTG 1178
Db 541 TTGTTTACCGGGGCGAGGCGACGCTGGACCTGGCTTCAAGGTGAAGGACATCCCTCTG 600
QY 1179 CAGCAGTGGCTCTTTAAACCATTTGACGATAAATCTTGTGGCCTGGACATGAATGCTCCCT 1238
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Db 661 GGGAGTGTCCGACATGGTGGGAAATCCCGTCTTTCACGGAGGACAGGACCGCATGAC 720
QY 1299 GTCTGTCTATCGCATATGCTTACAGAAACACTCTCTGGCCTTTGTGGGACCAAAAGTGG 1358
Db 721 GTCTGTCTATCGCATATGCTTACAGAAACACTCTCTGGCCTTTGTGGGACCAAAAGTGG 780
QY 1359 CAAGCTGAAGAAG 1371
Db 781 CAAGCTGAAGAAG 793

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Search completed: May 23, 2004, 13:05:11  
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, PRIOR FILING DATE: 1999-09-15
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, PRIOR FILING DATE: 1999-10-05
, PRIOR APPLICATION NUMBER: PCT/US99/28214
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, PRIOR APPLICATION NUMBER: PCT/US99/30999
, PRIOR FILING DATE: 1999-12-20
, PRIOR APPLICATION NUMBER: PCT/US00/00219
, PRIOR FILING DATE: 2000-01-05
, NUMBER OF SEQ ID NOS: 423
, SEQ ID NO 169
, LENGTH: 2477
, TYPE: DNA
, ORGANISM: Homo sapiens
US-09-907-794A-169

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Query Match	10.2k; Score 579.2; DB 4; Length 2477;
Best Local Similarity	67.4%; Pred. No. 1.4e-131;
Matches 837; Conservative 0; Mismatches 408; Indels 3; Gaps 1;	
Qy	151 TTCAATCACCTGGTGGATGAGACAGGACACATTTACTTGGGGGCGGTCAATCGG 210
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Qy	211 ATTTACAAGCTCTCCAGCGACCTGAAGGCTTTGGTGACGCATGAGACAGGGCCGACGAG 270
Db	1036 GTCTATAAGCTGACAGGCAACCTGACCATCCAGTGGCTCATGAAGACAGGGCCAGAAGAG 1095
Qy	271 GAGAACCCCAAGTGTTACCCACCCGCATCGTCCAGACCTGCAATGAGCCCTGACCAAC 330
Db	1096 GACAAACAAGTCTCGTTACCCGCCCTCATGTGACGCCCTGACGGAAGTGCTCACCCCTC 1155
Qy	331 ACCAACAAATGTCAACAAGATGCTCTCTCATAGACTTACAAGGAGAACGGCTGATTGCTGT 390
Db	1156 ACCAACAAATGTCAACAAGTGTCTCATCATTTGACTACTCTGAGAACCCTGTCTGGGCTGT 1215
Qy	391 GGGAGCCTGTACCAAGGCATCTCAAGCTGCTGAGGCTGAGAGACCTCTTCAAGCTGGGG 450
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Qy	451 GAGCCTTATCATAGAAGAGGACATATCTGTCAAGTGTCAACGAGAGCGCTCAGTCTTT 510
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Qy	511 GGAGTGATCGTCTCCTACAGCACTCGATGAGCAAGCTGTTCATTGCGACGGCAGTGGAT 570
Db	1336 GGGGTGATGTGGCGCTCTGAGGTGAGGATGGCAAGCTCTTCATCGGCACGGCTGTGGAT 1395
Qy	571 GGGAGGCCCGAGTATTTTCCACCACATCTCCAGCCGGAAAATGACCAAGAAGCTCTGAGCG 630
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Qy	631 GATGGCATGTTTCGGGTAGCTTTCATGATGAGTTCGTGGCGCTCGATGATTAGATCCCT 690
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Qy	691 TCGGACACCTTCACCATCATCCCTGACCTTTGATATCTACTATGTCTATGTTTAGCAGT 750
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Qy	751 GGCACCTTTGTCTACTTTTTGACCCCTCCAACTGAGA---TGGTGTCTCCACAGGCTCC 807
Db	1576 GGGGGCTTTGTCTACTTTCTCACTGTCTCAGCCCGAGACCCCTGAGGCTGTGGCCATCAAC 1635

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; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905,125A
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
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; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 169
; LENGTH: 2477
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-905-125A-169

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Query Match      10.2%; Score 579.2; DB 4; Length 2477;
Best Local Similarity 67.1%; Pred. No. 1.4e-131;
Matches 837; Conservative 0; Mismatches 408; Indels 3; Gaps 1;

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Qy	151	TTCAATCACTGGTGGTGGATGAGGACGACGACACATTTTACTTTGGGGCGGCAATCGG	210
Db	976	TTCAACCACTTGACCGCTCCCAAGGAGCGGGCGGCTATATGTGGGGCCATCAACCGG	1035
Qy	211	ATTTACAAAGCTCTCCAGCGACCTGAAGGTCTTTGGTGAAGCATGAGACAGGCGGCGAG	270
Db	1036	GTCTATAAGCTGACAGGCAACCTGACCATCCAGGTGGCTATAAGACAGGSCCAGAAG	1095
Qy	271	GACAAACCAAGTGTATCCACCCCGCATCTCCAGACCTGCATGAGCCCTGACCCACAC	330
Db	1096	GACAAACCAAGTCTGTTACCCCGCCCTCATCTGTGACGCGCTGACGAGGTCTCACCCCT	1155
Qy	331	ACCAACAATGTCAACAAGATGCTCTCTATAGACTACAAGGAGAACAGGCTGATTCGCTGT	390
Db	1156	ACCAACAATGTCAACAAGTGTCTCATCTGACTTACTGAGAACCGGCTCTGCGCTGT	1215
Qy	391	GGGAGCGTGTACCAAGGATCTGCAAGCTGTGAGGCTGGAGGACCTTCAAGTGGGG	450
Db	1216	GGGAGCGTGTACCAAGGATCTGCAAGTGTGCGGCTGGATGACCTTTCATCTGGTG	1275
Qy	451	GAGCCTTATCAAGAAGGACACTATCTGTGAGGTCAACGAGAGCGGCTCAGTCTTT	510
Db	1276	GAGCCATCCCAAGAAGGAGCACTACCTGTCCAGTGTCAACAGACCGGACCATGTAC	1335

Qy	511	GGAGTGATCGTCTCTACAGCAACCTGGATGACAACTGTTTATTGACCGGAGTGGAT	570
Db	1336	GGGTTGATTTGGCGCTGTAGGGTGAGATGGCAAGCTCTTCATCGGCACGGCTGTGGAT	1395
Qy	571	GGGAAGCCCGAGTATTTTCCCAACATCTCCAGCCGGAACCTGACCAAGAACTCTGAGCG	630
Db	1396	GGGAAGCAGGATTTACTTCCCGACCTGTCCAGCCGGAAGCTGCCCGGAGACCTTGAGTCC	1455
Qy	631	GATGCAATGTTCCGGTGAAGTCTTCCATGATGAGTTCTGTGGCTCGATGATTAAAGATCCCT	690
Db	1456	TCAGCCATGCTCGACTATGAGCTACAGCGATTTTGTCTCTCTCTCATCAAGATCCCT	1515
Qy	691	TCGGACACCTTCCACCATCATCCCTGACATTTGATATCTACTATGTCTATGTTTAGCAGT	750
Db	1516	TCAGACACCTTGGCCCTGGTCTCCCATTTTGCATCTTCTACATCTTACGCTTTGCTAGT	1575
Qy	751	GGCAACTTTTGTCTACTTTTTCACCTTCCAACTCAGA---TGGTGTCTCCACAGGCTCC	807
Db	1576	GGGGCTTTTGTCTACTTTTCTCAGTGTCCAGCCCGAGACCTTGGGGTGTGGCCTATCAAC	1635
Qy	808	ACCACCAAGGAGCAGGTGTATACATCCAAAGCTCTGAGGCTTTGCAAGGAGGACACAGCC	867
Db	1636	TCGGCTGGAGACCTCTTCTACACCTCAGCATCTGTGGGCTCTGCAAGGATGACCCCAAG	1695
Qy	868	TTCAACTCTATGAGGTGCCATTTGGCTGTGAGCCAGTGGGTGGAGTACCGCTG	927
Db	1696	TTCCACTCATAGTGTCCCTTCCCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTT	1755
Qy	928	CTGCAAGGTGCTCTACTCTGTCACAAAGCGGGCGGCTGTGTCAGGACCTTTGGAGTCCAT	987
Db	1756	CTGCAAGGTGCTCTACTCTGTCACAAAGCGGCTGAGGCTCTGTCAGGACCTTTCAATATCACC	1815
Qy	988	CCAGATGATGACCTCTCTTCAACCTCTTCCAAAGGCGCAGAGCGGAGAAATGAAATCC	1047
Db	1816	AGCCAGGACGATGTACTCTTTTGGCATCTTCTCCAAAGGCGCAGAGCGATATCACCCCG	1875
Qy	1048	CTGGATGATGCGGCTCTGTCATCTTCAAGCAGATAAATGACCGCATTAAGGAG	1107
Db	1876	CCGATGATCTGCGCTCTGTCATCTTCCATCCGCGCCATCACTTGCAGATCAAGGAG	1935
Qy	1108	CGGCTGCAAGTCTTTTGAACCGGCGCAGGCGCAGCTGAGCCTGGCTGCTGCTCAAGTGAAG	1167
Db	1936	CGCTGCAAGTCTTTTGAACCGGCGCAGGCGCAGCTGAGCCTGGCTGCTGCTGCTGCTGCTG	1995
Qy	1168	GACATCCCTGCGAGGCTCTTAAACCTTGAAGTAACTTCTGTGGCTGGACATG	1227
Db	1996	GAGCTCCAGTGACGAGCGCTCTCCCATCGATGATTAATCTTCTGTGGCTGGACATC	2055
Qy	1228	AATGCTCCCTGCGAGTGTCCGACATGCTGGAATTCCTGCTTCTTCAAGGAGCAGG	1287
Db	2056	ACCAGCCCTGGAGGCTCAACTCCAGTGGAGGCGCTGACCTGTACACACCGAGCAGG	2115
Qy	1288	GACCGATGAGTCTGTGATCGCATATGCTACAGACCACTCTCTGCGCTTGTGGGC	1347
Db	2116	GACCGATGAGTCTGTGATCGCATATGCTACAGACCACTCTCTGCGCTTGTGGGC	2175
Qy	1348	ACCAAGTGGCAAGCTGAAGAGATCCGGGTGGATGGACCCAGGGG	1395
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RESULT 3
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; Sequence 169, Application US/09902775A
; Patent No. 6686451
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen

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1036	DB	GTCTATAGCTGACAGCGAACTTGACCATCCAGGTGGCTCATAGACAGGGCCAGAGAG	1095
271	QY	GACAAACCCCAAGTGTATACCAACCCCGCATGCTTCAGACCTGCAATGAGCCCCCTGACCACC	330
1096	DB	GACAAACAAGTCTCTGTTACCGCGCCCTCATCGTGCAGCCCTGCAGCGAAGTGCTCACCCCTC	1155
331	QY	ACCAACAATGTCAACAAGATGTCCTCATAGACTACAAGGAGAAAGAGCTGATTGGCCCTGT	390
1156	DB	ACCAACAATGTCAACAAGCTGCTCATCTGACTACTCTGAGAACCCGCTGCTGCGCTGT	1215
391	QY	GGGAGCCTGTACCAAGGCACTCTGCAAGCTGCTGAGGCTGGAGGACCTCTTCAAGCTGGG	450
1216	DB	GGGAGCCTCTACCAAGGGGCTGCAAGCTGCTGGCGCTGGATGACCTCTTCACTCGTGGT	1275
451	QY	GAGCCTTATCATAGAAGAGGAGCACTATCTGTGAGTGTCAACGAGAGCGGCTCAGTCTTT	510
1276	DB	GAGCCATCCCAAGAAGGAGCACTACCTGTCCAGTGTCAACAAGACGGGACCATGTAC	1335
511	QY	GGAGTGATGCTCTCTACAGCAACCTGGATGACAGCTGTTTCATTGGCCACGGCAGTGAT	570
1336	DB	GGGTGATGTTGGCGCTCTGAGGCTGAGGATGCAAGCTCTTTCATCGGCACGGCTGTGGAT	1395
571	QY	GGGAAGCCCGAGTATTTTCCACCATCTCCAGCCGGAAACTGACCAAGAACTCTGAGCGG	630
1396	DB	GGGAAGCAGGATTACTTCCGAGCCCTGTCCAGCCGGAAGCTGCCCGAGACCCCTGAGTCC	1455
631	QY	GATGGCATGTTCCGGTAGCTCTCCATGATGATGATGTTCTGGCTCGATGATTAAAGATCCCT	690
1456	DB	TCAGCCCATGCTCGACATATGAGCTACACAGGATTTGTCTCTCTCTCATCAAGATCCCT	1515
691	QY	TCGACACACCTTCACCATCATCCCTGACTTTGATATCTACTATGTCTATGTTTTAGCAGT	750
1516	DB	TCAGACACCTTGGCCCTGGTCTCCCACTTTGACATCTTCTACATCAAGCTTTGCTAGT	1575
751	QY	GGCAACTTTTGCTACTTTTGGACCTCCGAACCTTGAGA--TGGTGTCTCCACGAGTCC	807
1576	DB	GGGGGCTTTGTCCTACTTTCTCATGTGCCAGCCGAGACCCCTGAGGGTGTGGCATCAAC	1635
808	QY	ACCACCAAGGAGCAGGTGTATACATCCAAAGCTCGTGAGCTTTGCAAGGAGACACAGCC	867
1636	DB	TCCGCTGGAGACCTTCTTACACTCAGCATCGTGGGCTCTGCAAGGATGACCCCAAG	1695
868	QY	TTCAACTCTTATGAGAGTGCCCATTTGGCTGTGAGCGCAGTGGGCTGAGTACCGCTG	927
1696	DB	TTCCACTCATACGTGTCCCTTGGCTGTGACCCGGCCGGGGTGGATACCGCTC	1755
928	QY	CTGCAGGCTGCTACCTGTGCCAAGCGGGGGCGCTGTGGCAGGACCTTTGGAGTCCAT	987
1756	DB	CTGCAGGCTGTTTACCTTGGCCAAAGCTGGGACTCACTGGCCAGGCTTCAATATCACC	1815
998	QY	CCAGATGATGACTGTCTTTACCGTCTTCCAGGGCCGAAGCGGAAATGAATGCC	1047
1816	DB	AGCCAGGACGATGTACTCTTTGGCATCTTCTCCAAAGGCGAGACGATATCACCAACCG	1875
1048	QY	CTGGATGAGTGGGCCCTGTGCATCTTTCATCTTTGAACGACAGATAAATGACCGCATTAAGAG	1107
1876	DB	CCGATGACTCTGGCCCTGTGGCTTCCCTATCCGGGCCATCAACTTCAGATCAAGAG	1935
1108	QY	CGGCTGCAGTCTTGTACGGGCGGAGGCACTGCGACTCGCTGGCTCAAGTGAAG	1167
1936	DB	CGCCTGCAGTCTCTCTACCAAGGCGAGGGCACTGGAGTCAATGGCTCTGGGGAG	1995
1168	QY	GACATCCCCCTGCAGCAGTGGCTCTTAAACATTGACGATAAATTCTGTGGCTGGACATG	1227
1996	DB	GACGTCCAGTGCACGAAGGCGCTGTCCCCATCGATGATAAATTCTGTGGACTGGACATC	2055
1228	QY	ATGCTCCCTCGGAGTGTCCGACATGGTGGTGAATTCCTGCTTTCACGAGGACAGG	1287
2056	DB	AACCAAGCCCCCTGGAGGCTCACTCCAGTGGAGGGCTGACCTGTACACCAACGACAG	2115
1288	QY	GACCGCATGAGCTGTGTATCGCATATGTCTACAAGAACCACTCTCTGCGCTTTGTGGGC	1347



Db 2116 GACCGCATGACCTCTGTGGCTCTACGTTTACAAACGGCTACAGCGTGGTGGGG 2175  
QY 1348 ACCAAAGTGGCAAGCTGAAGAGATCCGGTGGATGGACCCAGGGGC 1395  
Db 2176 ACTAAGAGTGGCAAGCTGAAGAGTAAAGAGTCTATGAGTTGAGATGC 2223

RESULT 4  
US-09-023-655-603  
; Sequence 603, Application US/09023655  
; Patent No. 6607879  
; GENERAL INFORMATION:  
; APPLICANT: Cocks, Benjamin G.  
; APPLICANT: Susan G. Stuart  
; APPLICANT: Jeffrey J. Sellmaner  
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE  
; TITLE OF INVENTION: EXPRESSION  
; NUMBER OF SEQUENCES: 1508  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
; STREET: 3174 PORTER DRIVE  
; CITY: PALO ALTO  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/023,655  
; FILING DATE: HEREWITH  
; CLASSIFICATION:  
; PRIOR APPLICATION NUMBER:  
; APPLICATION NUMBER:  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Zeller, Karen J.  
; REGISTRATION NUMBER: 37,071  
; REFERENCE/DOCKET NUMBER: PA-0001 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (650) 855-0555  
; TELEFAX: (650) 845-4166  
; INFORMATION FOR SEQ ID NO: 603:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3458 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: THYMNON04  
; CLONE: 3191066  
; US-09-023-655-603

Query Match 5.0%; Score 284.2; DB 4; Length 3458;  
Best Local Similarity 64.4%; Pred. No. 2e-59;  
Matches 440; Conservative 0; Mismatches 237; Indels 6; Gaps 1;

QY 5001 CCGGGGAGCAAGATGGTGTCTGAATCTACCTGACCCGACTCCTGGCCACTAAGGGCAC 5060  
Db 1658 CCATCCGAGAGGTCTCCGGAAATCTACTGACCCGCTGCTCCACCAAGGGCAC 1717  
QY 5061 ACTGCGAAGTTTGTGGATGACCTCTTTGAGACCATCTTCAGCAGGCACACCGTGGCTC 5120  
Db 1718 GTTGCGAAGTTTCTGGATGACCTGTTCAAGGCCATTCTGAGTA-----TCCGTGAAGA 1771  
QY 5121 TGCCCTGCCCTGGCCATCAAGTACATGTTTGACTTCTGGATGACGAGCTGATAACA 5180  
Db 1772 CAAGCCCCCACTGGCTGCANNACTTTTCGACTTCTGGANANCAAGCTGAGAGAG 1831  
QY 5181 TGGCATTTCATGACCCGACGTCGCCCATACCTGGAAGAGCAATTGCTGCCCTCGAGGTT 5240

Db 1832 GGAATCTCCGACCCCGACACCCCTACATCTGGAAGACCAACAGCCTTCTCTCGGTT 1891  
QY 5241 TTGGGTCAACATGATCAAGAACCCCGAGTTTGTGTTGACATCCATAGAAACAGCATCAC 5300  
Db 1892 CTGGGTGAACATCTCTGAAGAACCCCGAGTTTGTGTTGACATCGAAGACAGCACAT 1951  
QY 5301 AGACGCTGCTCTCTGTGGTGGCTCAGACCTTTCATGACTCTTCTCCACGTCAGAGCA 5360  
Db 1952 CGACGCTGCTCTTTCAGTTCATCGCGAGGCTTTCATCGACGCTGCTCAATCTCTGACT 2011  
QY 5361 CCGGCTGGGCAAGGACTCGCCCTCCAAAGCTGTGTATGCAAGGAGCATCCCGAGTGA 5420  
Db 2012 GCAGCTGGGCAAGGATTGCGCAACCAAGCTCTCTACGCAAGGAGATTCTCTGAGTA 2071  
QY 5421 CAAGAATGGGTGGAGAGTATTACTCAGACATAGGAGATGCGAGCCATCAGCGACCA 5480  
Db 2072 CCGAAGATCGTGCAGCGCTACTACAAGCAGATCCAGGACATGACCGCTCAGCGAGCA 2131  
QY 5481 AGACATGAACGCATACCTGCTGAGCAGTCCCGGATGCACATCAATGAGTTCAACACCAT 5540  
Db 2132 AGAGATGAATGCCCATCTGCGGAGGAGTCGAGGAAATACCAAGATGAGTTCAACACCAA 2191  
QY 5541 GAGTGCACTCTCAGAGATCTTCTCTATGTGGGCAATACAGGAGGAGATCTTTGGACC 5600  
Db 2192 TGTGGCCATGGCAGAGATTATAAGTACGCCAAGAGGTATCGGCCGACATCATGCCCCG 2251  
QY 5601 TCTGGACCAAGTACGACGAGTGTGGGAAAGCAGAACTGGGCTTACAACTAGAACCAATCAT 5660  
Db 2252 GCTGGAGGCCAACCCACGCGCGGAGGACACACTGACGACACAGTTTGGAGCGTGGT 2311  
QY 5661 AACCTCATGAGCTTAGACAGCT 5683  
Db 2312 GGCTTTGATGGAGGACAAATCT 2334

RESULT 5  
US-09-181-706-1  
; Sequence 1, Application US/09181706  
; Patent No. 6130068  
; GENERAL INFORMATION:  
; APPLICANT: Melanie K. Spriggs, Michael R. Comeau,  
; APPLICANT: Robert F. DuBose, Richard S. Johnson  
; TITLE OF INVENTION: VIRAL ENCODED SEMAPHORIN PROTEIN  
; TITLE OF INVENTION: RECEPTOR DNA AND POLYPEPTIDES  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Janis C. Henry  
; STREET: 51 University St.  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: US  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; FILING DATE: US/09/181,706  
; FILING DATE: October 28, 1998  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/958,598 (converted to a  
; APPLICATION NUMBER: Provisional, see below)  
; FILING DATE: October 28, 1997  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: --to be assigned-- (USN 08/958,598  
; APPLICATION NUMBER: conversion to Provisional application)  
; FILING DATE: October 26, 1998  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:

NAME: Henry, Janis C  
 REGISTRATION NUMBER: 34,347  
 REFERENCE/DOCKET NUMBER: 2631-A  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (206)470-4189  
 TELEFAX: (206)233-0644  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 4707 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 1..4707  
 US-09-181-706-1

Query Match 3.5%; Score 201.2; DB 3; Length 4707;  
 Best Local Similarity 49.1%; Pred. No. 4.3e-39;  
 Matches 824; Conservative 0; Mismatches 728; Indels 126; Gaps 6;

3935 TTCCGTTCTCGGACTATAGAACTTACACCATCGCGGTGCTGTTCACCGGAAATGGAAGCC 3994  
 3038 TTCCCTTCCTGACTCAACAATTTGCTCTGAGAACTTTCTTCCCTGAGTCAGGTGGCT 3097  
 3995 ACCCTGTCTCCGGGACCTTGAGTCCGGGCTACCGGAGGAGCGTGTGGAGAGGCC 4054  
 3098 TCACCCACATCTTCACTGAAGATATGATTAACAGAGACGCCAACAGAAATGAAAGTC 3157  
 4055 TGAAGCTTTTCGCCAGCTCATCAACAAAGGTGTCTGCTGTCTTCTATCCCGCAGCC 4114  
 3158 TCACAGCTTTGGATGCCCTTAATCTGTAATAAAGCTTCTTGTACTGTCATCCACACC 3217  
 4115 TTGAGTCCCGAGTAGTCTTCCATGCGCGACCGTGGCAAGCTGGCTCTCATCATGTA 4174  
 3218 TTGAAAACGAGAGAACTTTCTGTGAAGACAGGTGTCTGTGTGCTCTCTTCTTAACCA 3277  
 4175 CCGTGTGTCAGAGCAAGCTGGAGTACCCACTGATGTGTGAAGACAGCTGCTGGCCGACC 4234  
 3278 TTGCACTTGCAACCAAGCTGTCTACTGACAGCATCTTAGAGGTGCTGACACAGGACT 3337  
 4235 TCATGTACAAGACCTGGAGAGCAAGAACACACCTTAGCTGTCTCAGGAGAGCTGAGT 4294  
 3338 TGAT-----GGAAACAGTAGTAACATGACGCGCAACTCATGCTGAGACGACCGAGT 3391  
 4295 CAGTGGCTGAGAGATGCTGACCAATTTGTTTACTTTCTCTCTCTACAGTTCTCTCAAGG 4354  
 3392 CCGTCTGCAAAAACCTCTCAAACTGGATGTCGATGTCGCTCTGCTTCTGGATTTCTCGGG 3451  
 4355 AGTGTCTGGGGACCCCTCTTCTCCCTGTTCTGTGCCATCAAGCAGCAGATGGAGAAG 4414  
 3452 AGACTGTGGAGAGCCCTTCTATTGTGTGTGAGCAGCTCTGAACAGAAAATTAACAAGG 3511  
 4415 GCCCATGTAGCCCATCAGCGGCGAGCCGCTACTCTTCTGAGGAGAGCAAGCTCATCC 4474  
 3512 GTCCGCTGGATGTAATCACTTGTGAAGCCCTGTGACACATTAATGAAGACTGGCTGTGT 3571  
 4475 GCCAGCAGATTGACTTACAAAACCCCTGGTCTGTAGCTGTGTGAGCCGACGACAATGCCAACA 4534  
 3572 GGCAGTCCCGAATTCAGTACTGTGGCATTAACACGCTGCTTTTGAAAAAATCCCGGAAA 3631  
 4535 GC-----CCGNGTCCAGTAAGATCCTCAACTGTGACACCATCA 4576  
 3632 ACGAGAGTGCAGATGCTGTGCGAATATTTTCAGTCAATGTTCTCGACTGTGACACCATG 3691  
 4577 CTCAGTCAAGGAGAGAAATTTCTGATGCGATCTTCAAGAAATGTCCTTGTCTCCACCGGC 4636  
 3692 GCCAGCCAAAGAAAAGATTTTCCAGCATTTTAAAGCAAAATGGCTCTCTTATGAC 3751  
 4637 CCAAAGCTGCAGATATGGATCTGGAGTGGCGACAGGAAGTGGGCAAGGATGATCTTGC 4696

RESULT 6  
 US-09-458-791-1  
 ; Sequence 1, Application US/09458791  
 ; Patent No. 6174689  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Spriggs, Melanie  
 ; TITLE OF INVENTION: VIRAL ENCODED SEMAPHORIN PROTEIN  
 ; RECEPTOR DNA AND POLYPEPTIDES  
 ; NUMBER OF SEQUENCES: 10

Db 3752 TTCAGCTTAATGAATGGTCTTGAGCTTCAATGGGCACACGACGAGAAAGAACTTCTGG 3811  
 Qy 4697 AGGATGAAGACATCAACACCAAGATTGAGAAATGATTGGAGCCAGTGAACACACTGGCCC 4756  
 Db 3812 ACATCGACAGTCTCGTGAATCTTTGAAGATGGAATCAACCAAGCTTAAACACCAITGGCC 3871  
 Qy 4757 ACTACCAAGTCCAGATGGTTCGTTGGTGGCAATTAGTGTCCAAGCAGGTGACAGCCTATA 4816  
 Db 3872 ACTATGAGATATCAATGGATCCACTATAAAGTCTTTAAGAGATAGCAAAATTTTACTT 3931  
 Qy 4817 ACGCAGTGAACAACTCCACCGTCTCCAGGACCTCAGCAAGTAAATATGAAAAATGATCC 4876  
 Db 3932 CAGATGTGGAGTACTC-----GGATGACCACTGCCATTGATTTTA----- 3972  
 Qy 4877 GGTACAGGGCAGCCCGCAGCAGCTCCGCTCAAGGACACCTATGATCACTCTGACCTGG 4936  
 Db 3973 ----- 3972  
 Qy 4937 AGAGTGGAGTCAAGATGTGGCACCCTAGTGAAGAACCAAGAGCAGGAGACGAGAGAGG 4996  
 Db 3973 -----CCAGATTCCGAAGCATTCCAAGATGTGCAAGGAAAGAGAC-----ATC 4015  
 Qy 4997 GGGACCGGGGAGCAAGATGGTGTCTGAATCTACCTGACCCGACTCTCTGGCCACTAAGG 5056  
 Db 4016 GAGGAGAGCAAGTTCAAAAGTAAAGAAATGTATCTGCAAAAGCTCTGTGACCAAGG 4075  
 Qy 5057 GCACACTGCAGAACTTTGTGATGACCTCTTTGAGACCATCTTCAGCACCGGCACACCGTG 5116  
 Db 4076 TGGCAATTCATCTGTGCTTGAAAACTTTTAGAAGCATTTGGAGTTTACCCCAACAGCA 4135  
 Qy 5117 GCTGTGCCCTGCCCTGCCATCAAGTACATGTTTGTGATCTTCTGGATGCGAGCTGATA 5176  
 Db 4136 GAGCT-----CCATTTGCTATAAATACTTTTGTGACTTTTGGACCGCCAGGCTGAAA 4189  
 Qy 5177 AACATGGCATTCATGACCGCAGCTCCGCCATACCTGGAAGAGCAATTTGCTGCCCTCGA 5236  
 Db 4190 ACATAAATAACACAGATCTGACCTCGTACATATTTGAAAAACAAACAGCCTTCTCTTC 4249  
 Qy 5237 GGTGTTGGTCAACATGATCAAGAACCGGAGTTTGTGTTGATCTTCAATCCATGAAGACAGCA 5296  
 Db 4250 GCTTCTGGGTAAACATCTCTGAAGAACCTCAGTTTGTCTTTGACATTAAGAAAGACACCAC 4309  
 Qy 5297 TCACAGACGCTGCTCTCTGTGTGGCTCAGACCTTCATGCACTTGTCTTCCAGCTCAG 5356  
 Db 4310 ATATGAGCGGTGTTGTGCTGATGTCAGGACATTCATGATGATTTCTCTCAG 4369  
 Qy 5357 AGCACCGCTGGGCAAGACTCGCCCTCCAAACAGCTCTGTATGCCAGGACATCCCA 5416  
 Db 4370 AGCAGCAACTAGGGAAGGAAAGCACCACCTAATAAGCTTCTATGCCAAGGATATCCCA 4429  
 Qy 5417 GCTACAAGAAATTTGGGTGAGAGGTATTACTCAGACATAGGGAAGATGCCAGCATCAGCG 5476  
 Db 4430 CTTACAAGAGAAATTAATCTTATTAAGAGCATCAGGATTTGCTTCAATGTCTAT 4489  
 Qy 5477 ACCAAGACATGAACCATACCTGCTGAGCAGTCCCGATGCCAGTGAATGATGATTCAACA 5536  
 Db 4490 CCTCAGAAATGAAGAAATTTTAACTCAGGAATCTAAGAAACATGAAAAATGAATTAATG 4549  
 Qy 5537 CCATGAGTGCATCTCAGAGATCTTCTCTTGTGGCAAAATACAGCAGGAGATCCT 5594  
 Db 4550 AAGAAAGTGGCTTGACAGAAATTTTAAATAATCATCTGTAATATTTTGTATGATGATCT 4607

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Janis C. Henry  
STREET: 51 University St.  
CITY: Seattle  
STATE: WA  
COUNTRY: US  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: MS-DOS/Windows 95  
SOFTWARE: Word for Windows 95, 7.0a  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/458,791  
FILING DATE: 10-Dec-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/958,598  
FILING DATE: 28-OCT-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Henry, Janis C  
REGISTRATION NUMBER: 34,347  
REFERENCE/DOCKET NUMBER: 2631  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206)470-4189  
TELEFAX: (206)233-0644  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4707 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..4707  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-09-458-791-1

Query Match 3.5%; Score 201.2; DB 3; Length 4707;  
Best Local Similarity 49.1%; Pred. No. 4,3e-39;  
Matches 824; Conservative 0; Mismatches 728; Indels 126; Gaps 6;  
QY 3935 TTCGGTTCCTGGAGTATAGAACTTACCAATCGGGTGTCTCCAGAGAAATGAAGACC 3994  
DB 3038 TTCCTTCTGACTCAAAACATTTTGTCTCAGAACTTTCTTCTCCTGAGTCAGTGGCT 3097  
QY 3995 ACCCTGTCTCCGGGACCTTGAGTCCCGGCTACCGCAGGAGCGTGTGNGAAGGCC 4054  
DB 3098 TCACCCACATCTTCACTGAAGATATGCATAACAGAGACGCCAACAGAAATGAAGTC 3157  
QY 4055 TGAAGCTTTTCGCCAGCTCATCAACAAACAGAGTGTCTGTCTCTTCTATCCGACGC 4114  
DB 3158 TCACAGCTTTGGATGCCCTAATCTGTAATAAAAGCTTTCTGTACTGTCTATCCACACC 3217  
QY 4115 TTGAGTCCAGCGTACTTCTCATCGCGCGGTGGCAAGTGGCCCTCATCATGA 4174  
DB 3218 TTGAAGAGCAAGAACTTTCTGTGAAGCAGAGTGTCTGTTCCTCTTCTTAACA 3277  
QY 4175 CCGTGTGACAGCAAGTGGAGTACGCCACTGTATGTGTGAAGCAGTGTCTGCGCGACC 4234  
DB 3278 TTGCACTGCAAAACCAAGCTGGTCTACCTGACCAGATCTTAGAGGTGTGACCGGAGT 3337  
QY 4235 TCATTGACAGACCTGGAGGCAAGAACCCCTAAGTGTCTCAGGAGGACTGAGT 4294  
DB 3338 TGAAT-----GGAAAGTGTAGTAAATCATGCGGAAATCATGCTGAGACGCGGAGT 3391  
QY 4295 CAGTGTGAGAAAGTGTGACCAATTTGGTTTACTTCTCTCTTCTACAAAGTTCCTCAAG 4354  
DB 3392 CCGTGTGCAAAAACCTCTCAAAACCTGATGTCTGTCTGCTCTGCTGCTCTGCTGCT 3451

QY 4355 AGTGTGCTGGGAGGCCCTCTTCTCCCTGTTCTGTGCCATCAAGCAGCAGATGAGAAGG 4414  
DB 3452 AGACTGTGCGAGAGCCCTTCTAATTTGCTGGTGACGACTCTGAACAGAAAAATTAAACAGG 3511  
QY 4415 GCCCATTTACGCCCATCAAGGCGAGGCCGCTACTCTCTTGAAGGAGCAGAGTCAATCC 4474  
DB 3512 GTCCCGTGGATGAATCACTTGCAAAAGCCCTGTACACACTTAATGAAGACTGGCTGTGT 3571  
QY 4475 GCCAGCAGATTGACTACAAAACCCCTGGTCTCTGAGTGTGTGAGCCAGCAATGCCACA 4534  
DB 3572 GGCAGGTTCCGGAAATTCAGTACTGTGGCATTAAACGCTGCTTTTGAATAAAATCCCGGAAA 3631  
QY 4535 GC-----CCGAGGTCCCAAGTAAAGATCCTCAACTGTGACACCATTCG 4576  
DB 3632 ACCAGAGTGCAGATGTCTGTGGAATAATTCAGTCAATGTTCTCGACTGTGACACCATTCG 3691  
QY 4577 CTCAGGTCAAGGAGAGGATTCCTGGATGCCATCTTCAAGAAATGTCCTTCCCAACCGGC 4636  
DB 3692 GCCAAGCCAAAGAAAGATTTTCCAGCATTTCTTAAGCAAAAATGGCTCTCTCTTATGGAC 3751  
QY 4637 CCAAAGCTGCAGATATGGATCTGGAGTGGCGACAAAGGAAGTGGGCAAGGATGATTCGC 4696  
DB 3752 TTCAGCTTAATGAAATTTGCTTGTAGCTTCAATATGGGCAACGACAGAAAGAACTTCTGG 3811  
QY 4697 AGGATGAAGACATCACCAACCAAGATTGAGAAATGATTGGAAGCGACTGAACACACTGGCC 4756  
DB 3812 ACATCGACAGTTCCTCCGTGATTTCTTGAAGATGAATCAACCAAGTAAACACCATTCGACC 3871  
QY 4757 ACTACCAAGTGCAGATGTTCCGTGGTGGCATTTAGTGTCCAAAGCAGGTGACAGCCCTATA 4816  
DB 3872 ACTATGAGATATCAAAATGATCCACTATAAAAGTCTTTAAGAAAGATAGCAAAATTTACTT 3931  
QY 4817 AGCAGTGAACACTCCACCGCTCTCCAGGACTCAGCAAGTAAATATATGAACACATGATCC 4876  
DB 3932 CAGATGTGGAGTACTC-----GGATGACCACTGCCATTTGATTTTA----- 3972  
QY 4877 GGTACACGGGACGCCCGACAGCCTCCGCTCACGGACACCTATGATCATCTCTGACCTGG 4936  
DB 3973 ----- 3972  
QY 4937 AGAGTGGAGTCAAGATGTGGCACCCTAGTGAAGAACCCAGCAGCAGGACGAGAGGAGG 4996  
DB 3973 -----CCAGATTCGGAAGCATTCGAAGATGTGCAAGGAAGAGAC-----ATC 4015  
QY 4997 GGGACCGGGGAGCAAGATGTGTGAAATCTACCTGACCCGACTCTGTCGCCACTAAGG 5056  
DB 4016 GAGGGAAGCACAGTTCAAAGTAAAGAAATGTATCTTGACAAAGCTGCTGTCGACCAAGG 4075  
QY 5057 GCACACTGCAGAGTTTCTGGATGACCTCTTTGAGACCATCTTCAGCAGCAGCAGCAGCGTG 5116  
DB 4076 TGGCAATTCATCTGTGTGTTGAAAACCTTTTGAAGCATTTTGAAGTTTGAAGTTTACCCACAGCA 4135  
QY 5117 GCTCTGCCCTGCCCTGCCCATCAAGTACATGTTTGTGACTTCTCTGATGAGCAGGCTGATA 5176  
DB 4136 GAGCT-----CCAATTTGCTATAAAATACTTTTTTGTACTTTTGGACGCGCCAGGCTGAAA 4189  
QY 5177 AACATGGCAATTCATCACCGCAGCCTCCGCTACCTGGAAGAGCAATTTGCTGCGCCCTGA 5236  
DB 4190 ACAAAAAATCAAGATCTGACGCTGACATAATTTGGAACAAACAGCCTTCTCTCTC 4249  
QY 5237 GGTGTTGGTCAACATGATCAAGAACCCGAGTTTGTGTTGATCATCAATAAGAACAGCA 5296  
DB 4250 GCTTCTGGTAAACATCTCGAAGAACCTCAGTTTGTCTTTGACATTAAGAAAGACACAC 4309  
QY 5297 TCACAGACGCTGCTCTCTGTGTGGCTCAGACCTTCATGAGTCTTGTGCTCCAGCTCAG 5356  
DB 4310 ATATAGACGCTGTTTGTGATGATTTGCCAGGCAATCATGAGTGTGATTTTCTCTCAG 4369  
QY 5357 AGCACCGGTGGCGAAGGACTCGCCCTCCAAACAGAGTGTCTGTATGCCAAGGACATCCCA 5416  
DB 4370 AGCAGCAACTAGGGAAGGAGCACCACTAATAAGTCTCTATGCGCAAGGATATCCAA 4429  
QY 5417 GCTACAGAAATTTGGGTGGAGAGGATTATTACTCAGACATTAAGGAAGATCCAGCCATCAGG 5476

Db 4430 CCTACAAAGAGAGTAAATCTTATTAAAGCAATCAGGATTTGCTCCTCATGTCTAT 4489  
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Db 4490 CCTCAGAAATGGAAGAAATTTTAACTCAGGAATCTAAGAAACATGAATGAATTAATG 4549  
Qy 5537 CCATGAGTGCATCTCAGAGATCTTCTCTATGTGGGCAAAATACAGCGAGGAGATCCT 5594  
Db 4550 AAGAAGTGGCTTGACAGAAATTTACAATACATCGTAATAATATTTTGATGAGATTCT 4607

RESULT 7

US-09-459-066-1  
; Sequence 1, Application US/09459066  
; Patent No. 6187909  
; GENERAL INFORMATION:  
; APPLICANT: Spriggs, Melanie  
; TITLE OF INVENTION: VIRAL ENCODED SEMAPHORIN PROTEIN  
; TITLE OF INVENTION: RECEPTOR DNA AND POLYPEPTIDES  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Janis C. Henry  
; STREET: 51 University St.  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: US  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: MS-DOS/Windows 95  
; SOFTWARE: Word for Windows 95, 7.0a  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/459,066  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/958,598  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Henry, Janis C  
; REGISTRATION NUMBER: 34,347  
; REFERENCE/DOCKET NUMBER: 2631  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206)470-4189  
; TELEFAX: (206)233-0644  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4707 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: CDNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..4707  
; US-09-459-066-1

Query Match 3.5%; Score 201.2; DB 3; Length 4707;  
Best Local Similarity 49.1%; Pred. No. 4.3e-39;  
Matches 824; Conservative 0; Mismatches 728; Indels 126; Gaps 6;  
Qy 3935 TTCCGTTTCTGGACTATAGAACTTACACCATGCGGGTGTGTTCCCAAGGAATGAAGACC 3994  
Db 3038 TTCCCTTCTTGATACAAATTTTCTCTGAGAACTTTCTTCCCTGAGTCAGGTGGCT 3097  
Qy 3995 ACCGTGCTCCGGGACCTTGAGGTCCGGGCTACCGGCGAGGACGCTGTGGAGAAAGGCC 4054  
Db 3098 TCACCCACATCTTCACTGAAGATATGATACAGACGCGCAACGACAGAAATGAAGTC 3157

Qy 4055 TGAAGCTCTTCCGCCAGCTCATCAAAACAAGGTGTTCTGTGCTCTTCTCATCCGACGC 4114  
Db TCACAGCTTTGGATGCCCTAATCTGTAAATAAAGCTTTCTGTACTGTCTATCCACACCC 3217  
Qy 4115 TTGAGTCCCAAGCTAGTCTTCCATGCGCGACCGTGGCAACGTTGGCTCTACTCATCATGA 4174  
Db TTGAAAAGCAGAGAACTTTCTGTGAAGGACAGGTGTCTGTGTGCTCTCTTCTTAACCA 3277  
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Db TTGACATGCAAAACCAAGCTGGTCTACCTGACACGACATCCTAGAGGTGCTGACCGGACT 3337  
Qy 4235 TCATTGACAAACCTGGAGAGCAAGAACCAACCTTAAGCTGTGCTGCTCAGAGAGCTAGT 4294  
Db TGAT-----GGAACAGTGTAGTAACATGACGCGCAAACTCATGCTGAGACGACGCGAGT 3391  
Qy 4295 CAGTGGCTGAGAAGATCTGACCAATTTGTTTACTTTCTCTCTCTCAAAAGTCTCTCAAG 4354  
Db CCGTGTGCAAAACTCTCACAACCTGATGTCGCTCTGCTCTTCTGGATTTCTCCGG 3451  
Qy 4355 AGTGTGTGGGAGCCCTCTTCTCCCTGTGTGTCATCAAGCAGCAGATGAGAGAGG 4414  
Db AGACTGTCCGAGAGCCCTTCTATTGCTGTGTCAGCACTCTGAAACCAAAATTAACAAG 3511  
Qy 4415 GCCCATTTGAGCCCATCAGCGGCGAGCCGCTACTCTTTGAGCGAGCAAGCTCATCC 4474  
Db GTCCCGTGGATTAATCACTTGCAAGCCCTGTACACACTTAATGAGACTGCTGTGTGT 3571  
Qy 4475 GCCAGCAGATTGACTACAAAACCTGTGCTGAGCTGTGTGAGCCAGACAATGCCAAC 4534  
Db GGCAGGTTCCGGAATTCACTACTGTGCAATTAAGCAAAATGCTCTTCTTGAATAAATCCCGAAA 3631  
Qy 4535 QC-----CCGAGCTCCAGTAAAGATCCTCAACTGTGACACCATCA 4576  
Db ACAGAGTGCAGATGTCTGTGCGAATATTTCAAGCAATTTTCAAGCAAAATGCTCTCTTATGAC 3631  
Qy 4577 CTCAGGTCAGGAGAGATTTCTGATGCCATCTTCAAGAAATGTGCTTGTCCACCGCC 4636  
Db GCCAAGCCAAAGAAAGATTTTCAAGCAATTTTCAAGCAAAATGCTCTCTTATGAC 3751  
Qy 4637 CCAAGCTGCAGATATGATGTGAGTGGCAAGGAGTGGGGCAGAGTATCTTGC 4696  
Db TTCAGCTTAATGAAATTTGCTTGTGAGCTTCAATTTTCAAGCAAAATGCTCTCTTATGAC 3811  
Qy 4697 AGGATGAAGACATCACCAACCAAGATTTGAGATGATTTGAGAGCTGAAACACTGGGCC 4756  
Db ACATCGACAGTTCTCCGTGATTTTGAAGATGAATCACCAGCTAAACACCATTTGGCC 3871  
Qy 4757 ACTACAGGTGCAGATGTTCCGTGTTGGATTTAGTGTCCAGCAGGTGACAGCTATA 4816  
Db ACTATGAGATATCAATGGATCCACTATAAAGTCTTTAAGAGATAGCAAAATTTTACTT 3931  
Qy 4817 ACGCAGTGAACAACCTCCACCGTCTCCAGGACCTCAGCAAGTAAATATGAAAAACATGATCC 4876  
Db CAGATGTGAGTACTC-----GGATGACCACTGCCATTTGATTTTA----- 3972  
Qy 4877 GGTACACGGGAGCCCGCCAGACGCTCCGCTCAGGACACCTATGATCACTCTGACCTGG 4936  
Db ----- 3972  
Qy 4937 AGAGTGGAGTCAAGATGCGCACCTAGTGAAGAACCAAGCAGCAGGAGACCAAGAGGAGG 4996  
Db -----CCAGATTCGGAGCATTCAGAGATGTGCAAGGAAGAGAC-----ATC 4015  
Qy 4997 GGGACCGGGGAGCAGATGTTGTGAAATCTTACTGACCCGACTCTCTGGCCACTAAGG 5056  
Db GAGGGAAGCACAAGTTCAAAGTAAAGAAATGTATCTGACAAAGTGTGTCTGACCAAGG 4075  
Qy 5057 GCACACTCAGAAAGTTTGTGATGATCCTTTTGTAGACCATCTTTCAGCAGCGCACACCGCTG 5116  
Db TGGCAATTCATCTGTGCTTGAATAAATTTTGTAGAGCATTTTGTGATTTTACCAACAGCA 4135  
Qy 5117 GCTCTGCCCTGCCCTCGCCATCAAGTACATGTTTGAATTTCTGTGATGAGCAGGCTGATA 5176

Db 4136 GAGCT-----CCATTTGCTATAAAATACATTTTTTGTGACGCGCCAGGCTGAAA 4189  
Qy 5177 AACATGGCATTCATGACCGCAGCTCGCGCATACCTGGAAGAGCAATGCTGCCCCCTGA 5236  
Db 4190 ACAAATAATCAGATCCTGACGCTGACATATTTGGAATAACAAACAGCTTCCCTTC 4249  
Qy 5237 GGTGTTGGTCAACATGATCAAGAACCGGCGAGTTTGTGTTGATCATCCATAAGAACGCA 5296  
Db 4250 GCTTCTGGTAAACATCTGGAAGAACCTCAGTTTGTCTTGTGACATTAAGAGACACCAC 4309  
Qy 5297 TCACAGAGCGCTGCTCTCTGTGTGGTCTCAGACTTCATGACTCTTGTCTCCAGCTCAG 5356  
Db 4310 ATATAGCGGTGTTTGTGCTGATGTCACAGGATTCATGATGCAATTTCTCTCAG 4369  
Qy 5357 AGCACCGCTGGGAAGACTTCGCGCTCCAAACAGCTGCTGTATGCAAGACATCCCA 5416  
Db 4370 AGCAGCACTAGGGAAGAACCAACAAATAAAGCTTCTCTATGCAAGGATATCCAA 4429  
Qy 5417 GCTCAAGAATTGGTGGAGAGGATTAATCTCAGACATAGGGAAGATGCCAGCCATCAGCG 5476  
Db 4430 CCTCAAGAAGAGATAAATCTTATTAACAAGCAATCAGGATTTGCTCCATGTGAT 4489  
Qy 5477 ACCAAGACATGAACATACCTGCTGAGCAGTCCCGGATGCCATGAATGAGTTCAACA 5536  
Db 4490 CCTCAGAAATGAAGAAATTTTAACTCAGGAATCTAAGAAACATGAAATGAATTAATG 4549  
Qy 5537 CCATGAGTGCATCTCAGAGACTTCTCCTATGTGGCAATACAGCGAGAGATCCT 5594  
Db 4550 AAGAGTGGCTTGACAGAAATTTACAAATACATCGTAAATATTTTGTGAGATTCT 4607

RESULT 8

US-09-459-065-1  
; Sequence 1, Application US/09459065  
; Patent No. 6562949  
; GENERAL INFORMATION:  
; APPLICANT: Spriggs, Melanie  
; TITLE OF INVENTION: VIRAL ENCODED SEMAPHORIN PROTEIN  
; TITLE OF INVENTION: RECEPTOR DNA AND POLYPEPTIDES  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Janis C. Henry  
; STREET: 51 University St.  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: US  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: MS-DOS/Windows 95  
; SOFTWARE: Word for Windows 95, 7.0a  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/459,065  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/958,598  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Henry, Janis C  
; REGISTRATION NUMBER: 34,347  
; REFERENCE/DOCKET NUMBER: 2631  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206)470-4189  
; TELEFAX: (206)233-0644  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4707 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear

; MOLECULE TYPE: cDNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..4707  
US-09-459-065-1

Query Match 3.5%; Score 201.2; DB 4; Length 4707;  
Best Local Similarity 49.1%; Pred. No. 4.3e-39;  
Matches 824; Conservative 0; Mismatches 728; Indels 126; Gaps 6;

Qy 3935 TTCCGGTTCCTGGACTATAGAACTTACACCATCGGGTGTCTTCCAGGAATTAAGACC 3994  
Db 3038 TTCCCTTCTTCTGACTACAAACATTTTGTCTCAGAACTTTCTTCTCAGTGTGGCT 3097  
Qy 3995 ACCTGTCCTCCGGACCTTTGAGTCCCGGGTACCGGAGGAGCGTGTGGAGAAAGCC 4054  
Db 3098 TCACCACATCTTCACTGAAGATATGCAATAACAGAGACGCCAACACAGATGAAGTC 3157  
Qy 4055 TGAAGCTCTTCGCCAGCTCATCAACCAAGGTGTCTGCTGCTCTTTCATCCGACGC 4114  
Db 3158 TCACAGCTTTGGATGCCCTTAATCTGTATATAAAGCTTTCTTCTACTGTCTACACCC 3217  
Qy 4115 TTGAGTCCAGCGTGTCTTCCATGCGGACCGTGGCAACGTTGGCTCCTCATCATGA 4174  
Db 3218 TTGAAGAGCAGAAAGAACTTTTCTGTGAAGGACAGGTGTCTTGTGCTCTTCTTAACA 3277  
Qy 4175 CCGTGTGAGAGCAAGCTGGAGTACGCCACTGTGTGCTGAAGCAGCTGTGGCCGACC 4234  
Db 3278 TTGACTGCAACCAAGCTGTCTTCTACCTGACAGCATCTAGAGTGTGACAGGACT 3337  
Qy 4235 TCATTGACAAGAACCTGGAGAGCAAGAACCCCTAAGTGTCTGCTCAGAGGACTGAGT 4294  
Db 3338 TGAT-----GGAAACAGTGTAGTAATGTCAGCGCGAAACTCATGCTGAGACGCGAGT 3391  
Qy 4295 CAGTGTGAGAGATGCTGACCAATTTGTTTACTTCTCTCTCAAAATTCCTCAAGG 4354  
Db 3392 CCCTGTCGAAAGAACTTCTCACAACATGGAGTCCGTCTGCTTCTGATTTCTCGGG 3451  
Qy 4355 AGTGTGCTGGGAGCCCTCTTCTCCCTGTCTGTGCTCCATCAAGCAGCAGATGGAGAGG 4414  
Db 3452 AGACTGTGAGAGCCCTTCTATTGCTGTGACGACTCTGAACACAGAAATTAACAAGG 3511  
Qy 4415 GCCCATTTGAGCATCAGGGGAGCGCCGCTTCTCTTGTGAGCGAGGCAAGCTCATCC 4474  
Db 3512 GTCCCGTGGATGTAATCACTTGCAGAGCCCTGTACACACTTAATGAAGCTGCTGTGT 3571  
Qy 4475 GCCAGCAGATTGACTACAAACCCCTGCTGCTGAGCTGTGTGACGCCAGCAATGCCAACA 4534  
Db 3572 GGCAGTTCGGAATTCAGTACTGTGGCAATTAACGTCGTCTTTGAAAAAATCCCGAAA 3631  
Qy 4535 GC-----CCGAGGTCCAGTAAGATCCTCAACTGTGACACCATCA 4576  
Db 3632 ACAGAGTGCAGATGTCTGTCCGAATATTTTCACTCAATTTCTCGACTGTGACACCATG 3691  
Qy 4577 CTCAGGTCAAGGAGAGATTCTGGATGCCATCTTCAAGATGTGCTTGTCTCCACCGGC 4636  
Db 3692 GCCAAGCCAAAGAAAGATTTTCCAGCATCTTAAGCAAAATGGCTCTCTTATGAC 3751  
Qy 4637 CCAAAGCTGCAGATATGATGATCTGTGAGTGGCGACAAGGAATGGGGCAAGATGATCTGC 4696  
Db 3752 TTCAGCTTAATGAAATTTGGTCTTGAGCTTCAAAATGGGCACACGACAGAAAGAACTTCTGG 3811  
Qy 4697 AGGATGAGACATCCACCACCAAGATTGAGAAATGATTGGAAGCGACTGAACACACTGGCCC 4756  
Db 3812 ACATCGACAGTTCCTCCGTGATTTCTGAGATGGAATCACAAGCTTAACACCATTTGCC 3871  
Qy 4757 ACTACAGGTGCCAGATGGTTCCGTGTGGCATTTAGTGTCAAGAGAGGTGACAGCCTATA 4816  
Db 3872 ACTATGAGATATCAATGGATCCACTATAAAGTCTTTAAGAGATGACAAATTTTACTT 3931  
Qy 4817 ACGAGTGAACAACTCCACCGTCTCCAGGACCTCAGCAAGTAAATATGAAAAACATGATCC 4876

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Db 3932 CAGATGTGAGTACTC-----GGATGACCACTGCCATTTGATTTA----- 3972
Qy 4877 GGTACAGGGCAGCCCGACAGCCTCCGCTCAGGACACCTATGATCATCTCTGACCTGG 4936
Db 3973 -----CCGAATTCGGAAGCATTCCAAGATGTGCAAGGAAGAGAC-----ATC 4015
Qy 4937 AGAGTGGAGTCAAGATGTGGACCTAGTGAAGAACCCAGCAGCAGGAGACCAAGAGG 4996
Db 3973 -----CCGAATTCGGAAGCATTCCAAGATGTGCAAGGAAGAGAC-----ATC 4015
Qy 4997 GGGACCGGGGAGCAGATGGTGTCTGAATCTACTGACCCGACTCTCTGGCCACTAAGG 5056
Db 4016 GAGGGAGCACAAGTTCAAAGTAAAGAAATGTATCTGCAAAAGTGTCTGTGCGACCAAG 4075
Qy 5057 GCACACTGCAGAAAGTTTGTGGATGACCTCTTTGAGACCATCTTCAGCAGCGCACACCGTG 5116
Db 4076 TGCCAAATTCATCTGTGCTGAAATACTTTTAGAAGCATTTGGAGTTTAAACCAACAGCA 4135
Qy 5117 GCTCTGCCCTGCCCTGCATCAAGTACATGTTTGAATCTCTGATGAGCAGGCTGATA 5176
Db 4136 GAGCT-----CCATTTGTATATAAATCTTTTGTGACTTTTGGACGCCAGGCTGAAA 4189
Qy 5177 AACATGCGATTCATGACCGCAGCTCGGCATACCTGGAAGAGCAATTCCTGCCCCCTGA 5236
Db 4190 ACAAATAATCACAGATCCTGACGCTGTACATATTTTGGAAACAAACAGACGCTTCCTCTTC 4249
Qy 5237 GGTGTTGGGTCAACATGATCAAGAACCGGAGTTGTGTTGACATCCATAAGAACAGCA 5296
Db 4250 GCTTCTGGTAAACATCCTCGGAAGAACCCCTCAGTTTCTTTGACATTAAGAAAGACACCCAC 4309
Qy 5297 TCACAGAGCGCTGCTCTGCTGTGGTGGCTCAGACCTTCATGGAATCTTGCTCCACGTCAG 5356
Db 4310 ATATGAGCGCTGTTGTCACTGATGTTGCCAGCGCATTCATGATGATTTCTCTCACAG 4369
Qy 5357 AGCAGCGGTGGGCAAGGATCGCCCTCCAAAGCTGCTGTATGTCGAAGGACATCCCA 5416
Db 4370 AGCAGCAACTAGGGAAGGAAGACCAACTAATAAGCTTCTCTATGTCGAAGGATATCCCAA 4429
Qy 5417 GCTACAGAAATGGTGGAGGATTTACTCAGACATAGGAAGATGCGCAGCATCAGCG 5476
Db 4430 CCTACAAAGAAAGTAAATCTTTTAAAGCAATCAGGATTTGCTCCATTTGTCAT 4489
Qy 5477 ACCAAGCATGAACGCTACCTGCTGAGCAGTCCCGATGTCACATGAATGATTCACA 5536
Db 4490 CCTCAGAAATGGAAGATTTTAACTCAGGAATCTAAGAAACATGAATGAATTTAATG 4549
Qy 5537 CCATGAGTGCATCTCAGATCTTCTCCTATGTCGCAATACAGCAGGAGATCCT 5594
Db 4550 AAGAAATGGGCTTGACAGAAATTTTACAAATACATCGTAAATATTTTGTGAGATTTCT 4607

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RESULT 9

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US-09-328-475C-37/c
; Sequence 37, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; ARE DIFFERENTIALY REGULATED IN PROSTATE CANCER
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 37

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; LENGTH: 1024
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1024)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-37

Query Match
Best Local Similarity 1.5%; Score 86.4; DB 4; Length 1024;
Matches 148; Conservative 0; Mismatches 68; Indels 2; Gaps 2;

Qy 5472 CAGGACCAAGACATGACCCATA-CCTGGTGGAGAGTCCCGATGACATGAATGAG- 5529
Db 780 CAGTGACCAAGCCATGAATGCTTACCTCGCCGAGAGTCCCGCTGCACNCGTGGAGT 721
Qy 5530 TTCAACACCATGAGTGCACCTCTCAGAGATCTTCTCTATGCGGCAAAATACAGCGAGG 5589
Db 720 TTCAACATGTTGAGTGCCCCCAATGAGATCTCTCTATGTCAGCAAGTATAGTAGGAG 661
Qy 5590 ATCCTTGGACCTCTGGACCAAGATGACCATGTTGGGAGAGAACTGGCTTCAAACTA 5649
Db 660 CTCAATCGGGCCCTAGAGCAGGATGACAGGCGCGCGCAGCGCTGGCTTATAAGTG 601
Qy 5650 GAACAAGTCATAACCTCTCATGAGCTTAGACAGCTGAAA 5687
Db 600 GAGCAGCTCATTAATGCCATGTCCATTGAGAGCTGAGA 563

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RESULT 10

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US-09-313-294A-6281
; Sequence 6281, Application US/09313294A
; Patent No. 6476212
; GENERAL INFORMATION:
; APPLICANT: Laigudi, Raghunath V.
; APPLICANT: Ito, Laura Y.
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
; FILE REFERENCE: PL-0017 US
; CURRENT APPLICATION NUMBER: US/09/313,294A
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 7600
; SOFTWARE: PERL Program
; SEQ ID NO 6281
; LENGTH: 288
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. 6476212 700351536H1
; NAME/KEY: unsure
; LOCATION: 9, 19, 26, 50, 82, 109, 135, 175-176, 186, 197, 208, 217, 244
; OTHER INFORMATION: a, t, c, g, or other
US-09-313-294A-6281

Query Match
Best Local Similarity 1.0%; Score 57.8; DB 4; Length 288;
Matches 71; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

Qy 4685 GGATGATCTTGAGGATGAAGACATCACCAAGATTTGAGATGATTTGGAAGGACTGA 4744
Db 12 GGGTGTCTGCAANATGAGGACATCACCAAGATTTGAGTGAAGCGGCTCA 71
Qy 4745 ACACACTGCCCACTTACAGGTGCCAGATGTTCCGT 4781
Db 72 ACACACTGATNCAATATCAGGTGAGAGGGGTGTTCT 108

RESULT 11
US-08-232-463-14/c
; Sequence 14, Application US/08232463
; Patent No. 5670367

```

GENERAL INFORMATION:  
APPLICANT: DORNER, F.  
APPLICANT: SCHEIFLINGER, F.  
APPLICANT: FALKNER, F. G.  
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS  
NUMBER OF SEQUENCES: 52  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 1800 Diagonal Road, Suite 500  
CITY: Alexandria  
STATE: VA  
COUNTRY: USA  
ZIP: 22313-0299  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/232,463  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/935,313  
FILING DATE:  
APPLICATION NUMBER: EP 91 114 300.6  
FILING DATE: 26-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 30472/114 IMMU  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 836-9300  
TELEFAX: (703) 683-4109  
TELEX: 899149  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7218 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
CLONE: pTZ9pt-Fls  
US-08-232-463-14

Query Match 0.9%; Score 49.6; DB 1; Length 7218;  
Best Local Similarity 4.0%; Pred. No. 0.058;  
Matches 16; Conservative 219; Mismatches 163; Indels 0; Gaps 0;  
QY 4649 ATATGATCTGGAGTGGGACAGGAGTGGGCAAGGATGATCTTGCAGGATGAACA 4708  
DB 1443 ATTGTACRRR 1384  
QY 4709 TCACCACCAAGATTGGAATGATTGGAAGCGACTGAACACACTGGCCCACTACCAAGTGC 4768  
DB 1383 RR 1324  
QY 4769 CAGATGGTCCGGTGGGATTAAGTTCACAGCAGTGACAGCTAATACGAGTGAACA 4828  
DB 1323 RR 1264  
QY 4829 ACTCCACCGTCTCAGGACCTCAGCAAGTAAATATGAACATGATCCGGTACACGGCA 4888  
DB 1263 RR 1204  
QY 4889 GCGCCGACACCTCGCTACGGACACCTATGATATCTCTGACCTGGAGAGTGGATCA 4948  
DB 1203 RR 1144  
QY 4949 AGATGTGCACCTAGTGAAGACACACGACGACGACGACGACGACGACGACGACG 5008  
DB 1143 RR 1084

QY 5009 GCAAGATGTGTCTGAATCTACTGACCCGACTCCTG 5046  
DB 1083 RR 1046  
RESULT 12  
US-08-607-509-3  
Sequence 3, Application US/08607509  
Patent No. 5878735  
GENERAL INFORMATION:  
APPLICANT: Reed, Steven G.  
TITLE OF INVENTION: METHODS FOR ENHANCEMENT OF PROTECTIVE IMMUNE RESPONSES  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SEED and BERRY LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/607,509  
FILING DATE: 16-FEB-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Maki, David J.  
REGISTRATION NUMBER: 31,392  
REFERENCE/DOCKET NUMBER: 210121.404C3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1867 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 117..1325  
US-08-607-509-3  
Query Match 0.9%; Score 49.4; DB 2; Length 1867;  
Best Local Similarity 45.3%; Pred. No. 0.034;  
Matches 179; Conservative 0; Mismatches 216; Indels 0; Gaps 0;  
QY 4049 AAGGCTTGAAGCTCTTCCGCGAGCTCATCAACAAGGTTTCTCTGCTGCTTCATCC 4108  
DB 403 AGGCGCTGTCTCTCCCGCTCGGAGCTGGCCCTGCAGACGGCGGAGTGATCAGCC 462  
QY 4109 GCAAGCTTGAAGCTTCCGAGCTAGCTTCTCCATGCGCGACCGTGGCAACGTTGCCCTCCTCA 4168  
DB 463 GCATCGGTGAGTCTCTGCGAACAGCTCCAAAGTTCTCGAGACCTTTGTCGCGCGCAGC 522  
QY 4169 TCATGACCGTCTGTCAGAGCAGCTGAGTACGACCTGATGTCTGAAGCAGCTGCTGG 4228  
DB 523 GCGTGCAGGATGACTCGCAAGCTGCGAGCGCGCGCTCATCTGTCGCGCGCAGC 582  
QY 4229 CCGACCTCATTTGACAAAGAACCTGGAGAGCAAGAACCCCTAAGCTGCTGCTCAGGAGGA 4288  
DB 583 GCGCGTCTCGACGCTGATCAAGCGTGGCGCTGCGCACAGAGTGGCTGCGCTGCTGG 642  
QY 4289 CTGAGTCAAGTGGCTGAGAGATGCTGACCAATGTTTACTTTCTCTCTTACAGTTCC 4348  
DB 643 TGCTCGACGAGCTGATGAGATGCTGCTCAGGGCTTCGCGGACGAGTTTACGAGATCT 702  
QY 4349 TCAAGGAGTGTGTCGGGAGCGCCCTCTTCTCCCTGTTCTGTGCCATCAAGCAGCAGATGG 4408

Db 703 TCCGCTTCCTCCGAGGAGATCCAGGTCCGCTCTTCTCCGCCAGCATGTCGGAGGAGG 762  
QY 4409 AGAAGGGCCCATGACGATCAGCGGCGAGGCC 4443  
Db 763 TACTGGAGCTGACGAAGAGTTTCATCGCGAGCCCC 797

RESULT 13  
US-08-634-642-3  
; Sequence 3, Application US/08634642  
; Patent No. 5879687  
; GENERAL INFORMATION:  
; APPLICANT: Reed, Steven G.  
; TITLE OF INVENTION: METHODS FOR ENHANCEMENT OF  
; TITLE OF INVENTION: PROTECTIVE IMMUNE RESPONSES  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SEED and BERRY LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98104-7092  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/634,642  
; FILING DATE: 18-APR-1996  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Maki, David J.  
; REGISTRATION NUMBER: 31,392  
; REFERENCE/DOCKET NUMBER: 210121.404C4  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1867 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 117..1325  
; US-08-634-642-3

Query Match 0.9%; Score 49.4; DB 2; Length 1867;  
Best Local Similarity 45.3%; Pred. No. 0.034;  
Matches 179; Conservative 0; Mismatches 216; Indels 0; Gaps 0;

QY 4049 AAGGCTGAAGCTCTTCCGCCAGCTCATCAACAAGGTCTTCTGCTGCTCTTCATCC 4108  
Db 403 AAGGCTCTGCTCTCTCCCTCCACTCGGAGCTGGCCCTGCAGACGGCGAGGTATCAGCC 462

QY 4109 GCACGCTTGAGTCCAGCGTAGCTTCTCCATGCGCGACCGTGGCAAGTGGCTCTCACTCA 4168  
Db 463 GCATCGGTGAGTTCTGTGCGACAGCTCCAGTCTCGAGACCTTTGTGCGCGGCGCG 522

QY 4169 TCATGACCGTGTGCGAGCAAGCTGGAGTAGCGCCACTGATGTGCTGAGCAGCTGCTGG 4228  
Db 523 CGGTGCGAGGATGACCTGGCGAAGCTGCGAGCGCGGCTCATGCTTGGCGTGGCGCGG 582

QY 4229 CCGACTCATTTACAAGACCTGGAGAGCAAGAACCCCTTAAGTGTGCTCAGGAGGA 4288  
Db 583 GCGCGGTGTCGACGTGATCAAGCTGGCGCGCTCGGACAGAGTCGTGCGGCTGCTGG 642

QY 4289 CTGAGTCAGTGGCTGAGAGATGCTGACCAATGTTTACTTCTCTCTACAGTTCC 4348  
Db 643 TCGTCGACGAGGCTGATGAGATGCTGTCTCAGGGCTTCGCGGACCAAGATTACGAGATCT 702

QY 4349 TCAGGAGTGTGTGGGAGGCCCTTTCTCCCTGTTCTGTGTCATCAGCAGCATGG 4408  
Db 703 TCCGCTTCTCTGCGAAGGACATCCAGGTCCGCTCTTCTCCGCCAGCATGTCGGAGGAGG 762

QY 4409 AGAAGGGCCCATGACGATCAGCGGCGAGGCC 4443  
Db 763 TACTGGAGCTGACGAAGAGTTTCATCGCGAGCCCC 797

RESULT 14  
US-08-989-370-3  
; Sequence 3, Application US/08989370  
; Patent No. 6013268  
; GENERAL INFORMATION:  
; APPLICANT: Reed, Steven G.  
; TITLE OF INVENTION: METHODS FOR ENHANCEMENT OF PROTECTIVE IMMUNE RESPONSES  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SEED and BERRY  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98104-7092  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/989,370  
; FILING DATE: 12-DEC-1997  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Maki, David J.  
; REGISTRATION NUMBER: 31,392  
; REFERENCE/DOCKET NUMBER: 210121.404C5  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1867 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 117..1325  
; US-08-989-370-3

Query Match 0.9%; Score 49.4; DB 3; Length 1867;  
Best Local Similarity 45.3%; Pred. No. 0.034;  
Matches 179; Conservative 0; Mismatches 216; Indels 0; Gaps 0;

QY 4049 AAGGCTGAAGCTCTTCCGCCAGCTCATCAACAAGGTGTTCCTGCTGCTCTTCATCC 4108  
Db 403 AAGGCTCTGCTCTCTCCCTCCACTCGGAGCTGGCCCTGCAGACGGCGAGGTATCAGCC 462

QY 4109 GCACGCTTGAGTCCAGCGTAGCTTCTCCATGCGCGACCGTGGCAAGTGGCTCTCACTCA 4168  
Db 463 GCATCGGTGAGTTCTGTGCGACAGCTCCAGTCTCGAGACCTTTGTGCGCGGCGCG 522

QY 4169 TCATGACCGTGTGCGAGCAAGCTGGAGTAGCGCCACTGATGTGCTGAGCAGCTGCTGG 4228  
Db 523 CGGTGCGAGGATGACCTGGCGAAGCTGCGAGCGCGGCTCATGCTTGGCGTGGCGCGG 582

QY 4229 CCGACTCATTTACAAGACCTGGAGAGCAAGAACCCCTTAAGTGTGCTCAGGAGGA 4288  
Db 583 GCGCGGTGTCGACGTGATCAAGCTGGCGCGCTCGGACAGAGTCGTGCGGCTGCTGG 642

QY 4289 CTGAGTCAGTGGCTGAGAGATGCTGACCAATGTTGTTTACTTCTCTCTCTACAGTTCC 4348  
Db 4289 CTGAGTCAGTGGCTGAGAGATGCTGACCAATGTTGTTTACTTCTCTCTCTCTACAGTTCC 4348



Db 643 TGCTGACGAGGTGATGAGATGCTGCTCAGGGCTTCGGGACCAAGATTACGAGATCT 702  
Qy 4349 TCAAGGAGTGTGTGGGAGCCCTCTTCTCCCTGTGTGTCATCAAGCAGCAGATGG 4408  
Db 703 TCCGCTTCCTGCGGAGGACATCAGGTGCGCTCTTCTCGGACAGATCGCGGAGG 762  
Qy 4409 AGAAGGCCCATGAGCCATCAGGGCGAGGCC 4443  
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RESULT 15  
US-09-398-169-3  
; Sequence 3, Application US/09398169  
; Patent No. 6660840  
; GENERAL INFORMATION:  
; APPLICANT: Reed, Steven G.  
; TITLE OF INVENTION: METHODS FOR ENHANCEMENT OF PROTECTIVE IMMUNE RESPONSES  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SEED and BERRY  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98104-7092  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/398,169  
; FILING DATE: 17-Sep-1999  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/989,370  
; FILING DATE: 12-DEC-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Maki, David J.  
; REGISTRATION NUMBER: 31,392  
; REFERENCE/DOCKET NUMBER: 210121.404C5  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1867 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 117..1325  
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
US-09-398-169-3

Query Match 0.9%; Score 49.4; DB 4; Length 1867;  
Best Local Similarity 45.3%; Pred. No. 0.034;  
Matches 179; Conservative 0; Mismatches 216; Indels 0; Gaps 0;

Qy 4049 AAGGCTGAGCTCTTCGCCAGCTCATCAACAAGGTGTCTGCTGCTTTCATCC 4108  
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Qy 4109 GCACGCTTGAATCCAGCCTAGCTTTCATCGCGGACGGTGGCAACGTGGCTTCACTCA 4168  
Db 463 GCATCGGTGAGTTCCTGTGCAACAGCTCCAGTCTTCGAGACCTTTGTTCGGCGGACGCC 522  
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Qy 4229 CCGACCTCATTTGACAAGAACCTGGAGAGCAAGACCCCTAAGCTGCTGCTCAGGAGGA 4288  
Db 583 GCCGCGTTCGAGCGTGTATCAAGCGTGGCGCTGGCGACAGAGTCTGCTGCGCTGCTGG 642  
Qy 4289 CTGAGTCAGTGGCTGAGAAGATGCTGACCAATTGGTTTACTTTCTCTCTTACAAAGTTC 4348  
Db 643 TGCTCGACGAGGCTGATGAGATGCTGTCTCAGGGCTTCGCGGACCAAGATTTACGAGATCT 702  
Qy 4349 TCAAGGAGTGTGCTGGGAGGCCCTCTTCTCCCTGTTCTGTGTCATCAAGCAGCAGATGG 4408  
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Qy 4409 AGAAGGGGCCCATTTGACGCCATCAGCGGCGAGGCC 4443  
Db 763 TACTGGAGCTGACGAAGAAGTTTCATGCGGACCCC 797

Search completed: May 23, 2004, 11:09:07  
Job time : 271 secs



; PRIOR APPLICATION NUMBER: 60/236,135
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 60/237,434
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/238,321
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: 60/238,399
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,396
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/276,667
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/294,823
; PRIOR FILING DATE: 2001-05-31
; PRIOR APPLICATION NUMBER: 60/304,868
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 12
; LENGTH: 5691
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-964-956-12

Query Match 100.0%; Score 5691; DB 13; Length 5691;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5691; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAAGCCATGCTGGAACCTGGACCTGCTTCTCCACCTCTCTATGTTGGGATG 60
DB 1 ATGAAGCCATGCTGGAACCTGGACCTGCTTCTCTCCACCTCTCTATGTTGGGATG 60

QY 61 GGTCTCTCCATTTGCTCAACCGGAGCCGAGCCGCTGCTCCAGAGCAGCGGTCATT 120
DB 61 GGTCTCTCCATTTGCTCAACCGGAGCCGAGCCGCTGCTCCAGAGCAGCGGTCATT 120

QY 121 GTCACATTCGAGAGAGCCGCGAGGTTTCAATCACCTGGTGGATGAGAGACA 180
DB 121 GTCACATTCGAGAGAGCCGCGAGGTTTCAATCACCTGGTGGATGAGAGACA 180

QY 181 GGNACATTTACTTGGGGGCGTCAATCGATTTACAGCTCTCCAGACCTGAAGTC 240
DB 181 GGNACATTTACTTGGGGGCGTCAATCGATTTACAGCTCTCCAGACCTGAAGTC 240

QY 241 TTGGTGACGATGAGACAGGCGCGGAGGAGCAACCCCAAGTGTTCACCCCGGCATC 300
DB 241 TTGGTGACGATGAGACAGGCGCGGAGGAGCAACCCCAAGTGTTCACCCCGGCATC 300

QY 301 GTCCAGACCTGCAATGAGCCCTGACCAACCAACAAATGTCAACAGATGCTCTCAT 360
DB 301 GTCCAGACCTGCAATGAGCCCTGACCAACCAACAAATGTCAACAGATGCTCTCAT 360

QY 361 GACTACAAGAGAACAGGCTGATTGCTGTGGAGGCTGTACCAAGGCACTTCGAAGCTG 420
DB 361 GACTACAAGAGAACAGGCTGATTGCTGTGGAGGCTGTACCAAGGCACTTCGAAGCTG 420

QY 421 CTGAGGCTGGAGGACCTTTCAAGCTGGGGAGCCCTTATCAAGAGAGCACTATCTG 480
DB 421 CTGAGGCTGGAGGACCTTTCAAGCTGGGGAGCCCTTATCAAGAGAGCACTATCTG 480

QY 481 TCAGGTGTCAACAGAGCGGCTCAGTCTTTGGAGTGTGCTCTTACAGCAACCTGGAT 540
DB 481 TCAGGTGTCAACAGAGCGGCTCAGTCTTTGGAGTGTGCTCTTACAGCAACCTGGAT 540

QY 541 GACAAGCTGTTCAATGCGCAGGCTGGATGGGAGCCGAGTATTTTCCACCATCTCC 600
DB 541 GACAAGCTGTTCAATGCGCAGGCTGGATGGGAGCCGAGTATTTTCCACCATCTCC 600

QY 601 AGCGGAACTGACCAAGAACTCTGAGGCGGATGGCATGTTCCGCTACGCTTCCATGAT 660
DB 601 AGCGGAACTGACCAAGAACTCTGAGGCGGATGGCATGTTCCGCTACGCTTCCATGAT 660

QY 661 GAGTTCGTGCGCTCGATGATTAAGATCCCTTCGGAACCTTCACCATCATCCCTGACTTT 720

661 GAGTTCGTGCGCTCGATGATTAAGATCCCTTCGGAACCTTCACCATCATCCCTGACTTT 720
721 GATATCTACTATGCTATGTTTACAGTGGCAACTTGTCTACTTTTTGACCCCTCCAA 780
721 GATATCTACTATGCTATGTTTACAGTGGCAACTTGTCTACTTTTTGACCCCTCCAA 780
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961 GTGCTTGGCAGGACCTTGGAGTCCATCCAGATGATGACCTGCTCTTCCACCTTCTCC 1020
961 GTGCTTGGCAGGACCTTGGAGTCCATCCAGATGATGACCTGCTCTTCCACCTTCTCC 1020
1021 AAGGGCCAGAGCGGAAATGAAATCCCTGGATGAGTCCGCTCTGTCATCTTCTTTC 1080
1021 AAGGGCCAGAGCGGAAATGAAATCCCTGGATGAGTCCGCTCTGTCATCTTCTTTC 1080
1081 AAGCAGATTAATGACCGCATTAAGGAGCGCTGCTGCTTGTACCGGGCGAGGCAAG 1140
1081 AAGCAGATTAATGACCGCATTAAGGAGCGCTGCTGCTTGTACCGGGCGAGGCAAG 1140
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1141 CTGACCTGCGCTGCTCAAGGTGAAGGACATCCCTGCGAGAGTGGCTCTTTAAACATT 1200
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1201 GACGATTAATCTGTGGCTTGGACATGATGCTCCCTGGAGTGGCTGGAGTGGCTG 1260
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1321 AAGAACCACTCTCTGGCTTTGTGGGACCAAAAGTGGCAAGCTGAAGAGATCCGGTG 1380
1381 GATGACCCAGGGCAACGCTCCAGTATGAGACGCTGAGTGGTGGACCCCGGCCCA 1440
1381 GATGACCCAGGGCAACGCTCCAGTATGAGACGCTGAGTGGTGGACCCCGGCCCA 1440
1441 GTCTCTCGGATATGCGCTTCTCCAGGACCAAGCACTCTACATCATGTGAGAGG 1500
1441 GTCTCTCGGATATGCGCTTCTCCAGGACCAAGCACTCTACATCATGTGAGAGG 1500
1501 CAGCTCAGGAGTCCCTGAGGAGTCCCTGAGTATCAGAGCTGCGGAGTGGCTT 1560
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1561 GGTCTCAGCGACCCCACTGTGGCTGTGTGTGCTGCAACACGCTGCAACCGGAGG 1620
1621 CGGTGTGAGCGGTCCAAAGGAGCCCGGAGTTTGGCTCGGAGATGAAGAGTGTCTCG 1680
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1681 CTGACGCTTCCATCCCAATATCTCGCTCTCTCAGTACAACTGCTGCTGCTGCTG 1740
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Db 1741 ACGTACATGTCCGGAGCTGTGAGTGGCGTCAACTGACACCTTTGAGACCTGTGAG 1800  
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 Db 1801 ATGGATGGGCTGTGCTGGCAATCAGATCCAGTGTCTACTCCCTCAGCCCAAGAGGTG 1860  
 Qy 1861 CCCGGATCATCAGAGATGGGACCAACATGCTGTACAGCTTCAGCTCAAAATCAAAG 1920  
 Db 1861 CCCGGATCATCAGAGATGGGACCAACATGCTGTACAGCTTCAGCTCAAAATCAAAG 1920  
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 Db 1921 GAGACCGGCATGACCTTCGCGACCAACAGCTTTGTCTTTCAAAATTCAGCGTCCACAAT 1980  
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 Db 1981 TCGTGCCTGTCTGCTGGAGTTCATACGCTGCCACTGTGTAAATACCGCATGTC 2040  
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 Db 2041 TGACCCCATGACCCCAAGACCTGCTCTCCAGGAAGCGGAGTGAAGCTGCCGAGGAC 2100  
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 Db 2521 CAGGAGCGAGTGTGCTGAGTGTCTGTCGCAAAAGCAAGTGCACAAACCCCGCATC 2580  
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 Db 2581 ACAGAGATTAATCCCGTGACAGGCCCCGGGAGGGGCAACAAGTCACTATCCGAGG 2640  
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 Db 2641 GAGAACCTGGGCTGGAAATTCGCAATTCGCTCCCATGTCAGAGTTGCTGGGTGGAG 2700  
 Qy 2701 TGCAGCCCTTTAGTGGATGTTACATCCCTGCGAAGACAGATCGTGTGAGATGGGGAG 2760  
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QY 4141 CCGGACCGTGGCAACGTGCGCTCTACTCATCATGACCGTGTCTCAGAGCAAGCTGAGTAC 4200  
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QY 5641 TACAAACTAGAACCAAGTCATAACCTCATGAGCTTAGACAGCTGAATAAA 5691  
Db 5641 TACAAACTAGAACCAAGTCATAACCTCATGAGCTTAGACAGCTGAATAAA 5691

## RESULT 2

US-10-451-010-19  
; Sequence 19, Application US/10451010  
; Publication No. US20040082761A1  
; GENERAL INFORMATION:  
; APPLICANT: INCITE GENOMICS, INC.  
; APPLICANT: DUGGAN, Brendan M.  
; APPLICANT: XU, Yuming  
; APPLICANT: LEE, Sally  
; APPLICANT: LU, Dying Aina M.  
; APPLICANT: WARREN, Bridget A.  
; APPLICANT: YUE, Henry  
; APPLICANT: GIETZEN, Kimberly J.  
; APPLICANT: HONCHELL, Cynthia D.  
; APPLICANT: BURFORD, Neil  
; APPLICANT: BAUGHN, Mariah R.  
; APPLICANT: TANG, Y. Tom  
; APPLICANT: JACKSON, Jennifer L.  
; APPLICANT: GANDHI, Ameena R.  
; APPLICANT: KALLICK, Deborah A.  
; APPLICANT: BANDMAN, Olga  
; APPLICANT: GRAUL, Richard C.  
; APPLICANT: CHAWLA, Narinder K.  
; APPLICANT: LU, Yan  
; APPLICANT: RAMKUMAR, Javalaxmi  
; APPLICANT: YAO, Monique G.  
; APPLICANT: LAL, Preeti G.  
; TITLE OF INVENTION: CELL ADHESION PROTEINS

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; FILE REFERENCE: PF-0867 USN
; CURRENT APPLICATION NUMBER: US/10/451,010
; CURRENT FILING DATE: 2003-06-17
; PRIOR APPLICATION NUMBER: PCT/US01/49206
; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: US 60/256,542
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: US 60/259,604
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 60/260,101
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PERL Program
; SEQ ID NO 19
; LENGTH: 6367
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 7156379CB1
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 166
; OTHER INFORMATION: a, t, c, g, or other
; US-10-451-010-19

Query Match          99.8%; Score 5680.6; DB 17; Length 6367;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 568; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 ATGAAAGCCATGCCCTGGAACTGGACTGCGCTCTCTCCCACTCTCTCATGTGGGCATG 60
DB 566 ATGAAAGCCATGCCCTGGAACTGGACTGCGCTCTCTCCCACTCTCTCATGTGGGCATG 625
QY 61 GGCTCTCCACTTTGCTCACCGGCGACGCCAGCCCCCTGTCCAGAAAGCAGCGGTCAATT 120
DB 626 GGCTCTCCACTTTGCTCACCGGCGACGCCAGCCCCCTGTCCAGAAAGCAGCGGTCAATT 685
QY 121 GTCACATTCCGAGGAGAGCCCGCGAGGGTTTCAATCACTGGTGTGATGAGAGGACA 180
DB 686 GTCACATTCCGAGGAGAGCCCGCGAGGGTTTCAATCACTGGTGTGATGAGAGGACA 745
QY 181 GGACACATTTACTTTGGGGGGCGTCAATCGGATTTTACAAGCTCTCCAGCGACCTGAAGTTC 240
DB 746 GGACACATTTACTTTGGGGGGCGTCAATCGGATTTTACAAGCTCTCCAGCGACCTGAAGTTC 805
QY 241 TTGTTGACGATGAGACAGGGCCGAGCGAGGACAAACCCCAAGTGTATCCCAACCCCGCATC 300
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QY 301 GTCACAGCTCGAATGATGCCCTGACCAACCAACCAATGTCAACAGATGCTCTCTCAT 360
DB 866 GTCACAGCTCGAATGATGCCCTGACCAACCAACCAATGTCAACAGATGCTCTCTCAT 925
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QY 421 CTGAGGCTGGAGGACCTCTCAAGCTGGGGAGCCTTATCATAGAAGGAGGACTACTCTG 480
DB 986 CTGAGGCTGGAGGACCTCTTCAAGCTGGGGAGCCTTATCATAGAAGGAGGACTACTCTG 1045
QY 481 TCAGGTGTCAACGAGAGCGGCTCAGTCTTTGGAGTGATCGTCTCTTACAGCAACCTGGAT 540
DB 1046 TCAGGTGTCAACGAGAGCGGCTCAGTCTTTGGAGTGATCGTCTCTTACAGCAACCTGGAT 1105
QY 541 GACAGGCTGTTCATTTGCCACGCGACGTGATGGGAAGCCGAGTATTTTCCCAACCATCTCC 600
DB 1106 GACAGGCTGTTCATTTGCCACGCGACGTGATGGGAAGCCGAGTATTTTCCCAACCATCTCC 1165
QY 601 AGCCGGAAACTGACCAAGAACTCTGAGCGGAGTGGCATGTTTCGCGTACGCTCTCCATGAT 660
DB 1166 AGCCGGAAACTGACCAAGAACTCTGAGCGGAGTGGCATGTTTCGCGTACGCTCTCCATGAT 1225

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QY 1741 AGGTAAATGTCCTCGAGTGTGACGTGGCGTCAATGCTACCTTTGAGGACTGTGACAG 1800  
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QY 1801 ATGGATGGCTGGTGGTGGCAATCAGATCCAGTGTCTACTCCCTGACGACCAAGAGTG 1860  
Db 2366 ATGGATGGCTGGTGGTGGCAATCAGATCCAGTGTCTACTCCCTGACGACCAAGAGTG 2425  
QY 1861 CCCCAGATCATCACAGAGAAATGGGACCAACCATGTCGACAGCTTCAGCTCAAAATCAAG 1920  
Db 2426 CCCCAGATCATCACAGAGAAATGGGACCAACCATGTCGACAGCTTCAGCTCAAAATCAAG 2485  
QY 1921 GAGACGGGATGACCTTCCGAGCAGCAGCTTTGCTTCTACAAATGAGGCTGCACAAAT 1980  
Db 2486 GAGACGGGATGACCTTCCGAGCAGCAGCTTTGCTTCTACAAATGAGGCTGCACAAAT 2545  
QY 1981 TCGTGCTCTCTCGGTGGAGAGTCCATACCCCTGCACTGCTGTAATATACCGGATGTC 2040  
Db 2546 TCGTGCTCTCTCGGTGGAGAGTCCATACCCCTGCACTGCTGTAATATACCGGATGTC 2605  
QY 2041 TGCACCCATGACCCCAAGACCTGCTCTTCCAGGAGGCGGAGTGAAGTGCCTCCGAGGAC 2100  
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QY 2101 TGCCTCCAGCTGTGAGTGGACCAAGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2160  
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QY 2161 AGCTGAAGGCAAGAACCTCTCCGAGCCGAGTGTGGGACGCTGGCTACGAATGCAATC 2220  
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QY 2221 CTCACATTCAGGGCAGGAGCAGCAGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2280  
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QY 2281 CAGTGCCAGAACCTCTTATTCATGAGGAGTGGAGATCAACAACTGCTGCTGCTGCTGCT 2340  
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QY 2341 TTGACAGTGTGGGATGGGCACTTCAACATTTGACAAACCCAGCTCAGAAATGTTTAC 2400  
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QY 2581 ACAGAGATATTCCTGGTGAAGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2640  
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QY 2641 GAGAACCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2700  
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Db 3326 GCCAAGCCAGCAGCAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3385  
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Db 3386 TTATGGCCCGGCTCTCTACAGCTCTATTACTTCTATGACACTGACTCTCTCAGATCTGAAG 3445  
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Db 3506 GCCGGAAGCAACCTGTGTGTGATGTTTGAAGAGCCCTGTCTCTTCCACAGGCGATCT 3565  
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QY 3121 ACCATCTGCGGATTTGAGCCAGAAATGGAGCATTTGTCAGTGGAAACACACCCATCGCGTA 3180  
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QY 3301 CTGCTCTGGTCTCTGACCAAGTCTGAGCTGAGCTGAGAGGCGCCGAGGAGTTTGGCTTC 3360  
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Db 3926 ATCTGAGCAACCTGCAAGTCCCTCATCTCAACAGACCAACTTCACTACTATCCC 3985  
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QY 3901 CATGAGTCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3960



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Qy 3961 ACCATCGGGTGTCTTCCAGGAATTGAAGCAACCTCTGTCTCCGGACCTTGAAGTTC 4020  
Db 4526 ACCATCGGGTGTCTTCCAGGAATTGAAGCAACCTCTGTCTCCGGACCTTGAAGTTC 4585  
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Db 4586 CCGGGTACCGGAGAGCGTGTGGAGAAAGCGCTGAAGCTCTTCCGCCAGCTCATCAAC 4645  
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Qy 4861 TATGAAAACATGATCCGGTACACGGGACCGCCGACAGCTCCGCTCAGGACACCTATG 4920  
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Qy 5041 CTCTGCGCACTAAGGCACTGACAGATTTTGTGGATGACCTCTTTGAGACCATCTTC 5100  
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Db 6146 AGCGAGGAGATCTTGGACCTCTGACACCATGATGACAGTGGGAAAGCAGAAAATGGCC 6205  
Qy 5641 TACAAACTAGAACAAAGTCAATACCTCATGAGCTTTAGACAGCTGAAA 5687  
Db 6206 TACAAACTAGAACAAAGTCAATACCTCATGAGCTTTAGACAGCTGAGA 6252

RESULT 3  
US-10-175-523-95  
; Sequence 95, Application US/10175523  
; Publication No. US20030096264A1  
; GENERAL INFORMATION:  
; APPLICANT: Brockman, Jeffrey  
; APPLICANT: Evans, David  
; APPLICANT: Klimczak, Leszek  
; APPLICANT: Laeng, Pascal  
; APPLICANT: Palfreyman, Michael  
; APPLICANT: Rajan, Prithi  
; TITLE OF INVENTION: MULTI-PARAMETER HIGH THROUGHPUT SCREENING ASSAYS (MPHTS)  
; FILE REFERENCE: 3235/1J795-US3  
; CURRENT APPLICATION NUMBER: US/10/175,523  
; CURRENT FILING DATE: 2002-06-18  
; PRIOR APPLICATION NUMBER: US 60/299,151  
; PRIOR FILING DATE: 2001-06-18  
; PRIOR APPLICATION NUMBER: US 60/317,828  
; PRIOR FILING DATE: 2001-09-07  
; PRIOR APPLICATION NUMBER: US 60/325,150  
; PRIOR FILING DATE: 2001-09-25  
; PRIOR APPLICATION NUMBER: US 60/333,047  
; PRIOR FILING DATE: 2001-11-14  
; PRIOR APPLICATION NUMBER: US 60/349,936  
; PRIOR FILING DATE: 2002-01-18  
; PRIOR APPLICATION NUMBER: US 60/361,834



; PRIOR FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatenIn version 3.1
; SEQ ID NO 95
; LENGTH: 6730
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(6730)
; OTHER INFORMATION: where n may be a or g or c or t/u, unknown, or other
US-10-175-523-95

Query Match 48.8%; Score 2778.4; DB 15; Length 6730;
Best Local Similarity 69.3%; P-red. No. 0;
Matches 3858; Conservative 0; Mismatches 1691; Indels 15; Gaps 5;

Qy 137 AGCCGCCAGGGTTCAATCACCCTGGTGGATGAGGAGGACAGACACATTTACTTGG 196
Db 683 ATCGTACTGGACTTTCAACCACTTTGACTGTACACCGAAGAACAGGGGTGTGTATGG 742

Qy 197 GGCCCTCAATCGATTTTCAAGCTCTCCAGGACCTGAAGGTCTTTGGTACGACATGAGA 256
Db 743 GGGCTATCAATCGTGTCTACAGTTGACTTGGCAACCTCACCATCCAGGTGGCTCAACA 802

Qy 257 CAGGGCCGAGAGGACAAACCCCAAGTGTACCCACCCCGCATCGTCCAGACCTGCAATG 316
Db 803 CAGGGCCGAGAGGACAAACAGGCTTGTACCCACCCCTCATTTGTACAGCCCTTGAGTG 862

Qy 317 AGCCCTGACCAACCAACATGTCAACAAAGTGTCTCATAGACTTACAGGAGAACCA 376
Db 863 AAGTGTCTACACTCACCAACATGTCAACAACTACTGATCATTTGACTACTCTGAGATC 922

Qy 377 GGCTGATTTGCTGGAGGCTGTACAGGCACTGTGCAAGTGTGCAAGTGTGGAGGAC 436
Db 923 GCCTGTGGCTCTCGAAGCCTTACCAAGGTGTGTCAGGCTTTGCAAGTCTCCGACTAGATG 982

Qy 437 TCTTCAAGCTGGGGAGCCTTATCATAAAGAGGACACTATCTGTGAGGTGTCAACGAGA 496
Db 983 TCTTCACTCTGGTGGAGGACATCCACAGAGGAACTACTTGTCCAGTGTCAATPAGA 1042

Qy 497 GCGGCTCAGTCTTTGAGTGTATCGTCTCTACAGAACTGTGATGACAGCTGTTCATG 556
Db 1043 CAGGCACCATGTATGTGTGTGCTCTGAGGGGGAAGATGGCAAGCTTTTATCG 1102

Qy 557 CCAGGAGTGGAGGAGGAGGAGTATTTTCCACCATCTCCAGCCGGAACCTGACCA 616
Db 1103 GCATGTGTGGATGGCAAGAGATTTACTTCCCTACTGTGTCAGCCGCAAGTGCCTC 1162

Qy 617 AGAATCTGAGGGGATGGCATGTTCCGATACGTCTTCCATGATGAGTTGCGGCTCGA 676
Db 1163 GTGACCTGAGTCTTCAGCAATGCTGGACTATGAGCTCCACAGTGAATTTGTCTCCTCC 1222

Qy 677 TGATTAGATCCCTTCGACACACTTACCATCATCCCTGACTTTGATATCTACTATGTCT 736
Db 1223 TCATCAAGATTCCTCTGACACCTTAGCCCTGGTCTCTCACTTCGACATCTTCTACATCT 1282

Qy 737 ATGGTTTTAGCAGTGGCAACTTTGTCTACTTTTTGACCTTCCAACTTGAGATGGTCTC 796
Db 1283 ATGGCTTTGCGAGTGGGGGTTTGTCTACTTTCTCACTGTCCAGCCAGACACCCCTGAC 1342

Qy 797 CACAGGCTCA---CCACAGAGAGAGGAGTGTATACATCCAGCTCGTGGGTTTGA 853
Db 1343 GCATGGCCATCAATTCAGCTGGAGACCTTCTTATACCTCAAGAAATTTGGGCTCTGCA 1402

Qy 854 AGGAGGACACAGCCTTCAACTCTCTATGTAGAGGTGCCCATTTGGCTGTGAGCGCAGTGGG 913
Db 1403 AGGATGACCCCAAGTTTCACTCCCTATGTGTCCTGCTTTTGGCTGACACAGTCTGGG 1462

Qy 914 TGGAGTACCGCTGTGAGGCTGCTACCTGTCCAAAGCGGGGCGTGTGCTTGGCAGGA 973
Db 1463 TGGAAATATGCGCTTCTGAGGAGCTTACCTTGTGAAGCCAGGGGAAGCTCTAGCTCAGG 1522

Qy 974 CCCTTGGAGTCCATCCAGATGATGACCTGTCTTCCACCTCTTCCAAAGGGCCAGAGC 1033
Db 1523 CTTTCAACATCAGCAGCAGCAAGATGTCTGTGTTGCCATCTTTTCCAAAGGGCCAGAGC 1582

Qy 1034 GGAATATGAATCCCTGGATGAGTCCGCGCTGTGCATCTTTCATCTTTGAAGCAGATAAATG 1093
Db 1583 AGTACCAACACCCCTGTGATGACTCTGCTCTGTGCTTCCCACTCCGGGCACTCACT 1642

Qy 1094 ACCGATTTAAGGAGCGCTGCACTCTTGTGTACCGGGCGAGGGCACTGTGAGCTGGCCT 1153
Db 1643 TGCMAATCAAGGAGCGGTGTGAGTCTCTTACACGAGAGGGCACTTTGGAGCTCAACT 1702

Qy 1154 GGCTCAAGTGAAGGACATCCCTGAGCAGTGGCTCTTAACCATTTGACGATTAATCTCT 1213
Db 1703 GGCTGTGGGAAAGGATGTGAGTGCACCAAGGCGCTGTCCCAATCGATGATTAATCTCT 1762

Qy 1214 GTGCTCTGACATGAATGTCTCCCTGGAGTGTCCGACATGTGTCGTCGTCGTAATTCCTG 1273
Db 1763 GCGCTCTGGACATCAACAGCTCTGGAGGCTCCACTCTGTGGAGGACTGACCTGT 1822

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RESULT 4
US-10-312-352-70
; Sequence 70, Application US/10312352
; Publication No. US20040053824A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.; TANG, Y. Tom
; APPLICANT: YUE, Henry; AZIMZAI, Yalda
; APPLICANT: HE, Ann; BATRA, Sajeev
; APPLICANT: LO, Terence P.; NGUYEN, Damiel B.
; APPLICANT: BURRILL, John D.; MARCUS, Gregory A.
; APPLICANT: ZINGLER, Kurt A.; GANDHI, Ameena R.
; APPLICANT: LAL, Preeti G.; KEARNEY, Liam
; APPLICANT: BURFORD, Neil; YAO, Monique G.
; APPLICANT: CHAWLA, Narinder K.; KHAN, Vicki S.
; APPLICANT: BAUGHN, Mariah R.; HAPALIA, April, J.A.
; APPLICANT: POLICKY, Jennifer L.; AU-YOUNG, Janice K.
; APPLICANT: LU, Yan; BOROWSKI, Mark L.
; APPLICANT: LU, Dying Aina M.; RAMKUMAR, Jayalaxmi
; APPLICANT: YANG, Junning; GURURAJAN, Rajagopal
; APPLICANT: WARREN, Bridget A.; GIETZEN, Kimberly J.
; APPLICANT: XU, Yuming; KALLICK, Deborah A.
; APPLICANT: LEE, Ernestine A.; THANGAVELU, Kavitha
; APPLICANT: DELEGEANE, Angelo M.; LEE, Sally
; TITLE OF INVENTION: EXTRACELLULAR MATRIX AND CELL ADHESION MOLECULES
; FILE REFERENCE: PF-0794 USN
; CURRENT APPLICATION NUMBER: US/10/312,352
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; PRIOR FILING DATE: 2000-10-12
; PRIOR APPLICATION NUMBER: US 60/240,106
; PRIOR FILING DATE: 2000-10-12
; PRIOR APPLICATION NUMBER: US 60/244,021
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/248,887
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/249,570
; PRIOR FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PERL Program
; SEQ ID NO 70
; LENGTH: 6147
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; TYPE: DNA		1202	CCGGTGAAGCCACCAAGAGTGCAGCTGTGCTCTTACCGTTCAGGGCCATCAAGGA	1261
; ORGANISM: Homo sapiens		1095	CCGATTAAAGAGCGCTGAGTCTTTGTTACCGGGCGAGGCGACGCTGGACCTGGCCCTG	1154
; FEATURE:		1262	GAAGATTAAAGAGCGCATCCAGTCTCTGTACCGTGTGAGGCGAAGCTCTCCCTGCCCGTG	1321
; NAME/KEY: misc.feature		1155	GCTCAAGGTGAAGACATCCCTTCAGCAGTGCCTCTTAAACATTGACGATAAATCTTCTG	1214
; OTHER INFORMATION: Incyte ID No. US20040053824A1 7204554CB1		1322	CTGCTCAACAGAGAGCTGGGTGATCAACTCGCCCTGCAGATCGATGAGCACTTCTG	1381
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Best Local Similarity 68.4%; Pred. No. 0;		1275	CACGGAGCAGAGGACCGCATGACGCTGTCTATCGCATATGCTTCAAGAACCACTCTCT	1334
Matches 3811; Conservative		1442	CGTGGACAAAGATGATGSCCTGACCCCGTGGCTGCTTATGACTATCGGGCGCGACTGT	1501
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3357	CTTATCTT	GGACAAGT	CCAGTCC	GTCTCAT	CTCTCA	ACAAGCA	CTTCACT	3416
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3959	CTACAAGC	GCAGTCA	CGAGAT	GCTCAG	CGCAC	CACTCA	AGCGGCT	4018
3837	CAACCTGG	AGTCCG	GTGSCCT	CGAGT	GTCA	AGGAAG	CCTTTG	3896
4019	CAACCTGG	AGTCCG	GTGSCCT	CGAAT	GTCA	AGGAAG	CCTTTG	4078
3897	CATCCATG	AGCTGAC	CAGTGA	CTCGAT	GGAGC	CGGGAT	TCGTT	3956
4079	CATCCAG	AGCTGAC	CAATGAC	CTGAC	GGTGC	CGCAT	CCCCCT	4138
3957	TTACACCA	TGCGG	TGCTGTTCC	AGGAT	TGAAC	CA	CCCTGCT	4016
4139	ATATGC	ATCGGG	TGCTCTTT	CTGGGAT	TCGAG	ACCA	CCCTGCT	4198
4017	GGTCCCGG	GTACCG	GAGCGGT	GTGGAGA	AGGCCT	CTGA	AGCTCT	4076
4199	GGT-----	GCAGS	CCAATGT	GTGAGA	AGT	CGTGA	CACTGTT	4246
4077	CAACAACA	AGGTGTT	CTGTGTC	TTCTCAT	CCGAC	CGCTTG	AGTCC	4136
4247	GACCAAGA	ACATTC	CTGTGAC	CTTCTCAT	TCGCTCAT	TA	GACG	4306
4137	CATGCGG	ACCGTGG	CAACCGT	GGCCTCA	CTCAT	CA	TGAC	4196
4307	CATGCGGA	CCGCGG	NAATGT	GGCCTCG	CTCAT	TA	GACG	4366
4197	GTACGCC	ACTGTAT	GTGTGA	AGCAGT	GTCTG	GGCC	AGCTCAT	4256
4367	ATACGCC	CA	CAGGGT	GTCTCA	AGCAGT	GTCTT	CCGAC	4426
4257	CAGAAC	CA	CCCTTA	AGCTGTCT	CA	GGAG	CACTG	4316
4427	CAAGAA	CA	CCCCA	AGTGTCT	AC	TG	CCCG	4486
4317	CAATTTGG	TTACTTTT	CTCTCT	CTACA	AGTTT	CCTCA	AGAGT	4376

Db 4487 TAAGTGGTCAACCTTCTCTTGTATTAAGTTCTCAAGGAGTGGCTGGGGAGCCGCTGTT 4546  
Qy 4377 CTCCTCTGTTCTGTGTCATCAAGCAGCAGATGAGAGAGGCCCCCATTTGACGCCATCAGCGG 4436  
Db 4547 CATGCTGTACTGCGCCATCAAGCAGCAGATGAGAGAGGCCCCCATTTGACGCCATCAGCGG 4606  
Qy 4437 CGAGGCGCCCTACTCTGAGCGAGAGCAAGCTCATCCGCGCAGAGATGACTCAAAAC 4496  
Db 4607 TGAGGCAACGCTACTCTGAGTGAAGCAAGCTCATCCGCGCAGAGATGACTCAAGAC 4666  
Qy 4497 CTTGTCCTGAGTGTGTGTCAGCCCAAGCAATGCCAGCGCCGAGGTCCTCCAGTAAGAT 4556  
Db 4667 ACTGACCTGAACTGTGTGAACCTTGAGAAATGAGAAATGCACTGAGGTCGCGGTGAAGG 4726  
Qy 4557 CTTCAACTGTGACCACTCACTCAGTCAAGCAGAGAGATTTCTGATGCACTCTCAAGAA 4616  
Db 4727 GCTGGACTGTGACACCGTCAACCGCCCAAGGAGAGCTGCTGGACGCTGCTCAAGGG 4786  
Qy 4617 TGTGCTTGTCTCCACCGGCCCAAGCTGCAGATATGATCTGAGTGGAGTGGCAAGAG 4676  
Db 4787 CGTGGCCCTACTCTCCAGCGGCCCAAGGCCCGGACATGACCTGGAGTGGCGCGCCAGGGCGG 4846  
Qy 4677 TGCGGCAAGATGATCTTCAGAGTGAAGACATCAACCCACAGATTTGAGATTTGAA 4736  
Db 4847 CATGGCGCGCATCATCTGAGCAGAGAGAGCTCAACCAAGATTTGACAGATTTGAA 4906  
Qy 4737 GCACTGAACACACTGCGCCCACTTACAGGTGCCAGATGTTCCGTGGTGGCATTAGTGC 4796  
Db 4907 GAGGCTGAACACACTGCTCACTTACAGGTGACAGAGGCTCTCGGTGGCACTGCTGCC 4966  
Qy 4797 CAGCAGGTGACAGCTATTAAGCAGTGAACACTCAACCGCTCCAGAGCTCAGCAG 4856  
Db 4967 CAAGCAGAGCTCGCCTTACCAATCTCCACTCTCTCCACTTCAACAG---TCCTCAG 5023  
Qy 4857 TAAATATGAATAATGATCGGTGACAGGGGAGCGGAGCGCCAGCTCCGCTCAGGACACC 4916  
Db 5024 CAGATCAGAGAGATGCTGCGCAGCGCCAGCAGCGCCGAGCAGCTCGCGCAGCC 5083  
Qy 4917 TATGATCACTCTGACCTGAGAGTGGAGTCAAGATGTGGACCTAGTGAAGAACAGCA 4976  
Db 5084 CATGATCAGCCCGACTGAGAGCGGACCAAGCTGTGGACCTGTGTGAAGAACAGCA 5143  
Qy 4977 GCACGGAGACAGAGAGAGGGGACCGGGGAGCAAGATGTTGTCTGAATACTCCTGAC 5036  
Db 5144 CCACCTGACACAGCTGAGGCTGACCGCGGAGCAAGATGTTGTCTGGAGATCTACTTAC 5203  
Qy 5037 CCGACTCTGCGCCACTAAGGACACTGAGAGTGTGGAGTGTGGATGACCTTTTGAGACCAT 5096  
Db 5204 ACGCTACTGGCCACCAAGGCGCACTGAGAGATTTGTGGAGACCTGTTTGAGACCAT 5263  
Qy 5097 CTTTACGACGGCACACCGTGGCTCTGCGGCGCCCTGCGCATCAAGTACATGTTGACTT 5156  
Db 5264 CTTTACGACGGCACACCGGCGCTCAGCCCTGCGCTGGCCATCAAGTACATGTTGACTT 5323  
Qy 5157 CCGGATGAGCGGCTGATAAACATGGCTTCATGACCGCGCAGCTCCGCTACCTGGA 5216  
Db 5324 CTTGATGAGCGGCGCAAGCAGCAGATCCAGATGTGAGTGGCGCCACCTGGA 5383  
Qy 5217 GAGCAATGCTGCTGCTGAGGTTTGGGTCAACATGATCAAGAACCGGCGAGTTGTGTT 5276  
Db 5384 GAGCAATGCTGCTGCTGAGGTTTGGGTCAACATGATCAAGAACCGGCGAGTTGTGTT 5443  
Qy 5277 TGACATCCATAAGAACAGCATCACAGCGCTGCTCTGTTGGTGGCTCAGACCTTAT 5336  
Db 5444 CGACATTCACAGAACAGCATCACAGCGCTGCTCTGTTGGTGGCTCAGACCTTAT 5503  
Qy 5337 GGACTCTTGTCTCAAGTCAAGCAGCGGCTGGGCAAGGACTCGGCTCCCAACAGCTGCT 5396  
Db 5504 GGACTCTTGTCTCAAGTCAAGCAGCGGCTGGGCAAGGACTCGGCTCCCAACAGCTGCT 5563  
Qy 5397 GTATGCCAAGGATCCCAAGTCAAGATTCGGTGGAGAGTATTACTCAGACATAGG 5456

Db 5564 CTACGCCAAGGACATCCCAACTACAGAGCTGGTGGAGAGGTACTATGACAGATCGC 5623  
Qy 5457 GAAGATGCGAGCATCAGCAGCAAGACATGAACGATATACCTGGCTGAGCAGTCCCGAT 5516  
Db 5624 CAAGATGCGAGCATCAGCAGCAAGACATGAAGTGGTATCTGGCTGAGCAGTCCCGCT 5683  
Qy 5517 GCACATGATGATTTCAACACCATGAGTGCACCTCTCAGAGATCTTCTCTATGTTGGCAA 5576  
Db 5684 GACCTGAGCAGTTCAACAGCATGAGCGCTTGCACGAGATCTACTCTTACATCACC 5743  
Qy 5577 ATACAGCGAGGAGATCTTGGACCTCTTGGACCTCCTGACCAAGATGACAGTGTGGAAAGCAAACT 5636  
Db 5744 GTACAGGATGAGATCTTGGCAGCGCTTGGAGAGGATGAGCAGCGCGCGCAGCGCT 5803  
Qy 5637 GCGCTACCAACTAGAACAGTCAATAACCTCATGAGCTTAGACAGCTGA 5685  
Db 5804 GCGGAGCAAGCTGGAGCAGTGGTGGACACAGTGGCCTGAGCAGCTGA 5852

## RESULT 5

US-10-087-684-31  
; Sequence 31, Application US/10087684  
; Publication No. US20040029116A1  
; GENERAL INFORMATION:  
; APPLICANT: Edinger, Shlomit R.  
; APPLICANT: MacDougall, John R.  
; APPLICANT: Millet, Isabelle  
; APPLICANT: Ellerman, Karen  
; APPLICANT: Stone, David J.  
; APPLICANT: Grosse, William M.  
; APPLICANT: Lepley, Denise M.  
; APPLICANT: Rieger, Daniel K.  
; APPLICANT: Burgess, Catherine E.  
; APPLICANT: Casman, Stacie, J.  
; APPLICANT: Spytek, Kimberly A.  
; APPLICANT: Boldog, Ferenc L.  
; APPLICANT: Li, Li  
; APPLICANT: Padigaru, Muralidhara  
; APPLICANT: Mishra, Vishnu  
; APPLICANT: Shenoy, Suresh G.  
; APPLICANT: Pastelli, Luca  
; APPLICANT: Tchernev, Velizar T.  
; APPLICANT: Vernet, Corine A.M.  
; APPLICANT: Zerhusen, Bryan D.  
; APPLICANT: Malyankar, Uriel M.  
; APPLICANT: Guo, Xiaojia  
; APPLICANT: Miller, Charles E.  
; APPLICANT: Gangolli, Esha A.  
; TITLE OF INVENTION: PROTEINS AND NUCLEIC ACIDS ENCODING SAME  
; FILE REFERENCE: 21402-214 CIP  
; CURRENT APPLICATION NUMBER: US/10/087,684  
; PRIOR FILING DATE: 2003-03-10  
; PRIOR APPLICATION NUMBER: 60/253,834  
; PRIOR FILING DATE: 2000-11-29  
; PRIOR APPLICATION NUMBER: 60/250,926  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: 60/264,180  
; PRIOR FILING DATE: 2001-01-25  
; PRIOR APPLICATION NUMBER: 60/274,194  
; PRIOR FILING DATE: 2001-03-08  
; PRIOR APPLICATION NUMBER: 60/313,656  
; PRIOR FILING DATE: 2001-08-20  
; PRIOR APPLICATION NUMBER: 60/327,456  
; PRIOR FILING DATE: 2001-10-05  
; NUMBER OF SEQ ID NOS: 220  
; SOFTWARE: CuraSeqlist version 0.1  
; SEQ ID NO 31  
; LENGTH: 5895  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (23)..(5797)



US-10-087-684-31

Query Match				44.5%; Score 2533.8; DB 13; Length 5895;
Best Local Similarity				68.0%; Pred. No. 0;
Matches 3812; Conservative				0; Mismatches 1712; Indels 81; Gaps 17;
QY	141	CGCCAGGTTTCAATCAGCTGGTGGATGAGAGGACAGACATTTACTTGGGGC	200	
DB	217	CGACTGGGGCCCTACCCAGCTAGTGGTATGAGCAGACAGCGAGGTGTATGGGGC	276	
QY	201	CGTCAATCGGATTTTAAAGCTCTCCAGCGACCTGAAGGTCTTGGTGACGCATGAGACAGG	260	
DB	277	AGTGAACCCATCTATAAGCTGTGCGGGAACTGACACTGCTGCGGGCCCACTCACGGG	336	
QY	261	GCGGACGAGGACCAACCCAGTGTATCCACCCCGCATCTGTCAGACTGCGAAATGAGCC	320	
DB	337	CCCTGTGGAGGACCAACGAGAGTGTACCCCGCGCCAGCGTGTGCTGCGCCCAAGG	396	
QY	321	CTTGACACCAACCAATGTCAACAGATGCTCTCTATAGACTCAAGAGGAAACAGGCT	380	
DB	397	CTTGGGAGTACTGACAAAGCTCAACAGCTGCTGCTGGACTATGCGGCTAACCGCT	456	
QY	381	GATTGCTGTGGAGCTGTACAGGCACTGTCAAGCTGCTGAGGCTGGAGCACTCTT	440	
DB	457	GCTGGCTGTGGCAGCGCTTCCAGGGCATCTGCCAGTTCCCTGCTGTGGACGATCTCT	516	
QY	441	CAAGCTGGGGAGCCTTATCATAGAGAGGACACTATCTGTAGGTGTCAACGAGAGCGG	500	
DB	517	CAAACTGGGTGAGCCACACACCGTAAGGACACTACTGTCCAGGCTGCAGGAGGCGAG	576	
QY	501	CTCAGTCTTTGGAGTGTATGCTCTCCACA-----GCAACTGGATGACAGCTGTTAT	554	
DB	577	CAGCTGGCGGGGTGCTATTGCCGGGCCACCGGGCCAGGGCCAGGCTCTTCT	636	
QY	555	TGCCAGGAGTGGTGGAGCCCGAGTATTTTCCACCCTCCAGCGCGGAACTGAC	614	
DB	637	GGGACACCCCATGATGGCAAGTCCGAGTACTTCCCACTGTCAGCGCTCGGCTCAT	696	
QY	615	CAAGAACTCTGAGCGGATGGCATGTTCGGGTAGCTTCCATGATGAGTTCGGCCCTC	674	
DB	697	GGCCAAACAGAGGATGCCACATGTTCGGCTTCGTGTACCAAGGATGAGTTTGTGTATC	756	
QY	675	GATGATTAGATCCCTCGGACACCTTACCATCATCCCTGACTTGTATCTACTATGT	734	
DB	757	ACAGCTCAAGATCCCTTCGGACACGCTGTCAAGTTCCCGGCTTTGACATCTACTATGT	816	
QY	735	CTATGGTTTTAGCAGTGGCACTTTGTACTACTTTTTGACCTCCAACTGAGATGGTGC	794	
DB	817	GTACAGCTTCCGACAGCAGAGTTTGTCTACTACTCTCACGCTGCAGCTAGACACAGCT	876	
QY	795	TCCACAGGCTCCACCAAGGAGCAGGTGTATACATCCAGCTCGTAGGCTTTGCAA	854	
DB	877	GACCTCGCTGATCCCGCGGCGAGCACTTCTCACGTCCAAAGATCGTGGGCTCTGTGT	936	
QY	855	GGAGACACAGCTTCAACTCTATGTAGAGTGGCCATTTGGCTGTGAGCGCAGTGGGT	914	
DB	937	GGACGACCCCAATTTCTACTGCTAGTGTAGTTCCCATTTGGCTGCGAGCAGCGGGGT	996	
QY	915	GAGTACCGCTGTGAGGCTGCTCTGTCCAAAGCGGGGCGCTGTGGCAGGAC	974	
DB	997	GAGTACCGCTGTGTCAGGATGCTCTACTGAGCGGGCGCGCTGCGCCCAACCA	1056	
QY	975	CCTTGGAGTCCATCCAGATGATGACCTGCTCTTCAACCGCTCTTCCAAAGGCGCCAGAGCG	1034	
DB	1057	GCTGGGCTGGCTGAGGACAGGAGCGTGTCTTCTACTGTGTTCGCCAGGGCCAGAGAA	1116	
QY	1035	GAAATGAAATCCCTGGATGAGTGGCCCTGTGATCTTCTATGAGCAGATTAATGA	1094	
DB	1117	CGCGTGAAGCCACCAAGGAGTACGACTGTGCTGTCTTCACTGCTGAGGGCCATCAAGGA	1176	
QY	1095	CCGCAATTAAGGAGCGCTGAGTCTTGTATCCGGGGCGAGGCGCTGAGACCTGGGCTG	1154	
DB	1177	GAAGATTAGGAGCGCATCCAGTCTGTCTACCGTGTGTGAGGGCAAGCTCTCCCTGCGCTG	1236	

QY	1155	GCTCAAGGTGAGGACATCCCTGCGAGCAGTGGCTTTTAAACATTGACGATAACTTCTG	1214	
DB	1237	GCTGCTCAACAGGAGCTGGCTGCTATCACTCGCCCTGCGAGTCGATGACGACTTCTG	1296	
QY	1215	TGSCCTGGACATGAATGCTCCCTGGAGTGTCCGACATGCTGGTGGATTTCCCGTCTT	1274	
DB	1297	CGGCGAGGACTTCAACAGCCCTCGGGGGCAGTCAACATTGAGGGGACGCCCTGTT	1356	
QY	1275	CAGGAGGACAGGACCGGATGACGCTGTCTGCGCATATGTCTACAAGAACACACTCTCT	1334	
DB	1357	CGTGGACAGAGATGATGCGCTGACCGCGTGGCTGCTATGACTATCGGGGCGGACTGT	1416	
QY	1335	GGCCTTTTGTGGGACCAAAAGTGGCAGCTGAGTGAAGAGATCCGGGTGGATGGACCCA	1390	
DB	1417	GGTATTGCGCGGACACGGAAGTGGCGCATCCCAAGATCCTGGTGGACCTCTCAAAACC	1476	
QY	1391	-----GGGGCAACGCGCTTCCAGGACACGAGTGGTGGTGGACCCCGGCGCAGTCT	1445	
DB	1477	CGTGGCGCGCTGCGCTTGGCCTACGAGACGCTGTGGCCAGAGGGGAGCCCCATCT	1536	
QY	1446	CGGGATATGGCTTCTTCCAAAGGACACGAGCAACTCTTACATCATGTCTGAGAGGAGCT	1505	
DB	1537	CGGAGACCTCTGCTCTCAGCCCAACACACAGTACTCTTACGCCATGACCCGAGAGCAGT	1596	
QY	1506	CACGAGTCTCTGTGGAGTCTGTGTCTGATATCAGAGCTGCGGAGTGCCTTGGCTC	1565	
DB	1597	GACCGGGTGTCTGTGGAGAGCTGTGTGACAGTACACGCTCTGTGAGCTGTCTGGGTC	1656	
QY	1566	AGGCGACCCCACTGTGGCTGGTGTCTGTCACAAACAGTGCACCCGGAAGAGAGCGGT	1625	
DB	1657	ACGGGACCCCACTGTGGCTGGTGTCTGTGACAGCATGTCTGCGGGGGGACGCGCTG	1716	
QY	1626	TGAGCGGTCAAGAGGCGCGCAGGTTTGGCTCGGAGATGAGCAGTGTCTCGGCTGAC	1685	
DB	1717	TGAGCGAGCAGACAGGCGCCAGCGCTTGTCTGCGGACCTGTGTCAGTGTGTGACGCTGAC	1776	
QY	1686	GGTCCATCCCAACAAATATCTCCGTCTCTCAGTACAAAGTGC-----TGCTGGTCTTGGAGAC	1742	
DB	1777	TGTGAGCGCCGCAATGTGTCTGTACCATGTCTCCAGTGTCCAGTACTTGTGCTGCGAGC	1836	
QY	1743	GTACAAATCTCCGAGCTGTGAGTGGGTCACTGACACCTTTGAGGACCTGTGAGAGAT	1802	
DB	1837	CTGGAACTGTGCTGACCTCTCAGTGGCGTCACTGTCTCTTCGAGGACTTTCAGGAACTC	1896	
QY	1803	GGTGGGTGTCTGTGGCAATCAGATCCAGTGTCTTCTCCCTTCGAGCAAGAGAGTGGC	1862	
DB	1897	TGAGAGCTCTTGGAGGATGCGCGATCCACTGCGCTCACCTCCGCGCGGAGGTGGC	1956	
QY	1863	CGGGATCA-----TCACAGAGAAATGGGGAACAATGTCTGTAAGCTTCAAGTCAATC	1916	
DB	1957	GCCCATCACGCGGGCCAGGGGTGAGGGAGACACGCGGTGTGTAACCTCTACCTAAAGTC	2016	
QY	1917	AAAGGAGACCGCATGACCTTCCGCGACACAGCTTTCTTCTTACAAATTTGAGCGTCCA	1976	
DB	2017	CAAGGAGACAGGGAAGAGTTTGGCTGTGTGAGCTTCTCTTCTTCTTCTTCTTCTTCTTCT	2076	
QY	1977	CAATTCG---TGCCCTGTCTGTGGAGAGTCCATACCGCTGCGCACTGGTGTAAATACCG	2033	
DB	2077	CCAGTGGAGCTGCTGTCTGTGTCAACGGCTCTTCTCCCTGCGCACTGGTGTGCAATACCG	2136	
QY	2034	GATGTCTGACCCCATGACCCCAAGACCTGCTCTTCCAGGAGGCGCGAGTGAAGTGC	2093	
DB	2137	CCAGTGTGTGACACACACAGCTGGCTGACTGCGGCTTCTTGGAGGGCGGCTGTCAAGTGT	2196	
QY	2094	CGAGGACTGCGCCCGCAGCTGCTGCGAGTGGACAAAGATCTTGTGCTGCGGTGAGGTGATCA	2153	
DB	2197	TGAGGACTGCCACAGATCTGCGCTTCCACGCGAGATCTACGTGCGAGTGGAGTGGTAAA	2256	
QY	2154	GCTATACAGCTGAGGCGCAAGAACCTCCCGCAGCCCGAGTCTGCGGACGCTGGCTACCA	2213	
DB	2257	ACCATCACCTTGGCGCGCAGGAACTGTGCAACAGCCACAGTCAGGCGGACGCTGGATGTA	2316	

Qy	2214	ATGCATCTCAACATTACAGGCGAGGAGCAGCGAGTGGCCGCTTCAACAGCTC	2273
Db	2317	GTGCCTCTTTCCACATCCCGGGCAGCCCGCCGCTGTCAACGCCCTTCGCTTCAACAGCTC	2376
Qy	2274	CAGCGTACAGTGCAGAAACACCTCTTTATTCCTATGAAGGGATGGAGATCAACAACTCTGCC	2333
Db	2377	CAGCTTCGATGCCAAATTCCTCGTACTCTTACGAGGGGAACGATGTCAAGGACCTGCC	2436
Qy	2234	CCTGGAGTTTGACAGTCTGTGGAAATGGGCACCTTCAACATTGACAAACCCAGCTCAGAATAA	2393
Db	2437	AGTGAACCTGTCTAGTCTGTGGAAACGGCAACTTGTCTATTGACAAACCCACAGAAATCCCA	2496
Qy	2394	AGTTCACTCTTCAAGTGTGGAGCCATCGTGAGAGCTGCGGGCTGTGCTCAAGGCTGA	2453
Db	2497	GGGCACTCTTCAAGTGCCTCGCGAGAGCTCGGCTCTGCTCTCAAGGCCGA	2556
Qy	2454	CCAGACCTTCGATGTGGTGTGTCAGGCGCCAGGCCAGTGCACCTCTGCGCCACACTG	2513
Db	2557	CCCGCTTCGAGTGCAGATGTGTGCTGTGCGAGCGCCGCTGCTCCCTGCGACACCACTG	2616
Qy	2514	CCCTGCCCA---GGAGAGCAGTGGCTGGAGCTGTCTGTGTGCCAAAGCAAGTGCACAA	2570
Db	2617	CGTGTCCGACACACCTCTGCATCTGTGTGAATGACGCGCGTCAAGGAGCAGTGTGTGACCGA	2676
Qy	2571	CCCCCGCATCACAGAGATAATCCCGCTGTGACAGGCCCGCCGGAAGGGGGCACCAAGTCTAC	2630
Db	2677	CCCCAGATCTCAAGCTGTCCCCTGAGAGCGGCCCGAGCGAGGGCGGCACCGGCTCAC	2736
Qy	2631	TATCCGAGGGGAGAACTGTGGCTGTGAAATTTCCGACATCGCCTCCCATGTCAAGGTTGC	2690
Db	2737	TATCAAGGCGAGAACTGTGGGCTTGGATTCGAAAGACGTGCGCTGTGGGCGTCCGGTGGG	2796
Qy	2691	TGGCGTGGAGTCAGACCCCTTTAGTGGATGTTATCATCTTCAGAACACAGATCGTGTGCA	2750
Db	2797	CAAGTCTGTGCAGCCCTGTGAGAGCGAGTACATCAGTGCAGAGCAGATCGTCTGTGA	2856
Qy	2751	GATGGGGAGGCCAAGGCC---AGCCAGCATGAGGCTTGTGTGGAGATCTGGGTGGCTGT	2807
Db	2857	GATCGGGAGCGCAGCTCCGTGGCTGCCATGACGCCCTGCTGGTGGAGTGTGTGTGCGGA	2916
Qy	2808	GTGTGCGCTGAAATTCATGCCCCGCTCTCACAGCTCTATTATTCATGACACTGACTCT	2867
Db	2917	CTGTCTACCACTACCGCGCCCTGTGACCAAGCGCTTCACTTGTGACACCACTT	2976
Qy	2868	CTCAGATCTGAAGCCACCGCGGGGCCCATGTTCGGAGGAGCCCAAGTGCACATCACAG	2927
Db	2977	CTACCGTGTGAGCCCTCCCGTGGCCCTGTGTGAGGGGCGACCTGGATTGGCATCGAGG	3036
Qy	2928	CACCAACTGATCCGGAGACACGTTGTGTGATGTTTGGAAAGCAGCCCTGTCTCTT	2987
Db	3037	AAGCCACTGAACCGAGCAGTGAATGGCTGTGTGCGTGGTGGCGGCCCTGTCTCTT	3096
Qy	2988	CCACAGCGCATCTCCATCTCTACATTGTCTGCAACACACATCTCTCAGATGAGGTGCTAGA	3047
Db	3097	CTCTGTTCCAGGAGGAATCTCCGTGAGATCCCGTGTCTGACACCCCGCGGCAGAGCCC	3156
Qy	3048	GATGAAGGTGTCCGTGTCAGGTGGACAGGGCC-----AAGTCCACAGAGACCTGGT	3098
Db	3157	TGGCAGCGCTCCCATCATCATCAACATCAACCGCGCCCGAGCTCACCAACCCCTCAGGTGAA	3216
Qy	3099	CTTTTCAGTATGTGAAGACCCCACTCATGTCGGATTGAGCCAGAAATGGAGCATGTGCAG	3158
Db	3217	GTACMACTPACCGAGGACCCCACTCTGAGGATCGAATCCCGAGTGGAGCATCAACAG	3276
Qy	3159	TGGAAACACACCCATTCGCCGTATGGGGAGCCCACTGGAACCTCATACAGAACCCCCAGAT	3218
Db	3277	CGGTGGGACCTCTCTGACGGTCAAGGCACAGGCCAACTCTGCCCACTGTCCGTGAAACCCCAAT	3336
Qy	3219	CCGTGCCAAGCATGAGGAGGAGGACATCAATATCTGTGAGGTTCTGAACGCTACTGA	3278
Db	3337	CCGGGCCAAGTATGAGGCAATTGAG---AGGAGAACTGTCTGTGTGTACATGACACAC	3393
Qy	3279	GATGACCTGTGAGGCGCGCCGCTCGCTCTGGGTCTTGACACACAGTACAGACTGACCGA	3338

3394	Db	CATGTAATGCGCGCCCGCTGTGGCAACACCTGTGGGAGCCCAACAGAGCTGGGGGA	3453
3339	Qy	GAGCGCCGAGAGATTGSCCTTCATCCTTGGACAAAGTCAGTCCCTGTCTCATCTCAACAA	3398
3454	Db	GCGCGCGATGAGCTGGGCTTCGTATGGACAAAGTGGCGCTCCCTGTGTGCTCAACTC	3513
3399	Qy	GACCAACTTCACCTACTATCCCAACCGGTGTTTGGAGCCTTTGGTCCCTCAGGAATCCT	3458
3514	Db	CACCTCCCTTCTCTACTACCTTGACCCCGTACTGGAGCCACTGAGCCCACTGSCCTGCT	3573
3459	Qy	GGAGCTCAAGCCTGGCAGCCGCATCATCTTAAAGGGCAAGAACCTGTATCCCGCCTGTGGC	3518
3574	Db	GGAGCTGAAGCCAGCTCCCACTCATCTCAAGGGCGGAACCTCTTGGCACTT--GC	3630
3519	Qy	TGGGGGCAAGTGAAGCTGAACACTACATGCTGCTTGGGGAGAGCCGTGCACCGTCAAC	3578
3631	Db	ACCCGGCAACTCCCGACTCAACTACACGGTGTCTATCGGCTCCACACCTGTACCTCAC	3690
3579	Qy	CCTGTCCAGATGTCAGCTGCTCTGGAGTCCCCCAACCTCATCGGCAGGCACAAAGTCAAT	3638
3691	Db	CGTGTGGAGCGCAACTGCTGTGGAGGGCGCCAACTCACTGGCGAGCACAAGGTCAAC	3750
3639	Qy	GGCCGCTGTGCTGTGCATGGAGTACTCCCGGGGATGGTGTACATTGCCCGGACAGCCC	3698
3751	Db	GGTGGTGCAGGTGGCTTCGAGTTCCTGCCAGGGACACTGCAAGGTGTACTCGGACAGCT	3810
3699	Qy	GCTCAGCCTGCCCGCATCGTCAGCATCGCAGTGGCTGGCGGCTCCTCATCTTTTCAAT	3758
3811	Db	GCTGACGCTGCTTGCCATTTGGGCAATGGCGAGGCGGGGTCTCTGCTGCTGCTCAT	3870
3759	Qy	CGTGGCGCTGCTCATTTGCCCTATPAAACGCAAGTCCCGGAAGTGACTCAAGCTGAAGCG	3818
3871	Db	CGTGGCTGTGCTCATCGCCTCAAGCGCAAGTCAAGAGATGCTGACCGGACACTCAAGCG	3930
3819	Qy	GCTGCAGATGCAGATGGACAACTCGAGTCCCGTGTGGCCCTGGAGTGCAGAGAGCCCTT	3878
3931	Db	GCTGCAGCTCCAGATGGACAACTGGAGTCCCGGTGGCCCTCGAATGCAAGGAAGCCTT	3990
3879	Qy	TGCGAGCTGCGACAGGACATCCATGAGTGAACAGTGAACCTGATGGAGCCGGATTCC	3938
3991	Db	TGCAGAGCTGCGACAGACATCCAGAGCTGACCAATGACCTGGAGCGTCCCGGATCCC	4050
3939	Qy	GTCTCTGACTATAGAACTTACACATGCGGGTGTGTTCCAGAGAAATGAAGACACACC	3998
4051	Db	CTTCTCTTGACTACCGACATATGCCATGCGGGTGTCTTCTCTGGATCGAGACACACC	4110
3999	Qy	TGTCTCTCCGGGACCTTTGAGTCCCGGCTACCGGACGAGCGTGTGGAGAAAGGCTGAA	4058
4111	Db	TGTGCTCAAGGAGATGAGGTACAGGCCAA-----TGTGGAGAAGTCGCTGAC	4158
4059	Qy	GCTCTTCGCCAGCTCATCAACAAAGGTGTTCTGCTGTCTCTTCATCGCAAGCTTGA	4118
4159	Db	ACTGTTTGGGCAGCTGCTGACCAAGAAGCACTTCTGCTGACCTTCACTCGACGCTGGA	4218
4119	Qy	GTCCCGAGCTAGCTTCTCATGCGGACCGTGGCAACGTGGCTCACTCATCATGACCGT	4178
4219	Db	GGCACAGCGCAGCTTCTCCATGCGCACCGCGGGAATGTGGCTCGCTCATCATGACGGC	4278
4179	Qy	GCTGCGAGCAAGCTGGAGTACGCCACTGATGTGCTGAAGCAGCTGCTGGCGGACCTCAT	4238
4279	Db	CCTGCAAGGGGAGATGGAATACGCCACAGCGTGTCTCAAGCAGCTGCTTCCGACCTCAT	4338
4239	Qy	TGCACGAACCTCGAGAGCAAGAACCACCTCAAGCTG---CTGCTCAGGAGGACTGAGTC	4295
4339	Db	CGAGAGAACCTGGAGAGCAAGAACCAACCCCAAGCTGCTACTCGCGCGGCCAACTGAGTC	4398
4296	Qy	AGTGGCTGAGAAGATGCTGACCAATTTGTTTACTTCTCCTCTACAAGTTCTCTCAAGGA	4355
4399	Db	GGTGGCAGAGAAGATGCTAACTAACTGGTTTCACTCTCTCTGTTATAGTTCTCTCAAGGA	4458
4356	Qy	GTGTGCTTGGGAGCCCTCTTCTCCCTGTTCTGTGCCATCAAGCAGCAGATGAGAGGGG	4415



Db 4459 GTGGCTGGGAGCGCTGTTCTATCTGCTACTGCGCCATCAAGCAGCAGATGGAGAGG 4518  
 Qy 4416 CCCATTGACGCCATCAAGGCGAGCGCGCTATCTCTTTGAGCGAGGACAAGCTCATCCG 4475  
 Db 4519 CCCATTGACGCCATCAAGGCGAGCGCGCTATCTCTTTGAGCGAGGACAAGCTCATCCG 4578  
 Qy 4476 CCAGCAGATTGACTCAAAAACCTGCTCTGAGCTGTGTCAGCCCGAGCAATGCCAACAG 4535  
 Db 4579 GCAGCAGATTGACTCAAGACACTGACCCCTGAACCTGTGTGAACCTGTGAATGAGATGC 4638  
 Qy 4536 CCCGAGGTCCAGTAAAGATCCTCAATGTGACACCATCACTCAGGTCAAGGAGAAATG 4595  
 Db 4639 ACTGAGGTGCGGTGAGGCGCTGACTGTGACACGCTACCCAGGCGCAAGGAGAACT 4698  
 Qy 4596 TGTGATGCGATTTCAAGAAATGCTGCTGCTCCACCGGCCCAAGCTGCAGATATGGA 4655  
 Db 4699 GTTGACGCTGCTCAAGGGCGTCCCTTACTCCAGCGGCCCAAGCGCGCGCATGGA 4758  
 Qy 4656 TCTGAGTGGCGACAAAGGAAGTGGGCAAGGATGATTTGACGATGAAGACATCACCAC 4715  
 Db 4759 CTTGAGTGGCGCGAGGCGGATGCGCGCATCTCTGACGAGCAGGAGCTCACCAC 4818  
 Qy 4716 CAAAGATTGATGATGAGCGACTGAACACTGCGCCACTACCGAGTCCAGATGG 4775  
 Db 4819 CAAAGATTGATGATGAGCGACTGAACACTGCGCCACTACCGAGTCCAGATGG 4878  
 Qy 4776 TCCGCTGCTGATAGTGTCCAAAGCAGGTGACAGCTTATACGAGTGAACAACTCCAC 4835  
 Db 4879 GTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4938  
 Qy 4836 CGTCTCCAGACCTCAGCAGACCTATGATCTCTGACCTGAGAGTGGAGTCAAGATGTG 4895  
 Db 4939 CTTACCAAG--TCCCTCAGCAGATACGAGAGCATGCTGCGCACCGGCGAGCGCCGA 4995  
 Qy 4896 CAGCTCCGCTCAGCAGACCTATGATCTCTGACCTGAGAGTGGAGTCAAGATGTG 4955  
 Db 4996 CAGCTCCGCTCAGCAGACCTATGATCTCTGACCTGAGAGTGGAGTCAAGATGTG 5055  
 Qy 4956 GCACCTAGTGAAGAACACAGAGCAGCAGAGCAGAGAGGAGGAGGAGGAGGAGGAGGAGG 5015  
 Db 5056 GCACCTAGTGAAGAACACAGAGCAGCAGAGCAGAGAGGAGGAGGAGGAGGAGGAGGAGG 5115  
 Qy 5016 GGTGTCTGAAATCTACTGACCGGCTCTGCGGCACTA--AGGGCAGACTGCAAGATG 5072  
 Db 5116 GGTCTGGAGATCTCTTGAACCGGTACTGGCCACCAAGCAGGAGGAGGAGGAGGAGGAGG 5175  
 Qy 5073 TGTGATGACCTCTTTGAGACCATCTTACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 5132  
 Db 5176 TGTGAGACCTCTTTGAGACCATCTTACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 5235  
 Qy 5133 GGCATCAGTACATGTTGATCTCTGATGAGCAGGCTGATAAATGAGGATGATGATGATGATG 5192  
 Db 5236 GGCATCAGTACATGTTGATCTCTGATGAGCAGGCTGATAAATGAGGATGATGATGATGATG 5295  
 Qy 5193 CCGCAGCTCCGCATACCTGGAAGAGCAATT--GCCTGCCCTCAGGTTTGGGTCAA 5249  
 Db 5296 TGCTGAGTGGCGCACACCTGGAAGAGCAACTGAGCTGCCCTCAGGTTTGGGTCAA 5355  
 Qy 5250 CATGATCAAGAACCGCAGTTGTTGATCTTATGATCTTATGATCTTATGATCTTATGATCTT 5309  
 Db 5356 CGTATCAAGAACCGCAGTTGTTGATCTTATGATCTTATGATCTTATGATCTTATGATCTT 5415  
 Qy 5310 CCTCTCTGCTGCTCAGACCTTCTGATGAGTCTTGTCTCAGCTCAGAGCAGCAGCAGCAGC 5369  
 Db 5416 CTTGCTGGTGGTGGCCAGCCTTCTGATGAGTCTTGTCTCAGCTCAGAGCAGCAGCAGCAG 5475  
 Qy 5370 CAAAGACTCGCCCTCAAGAGCTGTGATGCAAGGATCTCCAGGATCTCCAGGATCTCCAGG 5429  
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 Qy 5430 GGTGGA--GAGGTATTACTCAGACATAGGGAAGATCCAGGATCTCCAGGATCTCCAGGAT 5486  
 Db 5536 GGTGGAAGGAGGTACTATGACAGATCGCCAGATCCAGGATCTCCAGGATCTCCAGGAT 5595

Qy 5487 GAACGCATACCTGGCTGAGCGTCCCGGATGCACATGAATGAGTTCAACACCATGAGTGC 5546  
 Db 5596 GATGGGTATCTGGCTGAGCGATCCCGCTGACCTGACCGATTCACACGATGAGCGC 5655  
 Qy 5547 ACTCTCAGAGATCTTCTCTATGTGGGCAATACAGCGA-----GGAGATCTTGGACC 5600  
 Db 5656 CTTGACGAGATCTACTCTTACATCAACCAAGTACAGGATGAGGTGAGATCTCTGCGCAG 5715  
 Qy 5601 TCTGACCCAGATGAGCGTGTGGGAGCAGAACTGGCCTACAACTAGAACAACTCAT 5660  
 Db 5716 CTTGGAAGGATGAGCG 5775  
 Qy 5661 AACCTCATGAGCTTAGACAGCTGA 5685  
 Db 5776 GGCACGATGCGCTGAGCAGCTGA 5800

RESULT 6  
 US-10-218-779-31  
 ; Sequence 31, Application US/10218779  
 ; Publication No. US2004002922A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Edinger, Shlomit  
 ; APPLICANT: MacDougall, John  
 ; APPLICANT: Millet, Isabelle  
 ; APPLICANT: Ellerman, Karen  
 ; APPLICANT: Stone, David  
 ; APPLICANT: Gerlach, Valerie  
 ; APPLICANT: Grosse, William  
 ; APPLICANT: Alsobrook II, John  
 ; APPLICANT: Lepley, Denise  
 ; APPLICANT: Rieger, Daniel  
 ; APPLICANT: Burgess, Catherine  
 ; APPLICANT: Casman, Stacie  
 ; APPLICANT: Spytek, Kimberly  
 ; APPLICANT: Boldog, Ferenc  
 ; APPLICANT: Li, Li  
 ; APPLICANT: Padigaru, Muralidhara  
 ; APPLICANT: Mishra, Vishnu  
 ; APPLICANT: Patturajan, Meera  
 ; APPLICANT: Shenoy, Suresh  
 ; APPLICANT: Rastelli, Luca  
 ; APPLICANT: Tchernev, Velizar  
 ; APPLICANT: Vernet, Corine  
 ; APPLICANT: Zerhusen, Bryan  
 ; APPLICANT: Malyankar, Uriel  
 ; APPLICANT: Guo, Xiaojia  
 ; APPLICANT: Miller, Charles  
 ; APPLICANT: Gangolli, Bsha  
 ; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same  
 ; FILE REFERENCE: 21402-214  
 ; CURRENT APPLICATION NUMBER: US/10/218,779  
 ; CURRENT FILING DATE: 2002-08-14  
 ; PRIOR APPLICATION NUMBER: 60/253,834  
 ; PRIOR FILING DATE: 2000-11-29  
 ; PRIOR APPLICATION NUMBER: 60/250,-926  
 ; PRIOR FILING DATE: 2000-11-30  
 ; PRIOR APPLICATION NUMBER: 60/264,180  
 ; PRIOR FILING DATE: 2001-01-25  
 ; PRIOR APPLICATION NUMBER: 60/313,656  
 ; PRIOR FILING DATE: 2001-08-20  
 ; PRIOR APPLICATION NUMBER: 60/327,456  
 ; PRIOR FILING DATE: 2001-10-05  
 ; NUMBER OF SEQ ID NOS: 216  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 31  
 ; LENGTH: 5895  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-10-218-779-31

Query Match 44.5%; Score 2533.8; DB 13; Length 5895;

Best Local Similarity 68.0%; Pred. No. 0; Matches 3812; Conservative 0; Mismatches 1712; Indels 81; Gaps 17;			
Qy	141	CGCCGAGGGTTTCAATCACCTGGTGGTGGATGAGAGGACAGACACATTTACTTGGGGC	200
Db	217	CGACTGGGGCTCACCCACCTAGTGGTGCATGAGCAGACAGGCGAGGTGTATGGGGC	276
Qy	201	CGTCAATCGAATTACAGCTTCCAGCGACCTGAAGGTCTTGGTGAAGCATGAGACAGG	260
Db	277	AGTGAACCGCATCTATAAGCTGCGGGGAACCTGACACTGCTGCGGGGCCACGTCACGG	336
Qy	261	GCGGGACGAGGACAAACCCAAAGTGTACCCACCCCGCATCGTCCAGACCTGCAATGAGCC	320
Db	337	CCCTGTGGAGGACAAAGAGAGTGTACCGCGCGCCAGCGTGCAGTCTCGCCCAAGG	396
Qy	321	CCTGACACACCAACCAATGTCAACAGATGCTCTCATAGACTACAGGACAAAGAGCT	380
Db	397	CCTGGGAGTACTGACAACTCAACAGCTGTGCTGTGCTGCTGCTGCTGCTGCTGCTGCT	456
Qy	381	GATTCCTGTGGAGCTGTACCAAGGCTATGCAAGCTGTGAGGCTGGAGGACCTCTT	440
Db	457	GCTGGCTGTGGCAGCGCTCCAGGGCATCTGCCAGTTCCTGCGTCTGGACGATCTCT	516
Qy	441	CAAGCTGGGGAGCCATTATCAAGAGAGGACATCTGTGCTGCTGCTGCTGCTGCTGCTGCT	500
Db	517	CAAACTGGGTGAGCCACACCGTAAAGGACACTACCTGTCCAGCTGCGAGGAGGACG	576
Qy	501	CTCAGTCTTTGGAGTGTCTCTTACCA-----GCAACCTGGATGACAGCTGTTTCA	554
Db	577	CAGCATGGCGGGGTGCTCATTCGCGGGCCACCGGGCCAGGGCCAGGCCAAGCTCTTCT	636
Qy	555	TGCCAGGAGTGGAGGAGCCGAGTATTTCCACCATCTCCAGCGGAACTGAC	614
Db	637	GGGCAACCCATCGATGGCAAGTCCGAGTACTTCCCACTGTCCAGCGCTGCGCTCAT	696
Qy	615	CAAGAACTCTGAGCGGATGGCATGTTCGCTGCTCTTCCATGATGATGCTGCTGCTGCT	674
Db	697	GGCCAAACGAGGAGTCCGACATGTTGCGTTCGTTGATACAGGATGATGTTGTCTATC	756
Qy	675	GATGATTAAGTCCCTCGGACACTTACCATCATCTGCTGCTGCTGCTGCTGCTGCTGCT	734
Db	757	ACAGTCAAGTCCCTTGGGACAGCTGTCCAGTTCGCGGCTTGTGATCTACTATGT	816
Qy	735	CTATGTTTTPAGCAGTGGCACTTTGCTACTTTTGTGCTTCCCTCCAACTGAGTGGTGT	794
Db	817	GTACAGCTTCCGAGCGAGCAGTTCCTGCTACTACTCTACCTCACGCTGACCTAGACAC	876
Qy	795	TCCACAGGCTCCACACCAAGAGCAGGTGTATATCATCCAGCTGCTGAGGCTTGC	854
Db	877	GACCTGCTGATGCGCGCGGCGAGCAGTCTTCCAGTCCAGATGCTGCGGCTCTGT	936
Qy	855	GGAGGACACAGCTTCAACTCTTATGTAGAGGTGCCCATTTGGCTGTGAGCGCAGTGGGT	914
Db	937	GGACGACCCCAATTTCTACTGCTAGCTTGGATTTCCCATTTGCTGCGAGCGGGGTGT	996
Qy	915	GGAGTACCGCTGCTGAGGCTGCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	974
Db	997	GGAGTACCGCTGCTGAGGATGCTTACTGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	1056
Qy	975	CCTTGGAGTCCATCCAGATGATGACCTGCTTCTTCCAGCTTCTTCCAAAGGCGCAAGCG	1034
Db	1057	GCTGGGCTGGCTGAGGACGAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1116
Qy	1035	GAAATGAATCCCTGGATGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1094
Db	1117	CCGCTGAGGCCAACAAAGAGTACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1176
Qy	1095	CCGATTAAAGGAGCGCTGAGTCTTGTGTTACCGGGCGGAGGCGAGCTGCTGCTGCTGCT	1154
Db	1177	GAAGATTAAAGGAGCGATCCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1236
Qy	1155	GCTCAAGGTGAAGGACATCCCTGCGAGTGGCTCTTAAACCATGAGCATTAATTCTG	1214

Db	1237	GCTGTCTAAAGAGGAGCTGGGCTGCATCAACTGCGCCCTGCAGATCGATGAGACTTCTG	1296
Qy	1215	TGGCTTGGACATGAATGCTCCCTGGGAGTGTCCACATGCTGGCTGGAATTCCTGCTT	1274
Db	1297	CGGCAAGGATTTCAACACGCTTGGGGGACAGTCAACCATTTGAGGGGACGCGCTGTT	1356
Qy	1275	CACGAGGACAGGAGCCGATGAGCTGTGTCTATCCATATGCTCTACAAGACCACTCTCT	1334
Db	1357	CGTGGACAAGGATGATGGCTTACCGCTGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCT	1416
Qy	1335	GGCTTTTGTGGGCAACAAAGTGGCAAGCTGAAGAGATCCGGGTGGATGGACCA-----	1390
Db	1417	GGTATTCGCGCGGACCGGAGTGGCGCATCCGCAAGATCTCTGTGTGGACCTCTCAACCC	1476
Qy	1391	-----GGGCAACGCGCTTCAAGATGAGACCGTGCAGGTGGCGCATCTGTGTGGACCT	1445
Db	1477	CGGTGGCGCGCTGCGCTTGGCTAGGAGCGTCTGTGGCGCCAGGAGGAGCGCCCATCT	1536
Qy	1446	CCGGGATATGGCTTCTCCAGGACCAAGAGCAACTCTACATCATGTCTCAGAGAGCAGCT	1505
Db	1537	GCGAGACCTCGTCTCAGCGCCCAACACACAGTACCTCTACGCCATGACCGAGAGCAGT	1596
Qy	1506	CACAGAGTCCCTGTGGAGTCTGTGTGCTGATCAGAGCTGCGGCGAGTGTGCTGCTGCT	1565
Db	1597	GACGCGGTGCTGTGTGGAGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1656
Qy	1566	AGCGGACCCCGCTGTGTGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1625
Db	1657	ACGGGACCCCGCTGTGTGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1716
Qy	1626	TGAGCGGTCCAGGAGCCCGGAGGTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1685
Db	1717	TGAGGAGCAGAGCAGGAGCCCGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1776
Qy	1686	GGTCCATCCCAACATATCTCCGTCTCTCAGTACCAACGCTG---TGCTGTGCTCTGGAG	1742
Db	1777	TGTGAGCGCCGCAATGTGTCTCACCATGTCTCCAGGTCCCGAGTACTTGTGTGTCAGG	1836
Qy	1743	GTACATATGCTCCGAGCTGTGAGCTGGCGTCAACTGCACTTGTGAGGACCTGTGAGAT	1802
Db	1837	CTGGAACGCTGCTGAGCTCTCAGCTGGCGTCAACTGCTTGTGAGGACTTCAAGGAATC	1896
Qy	1803	GGATGGGCTGTGTGGGCAATCAGATCCAGTGTCTCTCCCTGTCAGCAACAGGAGGTGCC	1862
Db	1897	TGAGAGCGTCTGGAGGATGGCGGATCCACTGCGCTCACCTCCGCGCGGAGGTGGC	1956
Qy	1863	CCGATCA-----TCACAGAGATGGGACCAACCATGTGTACAGCTTCACTCAATC	1916
Db	1957	GCCCATCACGCGGGGCGAGGTGAGGAGACAGCGGCTGTGTAACTCTACCTAAAGTC	2016
Qy	1917	AAAGGAGACCGGATGACCTTCCCGAGCACCAAGCTTGTCTTCTTACAAATTCAGCGTCCA	1976
Db	2017	CAAGGAGACAGGAGAAAGTGTGCTGTGTGCTTGTGTGTGTGTGTGTGTGTGTGTGTGT	2076
Qy	1977	CAATTCG---TGCTGTCTGT	2033
Db	2077	CCAGTCCAGCTGCTGT	2136
Qy	2034	GCATGTCTCACCCATGACCCCAAGACCTGCTCTTCCAGGAAGCGCGAGTGAAGTGCC	2093
Db	2137	CCAGTGTGCACACACCAAGTGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	2196
Qy	2094	CGAGGAGTCCCGGAGCTGTGCGAGTGGACAGATCCTGTGTGTGTGTGTGTGTGTGTGT	2153
Db	2197	TGAGGAGTCCCGGAGT	2256
Qy	2154	GCCTATCAGCTGAAGGCGCAAGACCTTCCCGAGCCCGAGTGTGGGAGCGTGTGCTACGA	2213
Db	2257	ACCCATCACCTTGGCGGACGGAACCTGTGCACAGCAGTCAAGGAGCGGTGTGATGA	2316
Qy	2214	ATGCATCTCAACATTCAGGAGGAGGAGGAGGAGTGTGTGTGTGTGTGTGTGTGTGTGT	2273
Db	2317	GTGCTCTTCTCCACATCCCGGCGAGCCCGCGCTGTCAACGCTTGTGCTTCAACAGCTC	2376

QY	2274	CAGCGTACAGTGCAGAAACACCTCTTATTCTATGAAGGATGGAGATCAACAACCTGCC	2333
DB	2377	CAGCGTGCAGTGCAGAAATTCCTCGTACTCTTACGAGGGGAAACGATGTGAGCGACTGCC	2436
QY	2334	CGTGGAGTTGACAGTGGTGGGAATGGGCACATTCACATTGACACCCAGCTCAGAAATAA	2393
DB	2437	AGTGAACCTCTCAGTCTGTTGGAAACGGCACTTTGTCAATTGACAAACCCACAGAATCCA	2496
QY	2394	AGTTACCTCTACAAGTGTGGAGCCATGCGTGAGAGCTGCGGCGTGTGCTCAAGGCTGA	2453
DB	2497	GGCGCACTCTACAAGTGCCTGGCGCTGCGGAGAGCTGCGGCTCTGCTCAAGGCCGA	2556
QY	2454	CCAGACTTCGCATGTGGCTGTGTCCAGGGGCCAGGCGAGTGACCCCTGGCGCAGCACTG	2513
DB	2557	CCGCGCTCTGAGTGGGAGTGGTGGCGGAGCGCGCTGCTCCCTCCGACACCACTG	2616
QY	2514	CCCTGCCCA--GGAGAGCCAGTGGCTGGAGCTGTCTGTTGCCAAAGCAAGTGACAAA	2570
DB	2617	CGTGGCGACACACCTGCATCTGTGATGCACGGCGTCAAGCAGCAGTTCGTGCACCGA	2676
QY	2571	CCCCCGCATCACAGAGATAATCCCGGTGACAGGCCGCCCGGAAAGGGGGGACCAAGGTCA	2630
DB	2677	CCCCAAGATCTCAAGCTGTCCCCGAGACGGGCGCGAGCGAGCGGCGGCGGCTCAC	2736
QY	2631	TATCCGAGGGAGAACTCGGSCCTGGAAATTCGCGACATCGCTCCCATGTCAAGTTGC	2690
DB	2737	TATCACAGCGAGAACTTGGGCTTGCATTCGAAGACGTGCTGCTGGGCGTGGCGTGG	2796
QY	2691	TGGCGTGGAGTGCAGCCCTTTAGTGGATGTTATCATCCCTGCAGAAACAGATCGTGTGA	2750
DB	2797	CAAGGTGCTGTGCAGCCCTGTGGAGAGCGAGTACATCAGTGCAGAGCAGATCGTCTGTA	2856
QY	2751	GATGGGGAGGCCAAGGCC--AGCCAGCATGAGGCTTCGTGGAGATCTGGGTGGCTGT	2807
DB	2857	GATCGGGAGCCAGCTCGGTGCGTGCCCATGACGCCCTGGTGGAGGTGTGTGCGGGA	2916
QY	2808	GTGTGGGCTGAATTCATGCGCCGCTCTCACAGCTCTATTATTTATGACACTGACTCT	2867
DB	2917	CTGCTCACCACTACCGGCGCTGTCAACCAAGCGCTTCACCTTGTGACACCAACCTT	2976
QY	2868	CTCAGATCTGAAGCCAGCGGGGGCCCATGTTCGGAGGGACCAAGTGACCATCACAGG	2927
DB	2977	CTACCGTGTGAGCCCTCCCGTGGGCTCTGTACAGGGGGCACCTGGATTGGCATCAGGG	3036
QY	2928	CACCAACTGAAATCCGGGAACAACGTGGTGTGATGTTTGGAAAGCAGGCCCTGTCTTT	2987
DB	3037	AAGCACTGAAACGAGCAGTGTATGTGGCTGTGTGCTGGTGGCGGGCCCTGTCTTT	3096
QY	2988	CCACAGGCGATCTCCATCTCTATGTGTGCAACACACATCTCTAGATGAGTGTGTAGA	3047
DB	3097	CTCCTGTGTCCAGGAGGAACCTCCCGTGAGATCCGCTGCTGACACCCCGGGCAGAGCCC	3156
QY	3048	GATGAAGTGTGGTGCAGGTGGACAGGGCC-----AAGATCCACAGACACTGGT	3098
DB	3157	TGGCAGCGCTCCCATCATCATCAATCAACCGCGCCAGGTCAACCACTGAGGTGAA	3216
QY	3099	CTTTTCAGTATGTGAAGACCCCACTGTGCGGATTGAGCCAGAAATGGAGCATTTGTGAG	3158
DB	3217	GTACAACCTACACCGAGGACCCCACTCTGAGGATCGACCCCGAGTGGAGCATCAACAG	3276
QY	3159	TGGAAACACACCATCGCGGTATGGGGGACCACTGGACCTCATACAGAACCCCGAGT	3218
DB	3277	CGGTGGGACCTCTCTGACGGTCAACGGCACCACTGGCCACTGCTCGTGAAACCCCGAAT	3336
QY	3219	CCGTGCCAAGCATGGAGGGAAGGAGCAATCAATATCTGTGAGTTCTGAACGCTACTGA	3278
DB	3337	CCGGGCCAAGTATGGAGCAATTGAG--AGGGAGNACTGCTGTGTGTACATGACACCAC	3393
QY	3279	GATGACCTGTACGGCGCCGCGCTCGTCTGGTCTGTGAACCAAGTTCAGACTGACCGGA	3338
DB	3394	CATGTTATCGCGCGCCGCTGTGTGGCCAACTCTGTGGCAGGCCACACAGAGTGGGGGA	3453

QY	3339	GAGGCCGAGGAGTTTGGCTTCATCTTGACAAACGTCCAGTCCCTCGCTCATCCTCAACNA	3399
DB	3454	GCGCCCGAATGAGCTGGGCTTCGTCAATGACAACGTGGCTCCCTCTTGTGCTCAACTC	3513
QY	3399	GACCACCTTCACCTACTATCCCACACCGGTGTTGAGGCCTTTGGTCCCTCAGGAATCCT	3458
DB	3514	CACCTCTTCTCTACTACCTGACCCCGTACTGGAGCCACTCAGCCCCACTGGCCTGCT	3573
QY	3459	GGAGCTCAAGCTGGGACGCGCCCATATCTTAAGGGCAAGAACCCTGATCCGGCTGTGGC	3518
DB	3574	GGAGCTCAAGCCAGCTCCCACTCATCTCTCAAGGGCCGGAACCTCTTCCCACT---GC	3630
QY	3519	TGGGGGCAACGTGAAGCTGAACCTACACTGTGCTGTGTTGGGAGAAGCCGTGACCCGTGAC	3578
DB	3631	ACC CGCACTCCGACTCAACTACAGGTGCTACTCGGCTCCACACCTGTACCCCTCAC	3690
QY	3579	CGTGTCAAGATGTCCAGCTGCTCTGAGTCCCCCAACCTCATCGGCAAGGACCAAGTGA	3638
DB	3691	CGTGTGGAGACGCAACTGCTGTGCGAGGCGCCCAACCTCACTGGGCAAGGACCAAGTCA	3750
QY	3639	GGCCGCTGTGGTGGCATGAGTACTCCCGGGGATGGGTATATTGCCCCCGGACAGCCC	3698
DB	3751	GGTGGTGTGAGGTGGCTTCGAGTTCCTCGCAGGGACACTGTGAGGTACTTCGGACAGCT	3810
QY	3699	GCTCAGGCTGCCCGCCATCGTCTCAGCATCGCAGTGGCTGGCGGCTCCTCATCATTTTCAT	3758
DB	3811	GCTGACGCTGCTCCCACTTGTGGCACTGGCGAGGCGGGGTCTCCTGCTGTGTCAT	3870
QY	3759	CGTGGCGTGCTCATTTGCCATAAAGCGAAGTCCCGGAAGTAGCTCAGCTCAGGTGAAGCG	3818
DB	3871	CGTGGCTGTGCTATCGCTTCAAGCGCAAGTCAAGAGTGTGACCGCACATCTCAAGCG	3930
QY	3819	GCTCAGATGAGATGGACAACCTGGAGTCCCGTGTGGCCCTGGAGTGCAGGAAGCCTT	3878
DB	3931	GCTGCAGCTCCAGATGGACAACTGGAGTCCCGGTGGCCCTCGAATGCAAGGAAGCCTT	3990
QY	3879	TGCCGAGCTGACGCGACATCATAGCTGAACAGTGAACCTGGAATGGAGCCGGGATTC	3938
DB	3991	TGCAGAGCTGACGACAGACATCCAAGAGCTGACCAATGACCTGGACGGTCCCGGACATCC	4050
QY	3939	GTTCTTGACATATAGAACCTTACACATGCGGGTCTGTTCCAGGAATTAAGACACACCC	3998
DB	4051	CTTCTTTGACTACCGGACATATGCAATGCGGGTCTCTTTCTGGGATCAGAGACACCC	4110
QY	3999	TGTCTCCGGACCTTGAGTCTCCGGCTACCGGACGAGCGTGTGGAGAAAGCCCTGAA	4058
DB	4111	TGTGCTCAAGGAGATGGAGGTACAGGCCAA-----TGTGGAGAAGTGGCTGAC	4158
QY	4059	GCTCTTCCCGCAGCTCATCAACACAGGTGTTCTGCTGCTTCATCCGACGCTTGA	4118
DB	4159	ACTGTTCCGGCAGCTGTGACCAAGAAGCACTTCTGCTGACCTTCAITCCGACGCTGGA	4218
QY	4119	GTCCAGCGGTAGCTTCTCCATGCGCGACCGTGGCAACGTGGCCCTCACTCATATGACCGT	4178
DB	4219	GGCA CAGCGAGCTTCTCCATGCGCACCGCGGGAATGTGGCTCGCTCATCATGACGGC	4278
QY	4179	GCTGACAGACGAGCTGGAGTAGCCACTGATGTCTGAAGCAGCTGCTGGCCGACCTCAT	4238
DB	4279	CCTGACGGCGGAGATGGAAATACGCCACAGGCGTGTCAAGCAGCTGTCTTCCGACCTCAT	4338
QY	4239	TGACAAGAACCTGGAGACCAAGAACCCCTTAAGCTG---CTGCTCAGGAGGACTGAGTC	4295
DB	4339	CGAGAAGAACCTGGAGACAGAGAACCCCAAGCTGCTACTGGCCGGCCAACTGAGTC	4398
QY	4296	AGTGGCTGAGAAGATGCTGAACAAATGGTTTTACTTTTCTCTCTACAGTTCTCTCAAGGA	4355
DB	4399	GGTGGCAGAGAAGATGCTAACTAACTGGTTCACTTCTTCTTGTATTAAGTTCTCTCAAGGA	4458
QY	4356	GTGTCTGGGAGCCCTCTTCTCCCTGTTCTGTGGCCATCAAGCAGCAGATGGAGAAGGG	4415
DB	4459	GTGGCTGTGGGAGCCGCTGTTCTATGCTGTACTGTGGCCATCAAGCAGCAGATGGAGAAGGG	4518
QY	4416	CCCCATTGACCCATCAACGGGCGAGGCCGCTATCTCTTGAAGCAGGACACACTCTCATCCG	4475

Db 4519 CCCATTGACGCCATCAGGTTGAGGACGCTACTCTCTGAGTGAGGACAAAGCTCATCGG 4578  
QY 4476 CCAGCAGATTGACTACAAAACCTGGTCTTCTGAGCTGTGTGAGCCAGCAAAATGCCAACAG 4535  
Db 4579 GCAGCAGATTGACTACAAAGACACTGACCTGAACTGTGTGAACTCTGAGAAATGAGAAATGC 4638  
QY 4536 CCCCAGGTCCTCCAGTAAAGATCTCTCACTGTGACACATCACTCAAGTCAAGGAGAGAT 4595  
Db 4639 ACCTGAGTGCCTGTGAAGGGCTGGAATGTGACACCGTCAACCGCCCAAGAGAGCT 4698  
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Db 4699 GCTGGAGGCTGCCCTTACAAAGGCGCTGCCCTACTCCAGGCGCCCAAGGCCGCGACATGA 4758  
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Db 4759 CTTGGATGGCGCCAGAGCGCGCATGGCGCGCATCTCTCCAGAGACGAGACGTCAACAC 4818  
QY 4716 CAAGATTGAGAAATGATTGGAAGGACTGAACACACTGGCCCACTACCGAGTGCAGATGG 4775  
Db 4819 CAAGATTGACAAAGATTGGAAGAGGCTGAACACACTGGCTCACTACCGAGTGCAGACGG 4878  
QY 4776 TTCCGTTGGTGCATTAGTGTCCAAAGCAGGTGACAGCTATAAGCGCAGTGAACACTCCAC 4835  
Db 4879 GTCTCGGTGGCATGTGCTCCAAAGCAGAGCTCGGCTTCAACATCTCCACTCTCCAC 4938  
QY 4836 CGTCTCCAGGACCTCAGCAAGTAAATATGAAACATGATCCGGTACACCGGCGAGCCCGGA 4895  
Db 4939 CTTCAACCAAG---TCCCTCAGCAGATACGAGAGCATGCTGCGCACGCGCCAGCAGCCCGGA 4995  
QY 4896 CAGCTCCGCTCAGGACACCTATGATCACTCTCTGACCTGGAGAGTGGAGTCAAGATNG 4955  
Db 4996 CAGCTCGGTGCGCGACGCCCATGATCAGCGCCGACCTGGAGAGCGGCACCAAGCTGTG 5055  
QY 4956 GCACCTAGTGAAGAACACAGAGCACGAGACCGAGAACGAGAGGGGACCGGGGAGCAAGAT 5015  
Db 5056 GCACCTGGTGAAGAACACAGCACCTGGACCGAGCGTGAAGGGTGAACCGGGGAGCAAGAT 5115  
QY 5016 GGTCTGTGAATCTTACCTGACCCGACCTCTGGCCACTA---AGGGCACACTGCAAGATT 5072  
Db 5116 GGTCTGGAGATCTTGTGACACGCTACTTGGCCACCGAGCAGGACACTGCAAGATT 5175  
QY 5073 TGTGGATGACCTCTTGAAGCAATCTTTCAGACCGGACACCGTGGCTGTGCTGCTGCCCT 5132  
Db 5176 TGTGGACACCTGTTTGAAGACCATCTTTCAGACCGGACACCGGGGCTGAGCCCTGCCGT 5235  
QY 5133 GGCATCAAGTACATGTTTGAATCTCTTGGATGAGCGCTGATAAAGATGGCATTCATGA 5192  
Db 5236 GGCATCAAGTACATGTTTGAATCTCTTGGATGAGCGGCGGACAGCAAGATCCAGCA 5295  
QY 5193 CCGGACGTCGCGCATACCTGGAAGAGCAATT---GCCCTGCCCTGAGGTTTGGGTCAA 5249  
Db 5296 TGCTGACGTGGCCACACCTGGAAGAGCACTGCGAGCTGCCCTGCGCTTCTGGGTGAA 5355  
QY 5250 CATGATCAAGAACCGCAGTTTGTGTTGATCATCCATAAGAACAGCATCACAGCCGCTG 5309  
Db 5356 CGTATCAAGAACCCACGTTTGTGTTGATTCATCAAGAACAGCATCACAGCCGCTG 5415  
QY 5310 CTTCTGTGTGTGTGAGACTCTTCACTGAGTCTTGTCTCAAGTCAAGACCGGCTGGG 5369  
Db 5416 CTTGTGTGTGTGTGAGGCTTCACTGAGTCTTGTCTTCCACTCTGAGCAAGCTGGG 5475  
QY 5370 CAAGGACTTCGCTTCCACAGCTGTGTGTTGATGCGCAAGACATCCCGAGTACAGAAATG 5429  
Db 5476 CAAGGACTTCACCTTCCACAGCTGTGTGTTGATTCAGCAAGACAGCATCCCGAGTGTG 5535  
QY 5430 GGTGA---GAGGTATTACTCAGACATAGGGAAGATGCCAGCATCAGGACCAAGACAT 5486  
Db 5536 GGTGAGAGGAGGTACTATGAGACATCGCCAAAGATGCCAGCCATCAGCGACAGGACAT 5595  
QY 5487 GAACGCATACCTGGTGTAGCAGTCCCGGATGCACATGAATGAGTTCAACACCATGATGC 5546

Db 5596 GAGTGCCTATCTGGCTGAGCAGTCCCGCTGCACTTGAGCCAGTTCAACAGCATGAGCGC 5655  
QY 5547 ACTTCTCAGAGATCTTCTCTATGTGGGCAAAATACAGCGA-----GGAGATCTTTGGACC 5600  
Db 5656 CTTGCACGAGATCTACTCTCTACATCAACCAAGTACAGGATGAGGTGCAGATCTTGCAGC 5715  
QY 5601 TCTGACCCAGATGAGCAGTGTGGAGAGCAGAAACTGGCTTCAAACTAGAACTCAATCAT 5660  
Db 5716 CTTGGAGAGATGAGCAGCGCGCGGCGAGCGGCTTCCGAGCAAGCTGAGCAGGTGT 5775  
QY 5661 AACCTCATGAGCTTAGACAGCTGA 5685  
Db 5776 GGACACGATGGCCTGAGCAGCTGA 5800

RESULT 7  
US-10-108-260A-802  
; Sequence 802, Application US/10108260A  
; Publication No. US20040005560A1  
; GENERAL INFORMATION:  
; APPLICANT: HELIX RESEARCH INSTITUTE  
; TITLE OF INVENTION: No. US20040005560A1e1 full length cDNA  
; FILE REFERENCE: HI-A0106  
; CURRENT APPLICATION NUMBER: US/10/108,260A  
; CURRENT FILING DATE: 2002-03-27  
; NUMBER OF SEQ ID NOS: 5458  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 802  
; LENGTH: 3666  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-108-260A-802

Query Match 20.3%; Score 1157.8; DB 16; Length 3666;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1159; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4527 TGCCAAACAGCCCGAGGTCCAGTAAAGATCTCTCAACTGTGACACCATCACTCAGTCAA 4586  
Db 1 TGCCAAACAGCCCGAGGTCCAGTAAAGATCTCTCAACTGTGACACCATCACTCAGTCAA 60  
QY 4587 GGAGAAATCTGATGCGCATCTTCAAGAAATGTCCTTCCACCGGCCCAAGCTGC 4646  
Db 61 GGAGAAATCTGATGCGCATCTTCAAGAAATGTCCTTCCACCGGCCCAAGCTGC 120  
QY 4647 AGATATGATCTGGAGTGGCGACAGGAAGTGGGCAAGGATGATCTTGCAGGATGAAGA 4706  
Db 121 AGATATGATCTGGAGTGGCGACAGGAAGTGGGCAAGGATGATCTTGCAGGATGAAGA 180  
QY 4707 CATCACCAACAGATTGAGAAATGATTGGAAGGACTGAACACACTGGCCCACTACAGGT 4766  
Db 181 CATCACCAACAGATTGAGAAATGATTGGAAGGACTGAACACACTGGCCCACTACAGGT 240  
QY 4767 GCCAGATGGTTCCGTGGTGGCATTAGTGTCCAAAGCAGGTGACAGCCCTATAACGCAAGTAA 4826  
Db 241 GCCAGATGGTTCCGTGGTGGCATTAGTGTCCAAAGCAGGTGACAGCCCTATAACGCAAGTAA 300  
QY 4827 CAATCCACCGTCTCCAGGACCTCAGCAAGTAAATGAAACATGATCCGGTACACGGG 4886  
Db 301 CAATCCACCGTCTCCAGGACCTCAGCAAGTAAATGAAACATGATCCGGTACACGGG 360  
QY 4887 CAGCCCGGACAGCCTCCGCTCAGCGACACCTATGATCACTCTCTGACCTTGCAGAGTGGAGT 4946  
Db 361 CAGCCCGGACAGCCTCCGCTCAGCGACACCTATGATCACTCTCTGACCTTGCAGAGTGGAGT 420  
QY 4947 CAAGATGTGGACCTAGTGAAGAACACAGGACGAGGACGAGAGAGGAGGAGCGGG 5006  
Db 421 CAAGATGTGGACCTAGTGAAGAACACAGGACGAGGACGAGAGAGGAGGAGCGGG 480  
QY 5007 GAGCAAGATGGTGTGAAATCTACCTGACCCGACCTCTTGGCCACTTAAGGGCACAATGCA 5066  
Db 481 GAGCAAGATGGTGTGAAATCTACCTGACCCGACCTCTTGGCCACTTAAGGGCACAATGCA 540

RESULT 8  
US-10-245-752-91  
; Sequence 91, Application US/10245752  
; Publication No. US20030064473A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin  
; APPLICANT: Eaton, Dan  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stephan, Jean-Phillippe  
; APPLICANT: Watanabe, Colin  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; APPLICANT: Fong, Sherman  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; TITLE OF INVENTION: ACIDS ENCODING THE SAME  
; FILE REFERENCE: P3630R1C66  
; CURRENT APPLICATION NUMBER: US/10/245,752  
; CURRENT FILING DATE: 2002-09-16  
; PRIOR APPLICATION NUMBER: 10/197942  
; PRIOR FILING DATE: 2002-07-18  
; PRIOR APPLICATION NUMBER: 60/059114  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/063046  
; PRIOR FILING DATE: 1997-10-24

Qy	879	TGTAGAGGTGCCCATTTGGCTGTGAGCGCAGTGGGGTGGAGTACCGGCTCTGTCAGGCTGC	938
Db	301	TGTAGAGGTGCCCATTTGGCTGTGAGCGCAGTGGGGTGGAGTACCGGCTCTGTCAGGCTGC	360
Qy	939	CTACCTGTCAAAGCGGGGGCCGTGTTGGCAGGACCCCTTGAGTGCCATCCAGATGATGA	998
Db	361	CTACCTGTCAAAGCGGGGGCCGTGTTGGCAGGACCCCTTGAGTGCCATCCAGATGATGA	420
Qy	999	CCTGCTCTTCACCGTCTTCTCCAAGGGCCAGAAAGCGGAAAATGAAATCCCTGGATCAGTC	1058
Db	421	CCTGCTCTTCACCGTCTTCTCCAAGGGCCAGAAAGCGGAAAATGAAATCCCTGGATCAGTC	480
Qy	1059	GGCCCTGTGCATCTTCATCTTTGAAGCAGATTAATGACCGCATTAAGAGCGGCTGCAGTC	1118
Db	481	GGCCCTGTGCATCTTCATCTTTGAAGCAGATTAATGACCGCATTAAGAGCGGCTGCAGTC	540
Qy	1119	TTGTTACCGGGGGAGGGCAGCTTGACCTGGGCTGCGCTCAAGGTGAAGACATCCCGTG	1178
Db	541	TTGTTACCGGGGGAGGGCAGCTTGACCTGGGCTGCGCTCAAGGTGAAGACATCCCGTG	600
Qy	1179	CAGCAGTGCCTCTTTAACCATTCACGATACTTCTGTGGCTGGACATGTAATCTCTCCCT	1238
Db	601	CAGCAGTGCCTCTTTAACCATTCACGATACTTCTGTGGCTGGACATGTAATCTCTCCCT	660
Qy	1239	GGGAGTGTCCGACATGTGTGGTGGAAATCCCGTCTTCCAGGAGGACAGGACCGCATGAC	1298
Db	661	GGGAGTGTCCGACATGTGTGGTGGAAATCCCGTCTTCCAGGAGGACAGGACCGCATGAC	720

QY 1299 GTCTGTATCGATATGTTACAGAACCACTCTCTGCGCTTTGTGGCCACCAAAAGTGG 1358  
 DB 721 GTCTGTATCGCATATGTTACAGAACCACTCTCTGCGCTTTGTGGCCACCAAAAGTGG 780  
 QY 1359 CAAGCTGAAGAAGATCC 1375  
 DB 781 CAAGCTGAAGAAGTGC 797

RESULT 9

US-10-245-859-91  
 ; Sequence 91, Application US/10245859  
 ; Publication No. US2003006447A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Baker, Kevin  
 ; APPLICANT: Baton, Dan  
 ; APPLICANT: Filvaroff, Ellen  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Grimaldi, J. Christopher  
 ; APPLICANT: Gurney, Austin  
 ; APPLICANT: Smith, Victoria  
 ; APPLICANT: Stephan, Jean-Phillippe  
 ; APPLICANT: Watanabe, Colin  
 ; APPLICANT: Wood, William  
 ; APPLICANT: Zhang, Zemin  
 ; APPLICANT: Fong, Sherman  
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
 ; FILE REFERENCE: P3630R1C78  
 ; CURRENT APPLICATION NUMBER: US/10/245,859  
 ; CURRENT FILING DATE: 2002-09-16  
 ; PRIOR APPLICATION NUMBER: 10/197942  
 ; PRIOR FILING DATE: 2002-07-18  
 ; PRIOR APPLICATION NUMBER: 60/059114  
 ; PRIOR FILING DATE: 1997-09-17  
 ; PRIOR APPLICATION NUMBER: 60/063046  
 ; PRIOR FILING DATE: 1997-10-24  
 ; PRIOR APPLICATION NUMBER: 60/065027  
 ; PRIOR FILING DATE: 1997-11-10  
 ; PRIOR APPLICATION NUMBER: 60/079689  
 ; PRIOR FILING DATE: 1998-03-27  
 ; PRIOR APPLICATION NUMBER: 60/086478  
 ; PRIOR FILING DATE: 1998-05-22  
 ; PRIOR APPLICATION NUMBER: 60/087607  
 ; PRIOR FILING DATE: 1998-06-02  
 ; PRIOR APPLICATION NUMBER: 60/089801  
 ; PRIOR FILING DATE: 1998-06-18  
 ; PRIOR APPLICATION NUMBER: 60/090557  
 ; PRIOR FILING DATE: 1998-06-24  
 ; PRIOR APPLICATION NUMBER: 60/090589  
 ; PRIOR FILING DATE: 1998-06-25  
 ; Remaining Prior Application data removed - See File Wrapper or PALM.  
 ; NUMBER OF SEQ ID NOS: 116  
 ; SEQ ID NO 91  
 ; LENGTH: 2597  
 ; TYPE: DNA  
 ; ORGANISM: Homo Sapien  
 US-10-245-859-91

Query Match 13.9%; Score 793.8; DB 13; Length 2597;  
 Best Local Similarity 99.7%; Pred. No. 6.3e-220;  
 Matches 795; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 579 CGAGTATTTCCACCATCTCCAGCGGAACTGACCAAGAACTCTGAGCGGATGGCAT 638  
 DB 1 CGAGTATTTCCACCATCTCCAGCGGAACTGACCAAGAACTCTGAGCGGATGGCAT 60  
 QY 639 GTTCGGGTACGTTCTCCATGATGAGTTCTGTCGCTCGATGATTAAGATCCCTTCGGACAC 698  
 DB 61 GTTCGGGTACGTTCTCCATGATGAGTTCTGTCGCTCGATGATTAAGATCCCTTCGGACAC 120  
 QY 699 CTTCCACCATCTCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 758

DB 121 CTTCCACCATCTCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 180  
 QY 759 TGTCTACTTTTGAACCTCCACCTGAGATGAGTGTCTCCACCAAGGTCCACCAAGGA 818  
 DB 181 TGTCTACTTTTGAACCTCCACCTGAGATGAGTGTCTCCACCAAGGTCCACCAAGGA 240  
 QY 819 GCAGGTGTATACATCAAGCTGCTGAGGTTTTCAGAGGAGGACACAGCTTCACTCCTA 878  
 DB 241 GCAGGTGTATACATCAAGCTGCTGAGGTTTTCAGAGGAGGACACAGCTTCACTCCTA 300  
 QY 879 TGTAGAGGTGCCCATTTGGCTGTGAGCGCAGTGGGTGGAGTACCGCTGCTGTCAGGCTGC 938  
 DB 301 TGTAGAGGTGCCCATTTGGCTGTGAGCGCAGTGGGTGGAGTACCGCTGCTGTCAGGCTGC 360  
 QY 939 CTACCTGTCCAAAGCGGGCGCTGCTGTCGACGACCCCTTGGAGTCCATCCAGATGATGA 998  
 DB 361 CTACCTGTCCAAAGCGGGCGCTGCTGTCGACGACCCCTTGGAGTCCATCCAGATGATGA 420  
 QY 999 CTTGCTCTTCCACCGCTCTTCTCCAAAGGCGCAGAGCGGAAATGAAATCCCTGGATGATC 1058  
 DB 421 CTTGCTCTTCCACCGCTCTTCTCCAAAGGCGCAGAGCGGAAATGAAATCCCTGGATGATC 480  
 QY 1059 GGGCCTGTGATCTTTCATCTTGAAGCAGATTAATGACCCGATTAAGAGCGGCTGCAGTC 1118  
 DB 481 GGGCCTGTGATCTTTCATCTTGAAGCAGATTAATGACCCGATTAAGAGCGGCTGCAGTC 540  
 QY 1119 TTGTTACCGGGCGAGGCGACGCTGACCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCT 1178  
 DB 541 TTGTTACCGGGCGAGGGCGACGCTGGACCTGGCTGGCTGGCTGGCTGGCTGGCTGGCT 600  
 QY 1179 CAGCAGTGGCTCTTAAACCATTTGACGATTAATGACGATTAATGACGATTAATGACGAT 1238  
 DB 601 CAGCAGTGGCTCTTAAACCATTTGACGATTAATGACGATTAATGACGATTAATGACGAT 660  
 QY 1239 GGGAGTGTCCGACATGGTGGCTGGAAATTCCTGGCTGGCTGGCTGGCTGGCTGGCTGGCT 1298  
 DB 661 GGGAGTGTCCGACATGGTGGCTGGAAATTCCTGGCTGGCTGGCTGGCTGGCTGGCTGGCT 720  
 QY 1299 GTCTGTATCGCATATGTTACAGAACCACTCTCTGCGCTTTGTGGCCACCAAAAGTGG 1358  
 DB 721 GTCTGTATCGCATATGTTACAGAACCACTCTCTGCGCTTTGTGGCCACCAAAAGTGG 780  
 QY 1359 CAAGCTGAAGAAGATCC 1375  
 DB 781 CAAGCTGAAGAAGTGC 797

RESULT 10

US-10-245-103-91  
 ; Sequence 91, Application US/10245103  
 ; Publication No. US20030068778A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Baker, Kevin  
 ; APPLICANT: Baton, Dan  
 ; APPLICANT: Filvaroff, Ellen  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Grimaldi, J. Christopher  
 ; APPLICANT: Gurney, Austin  
 ; APPLICANT: Smith, Victoria  
 ; APPLICANT: Stephan, Jean-Phillippe  
 ; APPLICANT: Watanabe, Colin  
 ; APPLICANT: Wood, William  
 ; APPLICANT: Zhang, Zemin  
 ; APPLICANT: Fong, Sherman  
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
 ; FILE REFERENCE: P3630R1C112  
 ; CURRENT APPLICATION NUMBER: US/10/245,103  
 ; CURRENT FILING DATE: 2002-09-17  
 ; PRIOR APPLICATION NUMBER: 10/197942  
 ; PRIOR FILING DATE: 2002-07-18  
 ; PRIOR APPLICATION NUMBER: 60/059114

; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 91
; LENGTH: 2597
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-245-103-91

Query Match
Best Local Similarity 13.9%; Score 793.8; DB 15; Length 2597;
Matches 795; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 579 CGAGTATTTTCCACCATCTCCAGCGGAACTGACCAAGAACTCTGAGCGGATGGCAT 638
DB 1 CGAGTATTTTCCACCATCTCCAGCGGAACTGACCAAGAACTCTGAGCGGATGGCAT 60

QY 639 GTTCGGTAGCTTTCCATGATGAGTTCTGCGGCTCGATTAAGATCCCTTCGGACAC 698
DB 61 GTTCGGTAGCTTTCCATGATGAGTTCTGCGGCTCGATTAAGATCCCTTCGGACAC 120

QY 699 CTTCCACCATCATCCCTGACCTTCTATCTACTATGCTAGTGTCTTACGAGTGGCACTT 758
DB 121 CTTCCACCATCATCCCTGACCTTCTATCTACTATGCTAGTGTCTTACGAGTGGCACTT 180

QY 759 TGTCTACTTTTGGACCTCCAACTGAGATGGTGTCTCCACAGGCTCCACCAAGGA 818
DB 181 TGTCTACTTTTGGACCTCCAACTGAGATGGTGTCTCCACAGGCTCCACCAAGGA 240

QY 819 GCAGGTGTATACATCCAACTGAGGCTTTGCAAGGAGGACACAGCTTCACTCTTA 878
DB 241 GCAGGTGTATACATCCAACTGAGGCTTTGCAAGGAGGACACAGCTTCACTCTTA 300

QY 879 TGTAGAGGTGCCATTTGGCTGTGAGCGCAGTGGGCTGAGTACCGCTGTCTGAGGCTGC 938
DB 301 TGTAGAGGTGCCATTTGGCTGTGAGCGCAGTGGGCTGAGTACCGCTGTCTGAGGCTGC 360

QY 939 CTACTGTTCAAAGCGGGGCGCTGCTTGGCAGACCCCTTGGAGTCCATCCAGATGTA 998
DB 361 CTACTGTTCAAAGCGGGGCGCTGCTTGGCAGACCCCTTGGAGTCCATCCAGATGTA 420

QY 999 CTTGCTCTTCCAGGCTTTCTCCAGGCGCAGAGCGGAAATGAATCCCTTGGATGATC 1058
DB 421 CTTGCTCTTCCAGGCTTTCTCCAGGCGCAGAGCGGAAATGAATCCCTTGGATGATC 480

QY 1059 GGCCCTGTGCACTTTCTTGAAGCAGATAAATGACCGCATTAAGAGCGGCTGCAGTC 1118
DB 481 GGCCCTGTGCACTTTCTTGAAGCAGATAAATGACCGCATTAAGAGCGGCTGCAGTC 540

QY 1119 TTGTTTACCGGGGCGAGGCGAGCTGGACCTGGCTGGCTCAAGGTGAAGGACATCCCTG 1178
DB 541 TTGTTTACCGGGGCGAGGCGAGCTGGACCTGGCTGGCTCAAGGTGAAGGACATCCCTG 600

QY 1179 CAGCAGTGCCTTTAAACCATTTGACATACTCTGTGGCTGGACATGAATGCTCCCT 1238
DB 601 CAGCAGTGCCTTTAAACCATTTGACATACTCTGTGGCTGGACATGAATGCTCCCT 660

QY 1239 GGGAGTGTCCGACATGCTGGTGGAAATTCGGCTTTCACGGAGACAGGACCGCATGAC 1298
DB 661 GGGAGTGTCCGACATGCTGGTGGAAATTCGGCTTTCACGGAGACAGGACCGCATGAC 720

QY 1299 GTCTGTCTATCGCATATGCTTACAGAAACCACTCTCTGCGCTTTGTGGGCGACCAAAAGTGG 1358
DB 721 GTCTGTCTATCGCATATGCTTACAGAAACCACTCTCTGCGCTTTGTGGGCGACCAAAAGTGG 780

QY 1359 CAAGCTGAAGAGATCC 1375
DB 781 CAAGCTGAAGAGATGTC 797

RESULT 11
US-10-245-107-91
; Sequence 91, Application US/10245107
; Publication No. US20030068779A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Eaton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Phillippe
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630R1C71
; CURRENT APPLICATION NUMBER: US/10/245.107
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 91
; LENGTH: 2597
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-245-107-91

Query Match
Best Local Similarity 13.9%; Score 793.8; DB 15; Length 2597;
Matches 795; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 579 CGAGTATTTTCCACCATCTCCAGCGGAACTGACCAAGAACTCTGAGCGGATGGCAT 638
DB 1 CGAGTATTTTCCACCATCTCCAGCGGAACTGACCAAGAACTCTGAGCGGATGGCAT 60

QY 639 GTTCGGTAGCTTTCCATGATGAGTTCTGCGGCTCGATTAAGATCCCTTCGGACAC 698



Db	61	GTTCGGGTACGTCCTTCCATGATGAGTTCGGGCTCGATGATTAAAGATCCCTTCGGACAC	120
Qy	699	CTTCACCATCATCCCTGACCTTTGATATCTACTATGCTCTATGGTTTTAGCAGTGGCAACTT	758
Db	121	CTTCACCATCATCCCTGACCTTTGATATCTACTATGCTCTATGGTTTTAGCAGTGGCAACTT	180
Qy	759	TGTCCTACTTTTTGACCCCTCCAACTTGATGTTGTTCTCCACCAAGGTCACCAACCAAGGA	818
Db	181	TGTCCTACTTTTTGACCCCTCCAACTTGATGTTGTTCTCCACCAAGGTCACCAACCAAGGA	240
Qy	819	GCAGGTGTATACATATCCAAAGCTCGTGAAGCTTTTGCAGGAGGACACAGCCCTTCAACTCCTA	878
Db	241	GCAGGTGTATACATATCCAAAGCTCGTGAAGCTTTTGCAGGAGGACACAGCCCTTCAACTCCTA	300
Qy	879	TGTAGAGGTGCCCATTTGGCTGTGAGCGCAGTGGGTGGATACGGCTGCTGCAGGCTGC	938
Db	301	TGTAGAGGTGCCCATTTGGCTGTGAGCGCAGTGGGTGGATACGGCTGCTGCAGGCTGC	360
Qy	939	CTACCTGTCCAAAGCGGGGCGGTGCTTGGCAGGACCCCTTGGAGTCCATCCAGATGATGA	998
Db	361	CTACCTGTCCAAAGCGGGGCGGTGCTTGGCAGGACCCCTTGGAGTCCATCCAGATGATGA	420
Qy	999	CCTGCTCTTCAACCGTCTTCTCCAAAGGCCAGAGACGGAAATGAATCCCTGATGATGC	1058
Db	421	CCTGCTCTTCAACCGTCTTCTCCAAAGGCCAGAGACGGAAATGAATCCCTGATGATGC	480
Qy	1059	GGCCCTGTGATCTTTCATCTTTGAAGCAGATAAATGACCGCATTTAAGAGAGCGGCTGCAGTC	1118
Db	481	GGCCCTGTGATCTTTCATCTTTGAAGCAGATAAATGACCGCATTTAAGAGAGCGGCTGCAGTC	540
Qy	1119	TTGTTACGGGGGCGAGGGCAGCTTGGACCTGGCCCTGGCTCAAGTGAAGACATCCCTG	1178
Db	541	TTGTTACGGGGGCGAGGGCAGCTTGGACCTGGCCCTGGCTCAAGTGAAGACATCCCTG	600
Qy	1179	CAGCAGTGCCTCTTTAACCATTCACGATAACTTCTGTGGCTGGACATGAATGCTCCCT	1238
Db	601	CAGCAGTGCCTCTTTAACCATTCACGATAACTTCTGTGGCTGGACATGAATGCTCCCT	660
Qy	1239	GGGAGTGTCCGACATGTGTGGTGAATTCCTCGTCTTCAAGGAGGACAGGACCGCATGAC	1298
Db	661	GGGAGTGTCCGACATGTGTGGTGAATTCCTCGTCTTCAAGGAGGACAGGACCGCATGAC	720
Qy	1299	GTCTGTCTATCGCATATGCTTACAGAACCACTCTCTGGCCTTTGTGGCACCAAAAGTGG	1358
Db	721	GTCTGTCTATCGCATATGCTTACAGAACCACTCTCTGGCCTTTGTGGCACCAAAAGTGG	780
Qy	1359	CAAGCTGAAGAAGATCC	1375
Db	781	CAAGCTGAAGAAGTGC	797

## RESULT 12

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US-10-245-143-91
; Sequence 91, Application US/10245143
; Publication No. US20030068780A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Eaton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Giddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Justin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe
; APPLICANT: Watambe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRIMMING
; FILE REFERENCE: P3630R1C30
; CURRENT APPLICATION NUMBER: US/10/245143
; CURRENT FILING DATE: 2002-09-16

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/	PRIOR APPLICATION NUMBER:	10/197942
/	PRIOR FILING DATE:	2002-07-18
/	PRIOR APPLICATION NUMBER:	60/059114
/	PRIOR FILING DATE:	1997-09-17
/	PRIOR APPLICATION NUMBER:	60/063046
/	PRIOR FILING DATE:	1997-10-24
/	PRIOR APPLICATION NUMBER:	60/065027
/	PRIOR FILING DATE:	1997-11-10
/	PRIOR APPLICATION NUMBER:	60/079689
/	PRIOR FILING DATE:	1998-03-27
/	PRIOR APPLICATION NUMBER:	60/086478
/	PRIOR FILING DATE:	1998-05-22
/	PRIOR APPLICATION NUMBER:	60/087607
/	PRIOR FILING DATE:	1998-06-02
/	PRIOR APPLICATION NUMBER:	60/089801
/	PRIOR FILING DATE:	1998-06-18
/	PRIOR APPLICATION NUMBER:	60/090557
/	PRIOR FILING DATE:	1998-06-24
/	PRIOR APPLICATION NUMBER:	60/090689
/	PRIOR FILING DATE:	1998-06-25
/	Remaining Prior Application data removed - See File Wrapper or PALM.	
/	NUMBER OF SEQ ID NOS:	116
/	SEQ ID NO	91
/	LENGTH:	2597
/	TYPE:	DNA
/	ORGANISM:	Homo Sapien
/	US-10-245-143-91	

  

Query Match	13.9%;	Score	793.8;	DB	15;	Length	2597;	
Best Local Similarity	99.7%;	Pred.	No. 6.3e-220;					
Matches	795;	Conservative	0;	Mismatches	2;	Indels	0; Gaps	0;

  

Qy	579	CGAGTATTTTCCACCACCTCTCCAGCGGGAAAATGACCAAGAACA	CTGTGAGCGGATGGCAT	638
Db	1	CGAGTATTTTCCACCACCTCTCCAGCGGGAAAATGACCAAGAACA	CTGTGAGCGGATGGCAT	60
Qy	639	GTTCCGGGTACGCTTCATCATGATGAGTTCGTGGCCTCGATGATTAAGATCCCTTCGGACAC	698	
Db	61	GTTCCGGGTACGCTTCATCATGATGAGTTCGTGGCCTCGATGATTAAGATCCCTTCGGACAC	120	
Qy	699	CTTCACACATCATCCCTGACTTTTGATATCTACTATGCTATGGTTTTAGCAGTGGCAACTT	758	
Db	121	CTTCACACATCATCCCTGACTTTTGATATCTACTATGCTATGGTTTTAGCAGTGGCAACTT	180	
Qy	759	TGTTACTATTTTGACCCCTCCAACTCGATGTTGTTCTCACAGGGTCCACCAACGAAGA	818	
Db	181	TGTTACTATTTTGACCCCTCCAACTCGATGTTGTTCTCACAGGGTCCACCAACGAAGA	240	
Qy	819	GCAGGTGTATACATCCAAGTCGTGAGGCTTTGCAAGGAGGACACAGCCTTCAACTCCTA	878	
Db	241	GCAGGTGTATACATCCAAGTCGTGAGGCTTTGCAAGGAGGACACAGCCTTCAACTCCTA	300	
Qy	879	TGTAGAGGTGCCCATTTGGCTGTGAGCGCAGTGGGGTGGAGTACCGCTGCTCGAGGCTGC	938	
Db	301	TGTAGAGGTGCCCATTTGGCTGTGAGCGCAGTGGGGTGGAGTACCGCTGCTCGAGGCTGC	360	
Qy	939	CTACCTGTCAAAGCGGGGCGGTGCTGGCAGGACCTTGGAGTCCATCCAGATCATGA	998	
Db	361	CTACCTGTCAAAGCGGGGCGGTGCTGGCAGGACCTTGGAGTCCATCCAGATCATGA	420	
Qy	999	CCTGCTCTTTCACCGTCTTTCTCCAAAGCGGCAGAGCGGAAAAATGAAATCCCTGGATGAGTC	1058	
Db	421	CCTGCTCTTTCACCGTCTTTCTCCAAAGCGGCAGAGCGGAAAAATGAAATCCCTGGATGAGTC	480	
Qy	1059	GGCCCTGTGCATCTTCACTTTGAAGCAGATAAATGACCGGATTAAGAGCGGCTGCAGTC	1118	
Db	481	GGCCCTGTGCATCTTCACTTTGAAGCAGATAAATGACCGGATTAAGAGCGGCTGCAGTC	540	
Qy	1119	TTGTTTACGGGGCGAGGGACCGCTGGACCTTGGCTCGGCTCAAGGTGAAGACATCCCTTG	1178	
Db	541	TTGTTTACGGGGCGAGGGACCGCTGGACCTTGGCTCGGCTCAAGGTGAAGACATCCCTTG	600	
Qy	1179	CAGCAGTGCCTCTTAAACATTACGATAACTCTTGTGGCCTGGACATGAATGCTCCCTT	1238	



[illegible]

RESULT 13

RESULT 13  
US-10-245-771-91  
Sequence 91, Application US/10245771  
Publication No. US20030068781A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin  
APPLICANT: Eaton, Dan  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Goddard, Audrey  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin  
APPLICANT: Smith, Victoria  
APPLICANT: Stephan, Jean-Philippe  
APPLICANT: Watanabe, Colin  
APPLICANT: Wood, William  
APPLICANT: Zhang, Zemin  
APPLICANT: Fong, Sherman  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
ACIDS ENCODING THE SAME  
FILE REFERENCE: P3630R1C98  
CURRENT APPLICATION NUMBER: US/10/245,771  
CURRENT FILING DATE: 2002-09-16  
PRIOR APPLICATION NUMBER: 10/197942  
PRIOR FILING DATE: 2002-07-18  
PRIOR APPLICATION NUMBER: 60/059114  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/063046  
PRIOR FILING DATE: 1997-10-24  
PRIOR APPLICATION NUMBER: 60/065027  
PRIOR FILING DATE: 1997-11-10  
PRIOR APPLICATION NUMBER: 60/079689  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/086478  
PRIOR FILING DATE: 1998-05-22  
PRIOR APPLICATION NUMBER: 60/087607  
PRIOR FILING DATE: 1998-06-02  
PRIOR APPLICATION NUMBER: 60/089801  
PRIOR FILING DATE: 1998-06-18  
PRIOR APPLICATION NUMBER: 60/090557  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090689  
PRIOR FILING DATE: 1998-06-25  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 116  
SEQ ID NO 91  
LENGTH: 2597  
TYPE: DNA  
ORGANISM: Homo Sapien  
US-10-245-771-91

	Query Match	13.9%	Score 793.8;	DB 15;	Length 2597;
	Best Local Similarity	99.7%	Fed. No. 6.3e-220;		
	Matches 795;	Conservative	0;	Mismatches 2;	Indels 0; Gaps 0;
Qy	579	CGAGTATTTTCCCACTCTCCAGCGCGAAACTGACCAAGAACTCTGAGCGCGATGGCAT	638		
Dy	1	CGAGTATTTTCCCACTCTCCAGCGCGAAACTGACCAAGAACTCTGAGCGCGATGGCAT	60		

Qy	639	GTTCGGGTACGCTCTTCCATGATGAGTTCGTGGCTCGATGATTAAGATCCCTTCGACAC	698
Db	61	GTTCGGGTACGCTCTTCCATGATGAGTTCGTGGCTCGATGAATGAATCCCTTCGACAC	120
Qy	699	CTTCACCATCATCCCTGACTTTGATATCTACTATGCTATGTTTGTAGCAGTGGCAACTT	758
Db	121	CTTCACCATCATCCCTGACTTTGATATCTACTATGCTATGTTTGTAGCAGTGGCAACTT	180
Qy	759	TGTCCTACTTTTGAACCCCTCGAACCTGAGATGGTGTCTCCACGAGGTCCACCAACCAAGGA	818
Db	181	TGTCCTACTTTTGAACCCCTCGAACCTGAGATGGTGTCTCCACGAGGTCCACCAACCAAGGA	240
Qy	819	GCAGGTGTATACATCCAAAGCTCGTGAAGCTTTTCCAAAGGAGGACACAGCCCTTCAACTCCTA	878
Db	241	GCAGGTGTATACATCCAAAGCTCGTGAAGCTTTTCCAAAGGAGGACACAGCCCTTCAACTCCTA	300
Qy	879	TGTAGAGGTGCCCATTTGGCTGTGAGCGCAGTGGGGTGGAGTACCGCTGCTGAGCGTGC	938
Db	301	TGTAGAGGTGCCCATTTGGCTGTGAGCGCAGTGGGGTGGAGTACCGCTGCTGAGCGTGC	360
Qy	939	CTACCTGTCCAAAGCGGGGCCGTGCTTGCGCAGGACCCCTTGGAGTCCATCCAGATGATGA	998
Db	361	CTACCTGTCCAAAGCGGGGCCGTGCTTGCGCAGGACCCCTTGGAGTCCATCCAGATGATGA	420
Qy	999	CTGCTCTTCCACCGTCTTTCTCCAAAGGCCAGAGCGGAAAAATGAAATCCCTGATGATGC	1058
Db	421	CTGCTCTTCCACCGTCTTTCTCCAAAGGCCAGAGCGGAAAAATGAAATCCCTGATGATGC	480
Qy	1059	GGCCCTGTGCATCTTCATCTTGAAGCAGATAAATGACCGCATTAAGAGCGGCTGCAGTC	1118
Db	481	GGCCCTGTGCATCTTCATCTTGAAGCAGATAAATGACCGCATTAAGAGCGGCTGCAGTC	540
Qy	1119	TTGTTACCGGGCGAGGCGACGCTGGACCTGGCTCGGCTCAAGGTGAAGACATCCCTCGT	1178
Db	541	TTGTTACCGGGCGAGGCGACGCTGGACCTGGCTCGGCTCAAGGTGAAGACATCCCTCGT	600
Qy	1179	CAGCAGTGCCTCTTTAACCATTCACGATACCTTCTGTGGCTCGACATGAATGCTCCCT	1238
Db	601	CAGCAGTGCCTCTTTAACCATTCACGATACCTTCTGTGGCTCGACATGAATGCTCCCT	660
Qy	1239	GGGAGTGTCCGACATGCTGCGTGAATTCCTGCTTTCACGGAGACAGGACCGCATGAC	1298
Db	661	GGGAGTGTCCGACATGCTGCGTGAATTCCTGCTTTCACGGAGACAGGACCGCATGAC	720
Qy	1299	GTCTGTCATCGCATATGCTTACAGACCACTCTCTGGCTTTGTGGCACCAAAAGTGG	1358
Db	721	GTCTGTCATCGCATATGCTTACAGACCACTCTCTGGCTTTGTGGCACCAAAAGTGG	780
Qy	1359	CAAGCTGAAGAAGATCC	1375
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## RESULT 14

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US-10-245-851-91
; Sequence 91, Application US/10245851
; Publication No. US20030068782A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Baton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Phillippe
; APPLICANT: Watambe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME

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FILE REFERENCE: P3630R1C93  
CURRENT APPLICATION NUMBER: US/10/245,851  
CURRENT FILING DATE: 2002-09-16  
PRIOR APPLICATION NUMBER: 10/197942  
PRIOR FILING DATE: 2002-07-18  
PRIOR APPLICATION NUMBER: 60/059114  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/063046  
PRIOR FILING DATE: 1997-10-24  
PRIOR APPLICATION NUMBER: 60/065027  
PRIOR FILING DATE: 1997-11-10  
PRIOR APPLICATION NUMBER: 60/079689  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/086478  
PRIOR FILING DATE: 1998-05-22  
PRIOR APPLICATION NUMBER: 60/087607  
PRIOR FILING DATE: 1998-06-02  
PRIOR APPLICATION NUMBER: 60/089801  
PRIOR FILING DATE: 1998-06-18  
PRIOR APPLICATION NUMBER: 60/090557  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090689  
PRIOR FILING DATE: 1998-06-25  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 116  
SEQ ID NO 91  
LENGTH: 2597  
TYPE: DNA  
ORGANISM: Homo Sapien  
US-10-245-851-91

Query Match  
Best Local Similarity 13.9%; Score 793.8; DB 15; Length 2597;  
Matches 795; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 579 CGAGTATTTTCCCACTCCAGCGGGAAGTCCAGCAAGAACTCTGAGGGGATGTCAT 638  
DB 1 CGAGTATTTTCCCACTCTCCAGCGGGAAGTCCAGCAAGAACTCTGAGGGGATGTCAT 60  
QY 639 GTTCGCTAGCTTTCCCAAGTATGATTCGTGGCTCGATGATTAAGATTCCTTCGACAC 698  
DB 61 GTTCGCTAGCTTTCCCAAGTATGATTCGTGGCTCGATGATTAAGATTCCTTCGACAC 120  
QY 699 CTTACCATCATCCCTGACTTTGATCTATCTATGCTATGCTTTTACAGTGGCACTT 758  
DB 121 CTTACCATCATCCCTGACTTTGATCTATCTATGCTATGCTTTTACAGTGGCACTT 180  
QY 759 TGTCTACTTTTGGACCTTCCAACTGAGATGGTGTCTCCACAGGCTCCACCAAGGA 818  
DB 181 TGTCTACTTTTGGACCTTCCAACTGAGATGGTGTCTCCACAGGCTCCACCAAGGA 240  
QY 819 GCAGTGTATACATCCAACTGCTGAGGCTTTGCAAGGAGCACAGGCTTCACTCTTA 878  
DB 241 GCAGTGTATACATCCAACTGCTGAGGCTTTGCAAGGAGCACAGGCTTCACTCTTA 300  
QY 879 TGTAGAGTGGCCATTGGCTGTGAGCGCAGTGGGTGAGTACCGCTGTGCGAGGCTGC 938  
DB 301 TGTAGAGTGGCCATTGGCTGTGAGCGCAGTGGGTGAGTACCGCTGTGCGAGGCTGC 360  
QY 939 CTACTGTCTCAAGCGGGGCGCTGCTGGCAGGACCTTTGAGTCCATCCAGATGTA 998  
DB 361 CTACTGTCTCAAGCGGGGCGCTGCTGGCAGGACCTTTGAGTCCATCCAGATGTA 420  
QY 999 CTTGCTCTTCCAGCTTCTTCCAAAGCGGCGGAAATGAAATCCCTGGATGACTC 1058  
DB 421 CTTGCTCTTCCAGCTTCTTCCAAAGCGGCGGAAATGAAATCCCTGGATGACTC 480  
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DB 481 GGCCTGTGCTATCTTCACTTTGAAGCAGATAATGACCGCATTAAGAGCGGCTGCACTC 540  
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DB 541 TTGTTTACCGGGGCGAGGCGACGCTGACCTGGCCTGGCTCAAGGTGAAGGACATCCCTG 600  
QY 1179 CAGCAGTGGCTCTTTAAGCATGACATACTTCTGTGGCTGGACATGATGCTCCCT 1238  
DB 601 CAGCAGTGGCTCTTTAAGCATGACATACTTCTGTGGCTGGACATGATGCTCCCT 660  
QY 1239 GGGAGTGTCCGACATGCTGGTGGAAATCCCGTCTTTCACGAGGACAGGACCGCATGAC 1298  
DB 661 GGGAGTGTCCGACATGCTGGTGGAAATCCCGTCTTTCACGAGGACAGGACCGCATGAC 720  
QY 1299 GTCTGTCTCATGATGCTCTACAGAACCACTCTCTGCGCTTTGTGGCCACCAAGTGG 1358  
DB 721 GTCTGTCTCATGATGCTCTACAGAACCACTCTCTGCGCTTTGTGGCCACCAAGTGG 780  
QY 1359 CAAGCTGAAGAAGATCC 1375  
DB 781 CAAGCTGAAGAAGTGC 797

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Sequence 91, Application US/10245883  
Publication No. US20030068783A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin  
APPLICANT: Eaton, Dan  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Goddard, Audrey  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin  
APPLICANT: Smith, Victoria  
APPLICANT: Stephan, Jean-Philippe  
APPLICANT: Watanabe, Colin  
APPLICANT: Wood, William  
APPLICANT: Zhang, Zemin  
APPLICANT: Fong, Sherman  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
TITLE OF INVENTION: ACIDS ENCODING THE SAME  
FILE REFERENCE: P3630R1C70  
CURRENT APPLICATION NUMBER: US/10/245,883  
CURRENT FILING DATE: 2002-09-16  
PRIOR APPLICATION NUMBER: 10/197942  
PRIOR FILING DATE: 2002-07-18  
PRIOR APPLICATION NUMBER: 60/059114  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/063046  
PRIOR FILING DATE: 1997-10-24  
PRIOR APPLICATION NUMBER: 60/065027  
PRIOR FILING DATE: 1997-11-10  
PRIOR APPLICATION NUMBER: 60/079689  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/086478  
PRIOR FILING DATE: 1998-05-22  
PRIOR APPLICATION NUMBER: 60/087607  
PRIOR FILING DATE: 1998-06-02  
PRIOR APPLICATION NUMBER: 60/089801  
PRIOR FILING DATE: 1998-06-18  
PRIOR APPLICATION NUMBER: 60/090557  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090689  
PRIOR FILING DATE: 1998-06-25  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 116  
SEQ ID NO 91  
LENGTH: 2597  
TYPE: DNA  
ORGANISM: Homo Sapien  
US-10-245-883-91

Query Match 13.9%; Score 793.8; DB 15; Length 2597;  
Best Local Similarity 99.7%; Pred. No. 6.3e-220;  
Matches 795; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 579 CGAGTATTTTCCGACCATCTCCAGCCGGAACTGACCAAGAACTCTGAGCGGATGGCAT 638  
Db 1 CGAGTATTTTCCGACCATCTCCAGCCGGAACTGACCAAGAACTCTGAGCGGATGGCAT 60  
QY 639 GTTCGGGTACGCTCTCCATCATGAGTTCCGTGGCCTCGATGATTAAGATCCCTTCGGACAC 698  
Db 61 GTTCGGGTACGCTCTCCATCATGAGTTCCGTGGCCTCGATGATTAAGATCCCTTCGGACAC 120  
QY 699 CTTACCATCATCCCTGACCTTTGATATCTACTATGTCTATGTTTGTAGAGTGGCACTT 758  
Db 121 CTTACCATCATCCCTGACCTTTGATATCTACTATGTCTATGTTTGTAGAGTGGCACTT 180  
QY 759 TGTCTACTTTTGGACCTCCAACTCAGATGTTCTCCACGAGGTCCACCAACCAAGGA 818  
Db 181 TGTCTACTTTTGGACCTCCAACTCAGATGTTCTCCACGAGGTCCACCAACCAAGGA 240  
QY 819 GCAGGTGTATACATCCAAAGCTGTGAGGCTTTGCAAGGAGGACACAGCCTTCAACTCCTA 878  
Db 241 GCAGGTGTATACATCCAAAGCTGTGAGGCTTTGCAAGGAGGACACAGCCTTCAACTCCTA 300  
QY 879 TGTAGAGTGGCCCATTTGGCTGTGAGCGCAGTGGGGTGGAGTACCGGCTGCTCAGGCTGC 938  
Db 301 TGTAGAGTGGCCCATTTGGCTGTGAGCGCAGTGGGGTGGAGTACCGGCTGCTCAGGCTGC 360  
QY 939 CTAACCTGTCCAAAGCGGGGCGGTGCTTGGCAGGACCTTGGAGTCCATCCAGATGATGA 998  
Db 361 CTAACCTGTCCAAAGCGGGGCGGTGCTTGGCAGGACCTTGGAGTCCATCCAGATGATGA 420  
QY 999 CTTGCTCTTCCACCGTCTTCTCCAAAGCGGCGGAAATGAAATCCCTGATGAGTC 1058  
Db 421 CTTGCTCTTCCACCGTCTTCTCCAAAGCGGCGGAAATGAAATCCCTGATGAGTC 480  
QY 1059 GGCCCTGTGCATCTTCACTTTGAAGCAGATAAATGACCCCATTTAAGGCGGCTGCAGTC 1118  
Db 481 GGCCCTGTGCATCTTCACTTTGAAGCAGATAAATGACCCCATTTAAGGCGGCTGCAGTC 540  
QY 1119 TTGTTACCGGGGAGGCGACGCTGACCTGGCTGGCTCAAGGTCAAGGACATCCCTG 1178  
Db 541 TTGTTACCGGGGAGGCGACGCTGACCTGGCTGGCTCAAGGTCAAGGACATCCCTG 600  
QY 1179 CAGCAGTGGCTCTTAACCATTAACGATAAATCTTGTGGCTGGACATGAATGCTCCCT 1238  
Db 601 CAGCAGTGGCTCTTAACCATTAACGATAAATCTTGTGGCTGGACATGAATGCTCCCT 660  
QY 1239 GGGAGTGTCCGACATGGTGGTGGATTCCTGCTTCCGAGGACAGGAGCGGATGAC 1298  
Db 661 GGGAGTGTCCGACATGGTGGTGGATTCCTGCTTCCGAGGACAGGAGCGGATGAC 720  
QY 1299 GTCTGTATCGCATATGCTTACAAAGAACCACTCTCTGGCTTTGTGGGCAACCAAGTGG 1358  
Db 721 GTCTGTATCGCATATGCTTACAAAGAACCACTCTCTGGCTTTGTGGGCAACCAAGTGG 780  
QY 1359 CAAGCTGAGAGATCC 1375  
Db 781 CAAGCTGAGAGGTGC 797

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Job time : 1479 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 25, 2004, 03:45:17 ; Search time 29 Seconds  
(without alignments)  
3375.270 Million cell updates/sec

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Perfect score: 9990  
Sequence: 1 MKAMPNWTCLLSHLMVGM.....QKLAYKLEQVITLMSLDNKK 1896

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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3	1351.5	13.5	552	4	US-09-902-775A-170
4	1349	13.5	1568	3	US-09-181-706-2
5	1349	13.5	1568	3	US-09-458-791-2
6	1349	13.5	1568	3	US-09-459-066-2
7	1349	13.5	1568	4	US-09-459-065-2
8	538.5	5.4	1404	4	US-09-345-473E-24
9	308	3.1	607	4	US-08-556-422A-4
10	263	2.6	888	4	US-09-077-940A-4
11	244.5	2.4	887	4	US-09-077-940A-2
12	228	2.3	1086	4	US-09-653-274-4
13	227	2.3	724	1	US-08-121-713D-62
14	227	2.3	724	1	US-08-835-268-62
15	227	2.3	724	1	US-09-060-692-62
16	227	2.3	724	3	US-08-833-391-62
17	227	2.3	724	4	US-09-060-610-62
18	227	2.3	724	5	PCT-US94-10151A-62
19	220	2.2	641	4	US-09-653-274-13
20	220	2.2	1070	4	US-09-653-274-8
21	207	2.1	730	1	US-08-121-713D-58
22	207	2.1	730	1	US-08-835-268-58
23	207	2.1	730	2	US-09-060-692-58
24	207	2.1	730	3	US-08-833-391-58
25	207	2.1	730	4	US-09-060-610-58
26	207	2.1	730	5	PCT-US94-10151A-58
27	200	2.0	771	1	US-08-121-713D-54

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29 200 2.0 771 2 US-09-060-692-54 Sequence 54, Appl  
30 200 2.0 771 3 US-08-833-391-54 Sequence 54, Appl  
31 200 2.0 771 4 US-09-060-610-54 Sequence 54, Appl  
32 200 2.0 771 5 PCT-US94-10151A-54 Sequence 54, Appl  
33 196.5 2.0 655 4 US-08-556-422A-3 Sequence 3, Appl  
34 186 1.9 712 1 US-08-121-713D-64 Sequence 64, Appl  
35 186 1.9 712 1 US-08-835-268-64 Sequence 64, Appl  
36 186 1.9 712 2 US-09-060-692-64 Sequence 64, Appl  
37 186 1.9 712 3 US-08-833-391-64 Sequence 64, Appl  
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42 185 1.9 650 2 US-09-060-692-60 Sequence 60, Appl  
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44 185 1.9 650 4 US-09-060-610-60 Sequence 60, Appl  
45 185 1.9 650 5 PCT-US94-10151A-60 Sequence 60, Appl

#### ALIGNMENTS

RESULT 1  
US-09-907-794A-170  
; Sequence 170, Application US/09907794A  
; Patent No. 6635468  
; GENERAL INFORMATION:  
; APPLICANT: Genentech, Inc.  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, A.  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth, J.  
; APPLICANT: Kijavini, Ivar J.  
; APPLICANT: Mather, Jennie P.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William, I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: 10466-14  
; CURRENT APPLICATION NUMBER: US/09/907,794A  
; CURRENT FILING DATE: 2001-07-17  
; PRIOR APPLICATION NUMBER: PCT/US00/04414  
; PRIOR FILING DATE: 2000-02-22  
; PRIOR APPLICATION NUMBER: US 60/143,048  
; PRIOR FILING DATE: 1999-07-07  
; PRIOR APPLICATION NUMBER: US 60/145,698  
; PRIOR FILING DATE: 1999-07-26  
; PRIOR APPLICATION NUMBER: US 60/146,222  
; PRIOR FILING DATE: 1999-07-28  
; PRIOR APPLICATION NUMBER: PCT/US99/20594  
; PRIOR FILING DATE: 1999-09-08  
; PRIOR APPLICATION NUMBER: PCT/US99/20944  
; PRIOR FILING DATE: 1999-09-13  
; PRIOR APPLICATION NUMBER: PCT/US99/21090  
; PRIOR FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: PCT/US99/21547

; PRIOR FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: PCT/US99/23089  
; PRIOR FILING DATE: 1999-10-05  
; PRIOR APPLICATION NUMBER: PCT/US99/28214  
; PRIOR FILING DATE: 1999-11-29  
; PRIOR APPLICATION NUMBER: PCT/US99/28313  
; PRIOR FILING DATE: 1999-11-30  
; PRIOR APPLICATION NUMBER: PCT/US99/28564  
; PRIOR FILING DATE: 1999-12-02  
; PRIOR APPLICATION NUMBER: PCT/US99/28565  
; PRIOR FILING DATE: 1999-12-02  
; PRIOR APPLICATION NUMBER: PCT/US99/30095  
; PRIOR FILING DATE: 1999-12-16  
; PRIOR APPLICATION NUMBER: PCT/US99/30911  
; PRIOR FILING DATE: 1999-12-20  
; PRIOR APPLICATION NUMBER: PCT/US99/30999  
; PRIOR FILING DATE: 1999-12-20  
; PRIOR APPLICATION NUMBER: PCT/US06/00219  
; PRIOR FILING DATE: 2000-01-05  
; NUMBER OF SEQ ID NOS: 423  
; SEQ ID NO 170  
; LENGTH: 552  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-907-794A-170

Query Match 13.5%; Score 1351.5; DB 4; Length 552;  
Best Local Similarity 51.6%; Pred. No. 8.4e-113;  
Matches 269; Conservative 81; Mismatches 116; Indels 55; Gaps 8;  
QY 23 STLLTRQAPLPSKOR-----SFVTFRCPEAE- 49  
DB 45 SRIIT--AAPLSEQWQWPALEVRDSVLLSVVWVLLAPPAGMPQSFTHSENRW 102  
QY 50 GFNLVVDERTGHIYLGAVNRVYKLSLKVLTHTGPDENPKCYPRIVQTCNEPIT 109  
DB 103 TFNHLTVHQGTGAVVYGAIRVYKLTGNTLIQVAHKTGPEEDKNSRYPPLIVQPCSEVLT 162  
QY 110 TTNVNVKLLIDYKENELIACGSLYOGICKLLLEDFKLGEYPYKHEHVLSCVNESGSV 169  
DB 163 LTNVNVKLLIDYSENRLLACGSLYOGVCKLLRLDOLFILVEPSHKHEHVLSCVNTGTM 222  
QY 170 FGIVSVSNLDDKFLIATAVDGRPEYPTTSSRKLTKNSEADGMFAIVFHDFFVASMIXI 229  
DB 223 YGVIVRSEGDGKFLIGTAVDGRQDYFPTLSSRKLPRDPRESSAMLDYELHSDVSSLIKI 282  
QY 230 PSDTFIIPFDIYVYVGFSSGNFVFLILOPEWSPPG---STTKEQVYTSKLVRLCKE 286  
DB 283 PSDTLAVSHFDIFYIYGFASGFGVFLTVQPE--TPEGVAINSAGDLFTYTRIVRLCKD 340  
QY 287 DTAFNSYVEVPICGERSGVYRLLQAAVLSKAGAVLGRTLGVHPDDLLFTVFSKGQKXK 346  
DB 341 DPXFSYVSLPFGCTRAGVEYRLLQAAVLSKAGAVLGRTLGVHPDDLLFTVFSKGQKXK 400  
QY 347 MKSLDESALCIFILKQINDRIKRLQSCYRGEGTLDLAKVKVDIPCCSALLTIDDNFCG 406  
DB 401 HHPDDSDALCAFTIRAINLQIKERLQSCYRGEGNLEMLLGRKDVQCTKAPVIDDNFCG 460  
QY 407 LDMNAPLGVSDMYRGIPVFTEDDRMTSVIAYVYKXHSIAFVTKSGKLLKRVVDGPRGN 466  
DB 461 LDINQPLGGTPEGLTLYTSRDMTSVASYVYNGSVYVFGTKSGKLLKRVV----- 514  
QY 467 ALOYE-----TVQVVDPGVPLRDMAFSK-DHEQLYIMSERQ 501  
DB 515 ---YEFRCNAIHLLSKESLLEGSYVWFRNYRQLYFLIGQR 552

RESULT 2  
US-09-905-125A-170  
; Sequence 170, Application US/09905125A  
; Patent No. 6664376  
; GENERAL INFORMATION:  
; APPLICANT: Genentech, Inc.

; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Geritsen, Mary E.  
; APPLICANT: Goddard, A.  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth, J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Mather, Jennie P.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William, I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: 10466-14  
; CURRENT APPLICATION NUMBER: US/09/905.125A  
; CURRENT FILING DATE: 2001-07-12  
; PRIOR APPLICATION NUMBER: PCT/US00/04414  
; PRIOR FILING DATE: 2000-02-22  
; PRIOR APPLICATION NUMBER: US 60/143,048  
; PRIOR FILING DATE: 1999-07-07  
; PRIOR APPLICATION NUMBER: US 60/145,698  
; PRIOR FILING DATE: 1999-07-26  
; PRIOR APPLICATION NUMBER: US 60/146,222  
; PRIOR FILING DATE: 1999-07-28  
; PRIOR APPLICATION NUMBER: PCT/US99/20594  
; PRIOR FILING DATE: 1999-09-08  
; PRIOR APPLICATION NUMBER: PCT/US99/20944  
; PRIOR FILING DATE: 1999-09-13  
; PRIOR APPLICATION NUMBER: PCT/US99/21090  
; PRIOR FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: PCT/US99/21547  
; PRIOR FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: PCT/US99/23089  
; PRIOR FILING DATE: 1999-10-05  
; PRIOR APPLICATION NUMBER: PCT/US99/28214  
; PRIOR FILING DATE: 1999-11-29  
; PRIOR APPLICATION NUMBER: PCT/US99/28313  
; PRIOR FILING DATE: 1999-11-30  
; PRIOR APPLICATION NUMBER: PCT/US99/28564  
; PRIOR FILING DATE: 1999-12-02  
; PRIOR APPLICATION NUMBER: PCT/US99/28565  
; PRIOR FILING DATE: 1999-12-02  
; PRIOR APPLICATION NUMBER: PCT/US99/30095  
; PRIOR FILING DATE: 1999-12-16  
; PRIOR APPLICATION NUMBER: PCT/US99/30911  
; PRIOR FILING DATE: 1999-12-20  
; PRIOR APPLICATION NUMBER: PCT/US99/30999  
; PRIOR FILING DATE: 1999-12-20  
; PRIOR APPLICATION NUMBER: PCT/US00/00219  
; PRIOR FILING DATE: 2000-01-05  
; NUMBER OF SEQ ID NOS: 423  
; SEQ ID NO 170  
; LENGTH: 552  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-905-125A-170

Query Match 13.5%; Score 1351.5; DB 4; Length 552;  
Best Local Similarity 51.6%; Pred. No. 8.4e-113;  
Matches 269; Conservative 81; Mismatches 116; Indels 55; Gaps 8;

QY 23 STLLTRQAPAPLSQOKR-----SFVTRGEPAE- 49  
Db 45 SRLLT--AAPLSMEQRPWRALEVDSSRVLLSVVLLAPPAGMPQFSTPHSENRDW 102  
QY 50 GFNHLVVDERTGHLYLGAVNRIYKLSDDLKVLVTHETGPDNDPKCYPRIVOTCNEPLT 109  
Db 103 TFNHLTVHQGTGAVYVGVGAINRYKLTGNLTQVAKHTGPEEDNKSRYPPPLIVQPCSEVLT 162  
QY 110 TTNNVNMKLLIDYKENRLIACGSLYQGIKLLRLLEDLFLKGEYPYHKEHYLSGVNBSGSV 169  
Db 163 LTNNVNMKLLIDYSENRLIACGSLYQGVCKLLRLDDLLFILVPSHKEHYLSVNVKTGTM 222  
QY 170 FGVIVSYNLDKDLFIATAVDGKPEYPTTISRKLTKNSADGMFAVYHDFVASMIKI 229  
Db 223 YGVIVRSEGEDEGLFVGTAVDGKQDFFPTLSRKLPRDPSSAMLDYELHSDDFVSSLIKI 282  
QY 230 PSDTFTIIPDPIYVYVGFSSGNFVYFLTLQPEMVSPPG---STTKEQVYTSKLVRLCKE 286  
Db 283 PSDTLALVSHDFIYVYGFASGGFVYFLTVQPE--TPEGVAINSAGDLFYTSRIVRLCKD 340  
QY 287 DTAFNSVYVPIGCRSGVYRLLQAAVLSKAGAVLRTGLCVHPDDDLLFTVFSKGOKRK 346  
Db 341 DPKEFHSVSLPFGCTRAGVEYRLQAYLAKPGDSLQAQAFNITSQDDVLFVFAIFSKGOKQY 400  
QY 347 MKSLDESALCIFIILKQINDRIKERLQSCYRGEGLDLAWLKVDI PCSSALLTIDNFCG 406  
Db 401 HHPDDSALCAFPPIRINLQIKERLQSCYQEGNLELWLLGKDVQCTKAPVPIDNFCG 460  
QY 407 LDMAPLGVSDMVRGIPVFTEDRDMTIVYVYKXSLAFVGTSGKLLKIRVDGPRGN 466  
Db 461 LDINQPLGSGTVEGLTLTYTTSRDMTIVASVYVNGYSWVFGTSGKLLKVRV----- 514  
QY 467 ALOVE-----TVQVNDPGVLRDMAFSK-DHEQLVIMSERQ 501  
Db 515 ---YEFRCNAIHLKSLEGSLEGSYWRNFRNQLFLGEQR 552

RESULT 3

US-09-902-775A-170  
; Sequence 170, Application US/09902775A  
; Patent No. 6686431  
; GENERAL INFORMATION:  
; APPLICANT: Genentech, Inc.  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Botstein, David  
; APPLICANT: Desnucy, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, A.  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth, J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Mather, Jennie P.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William, I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: 10466-14  
; CURRENT APPLICATION NUMBER: US/09/902, 775A  
; CURRENT FILING DATE: 2001-07-10

; PRIOR APPLICATION NUMBER: PCT/US00/04414  
; PRIOR FILING DATE: 2000-02-22  
; PRIOR APPLICATION NUMBER: US 60/143,048  
; PRIOR FILING DATE: 1999-07-07  
; PRIOR APPLICATION NUMBER: US 60/145,698  
; PRIOR FILING DATE: 1999-07-26  
; PRIOR APPLICATION NUMBER: US 60/146,222  
; PRIOR FILING DATE: 1999-07-28  
; PRIOR APPLICATION NUMBER: PCT/US99/20594  
; PRIOR FILING DATE: 1999-09-08  
; PRIOR APPLICATION NUMBER: PCT/US99/20944  
; PRIOR FILING DATE: 1999-09-13  
; PRIOR APPLICATION NUMBER: PCT/US99/21090  
; PRIOR FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: PCT/US99/21547  
; PRIOR FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: PCT/US99/23089  
; PRIOR FILING DATE: 1999-10-05  
; PRIOR APPLICATION NUMBER: PCT/US99/28214  
; PRIOR FILING DATE: 1999-11-29  
; PRIOR APPLICATION NUMBER: PCT/US99/28313  
; PRIOR FILING DATE: 1999-11-30  
; PRIOR APPLICATION NUMBER: PCT/US99/28564  
; PRIOR FILING DATE: 1999-12-02  
; PRIOR APPLICATION NUMBER: PCT/US99/28565  
; PRIOR FILING DATE: 1999-12-02  
; PRIOR APPLICATION NUMBER: PCT/US99/30095  
; PRIOR FILING DATE: 1999-12-16  
; PRIOR APPLICATION NUMBER: PCT/US99/30911  
; PRIOR FILING DATE: 1999-12-20  
; PRIOR APPLICATION NUMBER: PCT/US99/30999  
; PRIOR FILING DATE: 1999-12-20  
; PRIOR APPLICATION NUMBER: PCT/US00/00219  
; PRIOR FILING DATE: 2000-01-05  
; NUMBER OF SEQ ID NOS: 423  
; SEQ ID NO 170  
; LENGTH: 552  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-902-775A-170

Query Match 13.5%; Score 1351.5; DB 4; Length 552;  
Best Local Similarity 51.6%; Pred. No. 84e-113;  
Matches 269; Conservative 81; Mismatches 116; Indels 55; Gaps 8;

QY 23 STLLTRQAPAPLSQOKR-----SFVTRGEPAE- 49  
Db 45 SRLLT--AAPLSMEQRPWRALEVDSSRVLLSVVLLAPPAGMPQFSTPHSENRDW 102  
QY 50 GFNHLVVDERTGHLYLGAVNRIYKLSDDLKVLVTHETGPDNDPKCYPRIVOTCNEPLT 109  
Db 103 TFNHLTVHQGTGAVYVGVGAINRYKLTGNLTQVAKHTGPEEDNKSRYPPPLIVQPCSEVLT 162  
QY 110 TTNNVNMKLLIDYKENRLIACGSLYQGIKLLRLLEDLFLKGEYPYHKEHYLSGVNBSGSV 169  
Db 163 LTNNVNMKLLIDYSENRLIACGSLYQGVCKLLRLDDLLFILVPSHKEHYLSVNVKTGTM 222  
QY 170 FGVIVSYNLDKDLFIATAVDGKPEYPTTISRKLTKNSADGMFAVYHDFVASMIKI 229  
Db 223 YGVIVRSEGEDEGLFVGTAVDGKQDFFPTLSRKLPRDPSSAMLDYELHSDDFVSSLIKI 282  
QY 230 PSDTFTIIPDPIYVYVGFSSGNFVYFLTLQPEMVSPPG---STTKEQVYTSKLVRLCKE 286  
Db 283 PSDTLALVSHDFIYVYGFASGGFVYFLTVQPE--TPEGVAINSAGDLFYTSRIVRLCKD 340  
QY 287 DTAFNSVYVPIGCRSGVYRLLQAAVLSKAGAVLRTGLCVHPDDDLLFTVFSKGOKRK 346  
Db 341 DPKEFHSVSLPFGCTRAGVEYRLQAYLAKPGDSLQAQAFNITSQDDVLFVFAIFSKGOKQY 400  
QY 347 MKSLDESALCIFIILKQINDRIKERLQSCYRGEGLDLAWLKVDI PCSSALLTIDNFCG 406  
Db 401 HHPDDSALCAFPPIRINLQIKERLQSCYQEGNLELWLLGKDVQCTKAPVPIDNFCG 460

QY 407 LDVNAFLGVSDMVRGIPVFTEDDRMTSVIATYVKNHSLAFVTKSGKLLKIRVDGPRN 466  
Db 461 LDINQPLGGSTPVEGLTLYTSDRMTSVASVYVNGYSVVFVTKSGKLLKVRV----- 514  
QY 467 ALOVE-----TVQVDPGVPLRDMAFSK-DHEQLYIMSRQ 501  
Db 515 ---YEPSCNAIHLLESLEGSYMWRFNRQLYFLGEOR 552

RESULT 4

US-09-181-706-2  
; Sequence 2, Application US/09181706  
; Patent No. 6130068  
; GENERAL INFORMATION:  
; APPLICANT: Melanie K. Spriggs, Michael R. Coneau,  
; APPLICANT: Robert F. Dubose, Richard S. Johnson  
; TITLE OF INVENTION: VIRAL ENCODED SEMAPHORIN PROTEIN  
; TITLE OF INVENTION: RECEPTOR DNA AND POLYPEPTIDES  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Janis C. Henry  
; STREET: 51 University St.  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: US  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/181,706  
; FILING DATE: October 28, 1998  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/958,598 (converted to a  
; APPLICATION NUMBER: Provisional, see below)  
; FILING DATE: October 28, 1997  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: --to be assigned-- (USN 08/958,598  
; APPLICATION NUMBER: conversion to Provisional application)  
; FILING DATE: October 26, 1998  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Henry, Janis C  
; REGISTRATION NUMBER: 34,347  
; REFERENCE/DOCKET NUMBER: 2631-A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206)470-4189  
; TELEFAX: (206)233-0644  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1568 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-181-706-2

Query Match 13.5%; Score 1349; DB 3; Length 1568;  
Best Local Similarity 24.8%; Pred. No. 1e-111;  
Matches 480; Conservative 291; Mismatches 591; Indels 576; Gaps 74;  
QY 72 YKLSDDLKVLVTHETGPDENPKYPPRIVQTCNEPLTTT-----NNVAKMLLDYK 123  
Db 70 YSLEHLSRLYRDQAG-----NCTEPVSLAPPARPFGSFSK-LLLPYR 113  
QY 124 ENR-----LIACGSLYQGICKLLRLDLFLKGEYPYHKEHYLSGV-----NESGSVFGV 172  
Db 114 EGAAGLGGLLLTGTDFRGACEVRPLGNL-----SRNSLRNGTEVWSCHPQGSTAGV 165  
QY 173 IVSYNSLDDKLFLIA-----TAVDGKPEYFPTISSRKLTKNS 208

Db 166 VYR-AGRNRYLAVAATYVLPPEPETASRCNPAASDHDHTAIALKOTEGSLATQELGRK 224  
QY 209 EADGMFAVFDHDFV-ASMIKIPSDTFTIIPDFIYVYVGFSSGNFVYFTLTQPEMVSPP 267  
Db 225 LCEGAGSLHFVDAFLWNGSIYFP-----YYPYNTSG-----AATGWESMARIA 268  
QY 268 GSTTKEQVYTSKLVRLCKEDTAFNSYVEVPIGERSGVE-YRLQAAVLSKAGAVLGRTL 326  
Db 269 QST-----EVLFGQ--QASLDGCGHPDGRRLLSLSSLEA----- 302  
QY 327 GVHPDDLLFTVFS--KGOKRKMKSDBESALCIFIILKQINDRIKERLOSQYRGEGTDLDA 384  
Db 303 -----LDVWAGVFAAAGEGERSPTTALCLFRMSEIQARAK-----VS 344  
QY 385 W-LVKDIPCSSALLTIDNFCGLDMNAPLGVSVMVRGIPVFTEDDRMTSVIAYVKNH 443  
Db 345 WDFKTAESHCKEG-----DQP-----ERVQPIASSTLIHSDLSVYGVVWNR 387  
QY 444 SLAFVGTSGKLLKIRVDGPRGNALQYETVQV-----DPGPVLRDMASKD 490  
Db 388 TVLFLGTGDLKVL-----GENLTSCPEVIYEIETPVPFKLVDPV-----K 435  
QY 491 HEQYIMSERQLTRVPVESCQYQSCGECGLSGDPHCGWCVLHNTCTRKERCERSKEPRR 550  
Db 436 NIYIYLTAGEVRRIRVANCNKHKSCSECLTATDPHCGWCHSLQRCFTQGD----- 487  
QY 551 FASEMKQCVRLTVHPNNISVSQYNNVLLVETVYVPELSAGVNCFTEDLSEMDGLVGNQI 610  
Db 488 -----VHSENL-----NWLDSG----- 502  
QY 611 QCYSPAKEVPRIITENGDDHHVQLQKSKETGMTFASTSFVYNCVHNSCL-SCVESP 669  
Db 503 -----AKKCPKI-----QIIRSSKEKTTVTWVGSF-----SPRHSKCMYKVDSS 542  
QY 670 YRCHWKYRVHCTHDPKTCSPQEGRVKLPEDCPQLLRVDKLLVPVEVVKPTLAKNLPQ 729  
Db 543 -----RELQ-----QNKSQ 551  
QY 730 PQSGQGYECILNTQSGSEQRVPALRNFSSVQCCQTSYSYEGMEINNLVVELTVVW--G 787  
Db 552 PNR-----TCTCSI-----PTRAIVKDVVVVWVMSFGS-----WNLS 585  
QY 788 HFNDINPAQNKVHLKYCGAMPRESCLCLKADPDFACGCGQPGGCTLRQHCAPAESQWLE 847  
Db 586 RNFNTN-----CSSLKE-CPACVET-----GCWCKSARRC----- 615  
QY 848 LSGAKSKCTNPRITEIIPVTGPREGGTKVTIRGENLGLFPRDIASHVKVAGVECSPLVDG 907  
Db 616 -----IHPFTA-----CDP-----S 625  
QY 908 YIPABQIVCEM-----GEAKPSOHAGFVEICVACRPEFMARSQLYYFTLTSLDKP 961  
Db 626 DYERNQEQCPVAVENTSGGRPKENK-----NRTNQLQVY-----IKSIEP 669  
QY 962 SRGPMGGTQVTITGTNLNAGSNV-VVMFGKQPC-----LFHRRSPSYIVCNTSSDEV 1014  
Db 670 QKVSTLGSNVIVTGANFTRASNITMLKGTSTCDKDVQVSHVLNTHMKSFLPSRKK- 728  
QY 1015 LEMK-VSVQVDRAKIHQDLVFQYVEDPTVIRIEPMSIVSGNTPIAVGTHLDLIQNPQI 1073  
Db 729 -EMKDVCIQFDGNGCNSVGSLSYIALPHCSLIFFATTWISGQNTIMMGRNFDVND--L 785  
QY 1074 RAKHGGKEHINICEVLNATENTCOAPALALGPDHQSOLDTERPEPFGFTLDNVQSILLINK 1133  
Db 786 IISHELKGINVSECVATYCGFLAPSL-----KSKKRVTVTKLRVQD 830  
QY 1134 T-----NFTYYPNPVFEAFGSGILELKPGTPIILKGNLIPPVAGGNVKLYTVLGEK 1188  
Db 831 TVLDGQTLQYREDPRFTGYR-----VESEVDTELEVKIQ-----KENDNFNISK 875  
QY 1189 PCTVTV-----SDVQLLCESPLI-----GRHKWARYVGGMEYS 1222

Db 876 DIEITLFGHNGQLNCSPENITRNQDLATLILCKIKGIKTASTIANSSKKVVKLGNLE-- 933  
Qy 1223 PGMVYIAPDS-PLSLPAIVSTAVAGGLLIIFVAVLIAVYKRSRESDLTLKRLQWQMDNL 1281  
Db 934 ---LVVEQESVSTWYFIVLVPV---LLVIVFAVGVTRHKSKE--LSRQSQ-QUELL 984  
Qy 1282 ESRVALECKEAFELQTDIHELTSLDGAG-IPFLDYRTYMRVLF--GIEDHPVLRDL 1338  
Db 985 ESELKEIRIDGFAELQMDKLDV---VDSFGTVPLDYKHFALRTFFPESGGFTHTFTEDM 1041  
Qy 1339 EYPGVRQREVEKGLKFLA--QLINNKVLLSFIRLESQRSFMRDRGNVASLWVLOS 1396  
Db 1042 ---HNRDANDKNESLTALDALKCNKSLFVTVIHTLEKQKFSVKDRCLFASFITIALQT 1097  
Qy 1397 KLEVATDVLKQALLADLIDKNLESKNHPKLLARRTESVAEKMLTNWFTLLYKFLKECAGE 1456  
Db 1098 KLVYLTSLILEVLRDLMSQC--SNMQPKMLARRTESVVEKLLTNWMSVCLSGFLREITVE 1155  
Qy 1457 ELFSLFCALQKQMEKGPDAITGEARYSLSEDKLIROQIDYKTLVLSCV---SPDNANSP 1513  
Db 1156 PFYLLVTLTNQINKPGVDVITCKALYTLINEDWLLWQVPEFSTVALNVVFEKIPENESAD 1215  
Qy 1514 ---EVPVKILNCDDTITQVEKILDAIFKNVPCSHRPKAADMDLEWROQSGARMILQDEDI 1570  
Db 1216 VCRNISVNVLDCTTIGQAKEKIFQAFLSKNGSPYGLQNEIGLELQWGTROKELIDIDSS 1275  
Qy 1571 TTKIENDMKRLNTLAHYQVPGSVVALVSKQVATYNNSTVSTASKEYENMIRYTG 1630  
Db 1276 SVILEDGITKLTNGHYEISNGSTIKV-----FKKIANFTSD 1312  
Qy 1631 PDSLRSRPMTITPDESQVGMVHLVKNHEHGDQKEGDRGSK--MYSEIYLRILATKGT 1688  
Db 1313 VEYSDHCHLLPDSQA---FQVQGRKH-----RGKHFKVKEMILYKLTJSTKVAI 1361  
Qy 1689 QKFVDDLFETIFSTAHRSALPLAIAKYMFDLDEQADKHGIDHPHRTWKSNCPLR 1748  
Db 1362 HSVLEKLFRSIWSLEN--SRAPFAIKYFFDLDAQAENKKTIDPDVHVHWTNSLPLRF 1419  
Qy 1749 VNMINKPQFVEDIHKNSITDACLVSVAQTFWDSCSTSEHRLGKDSPSNKLKAYKDIP 1808  
Db 1420 VNILKNQFVFDIKTTHIDGCLSVIAQAFMDAPSLTEQQGKGAAPTNNLYAKDIPYK 1479  
Qy 1809 NWVERYSYDGRMFAISQDMNAYLAQSRMHNEFTMSALSEIFSVMGYSBEILGPL 1868  
Db 1480 BEVSKYKAIRDLPLLSSEMEEFITQSKKHENEFEVEALTEIYKIVYVYFDEILNKL 1539  
Qy 1869 DHD---DOGGKQKLAYKL 1883  
Db 1540 EREGLLEAQKQLLHVK 1557

RESULT 5

US-09-458-791-2  
; Sequence 2, Application US/09458791  
; Patent No. 6174689

; GENERAL INFORMATION:  
; APPLICANT: Spriggs, Melanie  
; TITLE OF INVENTION: VIRAL ENCODED SEMAPHORIN PROTEIN  
; RECEPTOR DNA AND POLYPEPTIDES

; NUMBER OF SEQUENCES: 10

; CORRESPONDENCE ADDRESS: 10

; ADDRESSEE: Janis C. Henry

; STREET: 51 University St.

; CITY: Seattle

; STATE: WA

; COUNTRY: US

; ZIP: 98101

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk.

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: MS-DOS/Windows 95

; SOFTWARE: Word for Windows 95, 7.0a

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/458,791  
; FILING DATE: 10-Dec-1999  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/958,598  
; FILING DATE: 28-OCT-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Henry, Janis C  
; REGISTRATION NUMBER: 34,347  
; REFERENCE/DOCKET NUMBER: 2631  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206)470-4189  
; TELEFAX: (206)233-0644  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1569 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-09-458-791-2

Query Match 13.5%; Score 1349; DB 3; Length 1568;  
Best Local Similarity 24.8%; Pred. No. 1e-111;  
Matches 480; Conservative 291; Mismatches 591; Indels 576; Gaps 74;  
Qy 72 YKLSLDKVLVTHETGPEEDNPKYPPRIQVTCNEPLTTT-----NNVNKMLLDYK 123  
Db 70 YSLEHSLRLYRQAG-----NCTEPVSLAPPARPGRGFSFK-LLLPYR 113  
Qy 124 ENR-----LIAGSLYQGIKLLRLLEDLFKLGEVHKKEHYLSGV-----NESGVSFVG 172  
Db 114 EGAAGLGGLLLTGWTDFRACEVVRPLGNL-----SRNSLRNGTEVVSCHPOGSTAGV 165  
Qy 173 IVSYSLNDDKLFKA-----TAVDGKPEYFTISRKLTKNS 208  
Db 166 VYR-AGNNRWYLAVAATVYLPETASRCNPAASDHDTAIALKOTEGRSLATQELGRLK 224  
Qy 209 EADGMFAVYFHDFFV-ASMKTPSDFTIIPDIDYVYVGFSSGNFVYLTLOPEMVSP 267  
Db 225 LCEGAGSLHFDVDAFLWNGSIYFP-----YYPNYTSG-----AATGPFWSARIA 268  
Qy 268 GSTTKQVYTSKLVRCKEDTAFNSYVEVPICGERSGVE-YRLLQAAVLSKAGAVLGR 326  
Db 269 QST-----EVLFQG--QASLDGCHGHPDGRLLLSLSLVEA----- 302  
Qy 327 GVHPDDDLFTVFS--KGQKRKMSLDESALCIFILKQINDRIKERLQSGRGEGLDLA 384  
Db 303 -----LDWAGVFSAAAGEQERRSPTTTALCLFRMSEIQARAKR-----VS 344  
Qy 385 W-LKVKDIPCSSALLTIDDNFCGLDMNAPLVGSDVMRGIPVFTEDRDMTSTVIAYVYKH 443  
Db 345 WDKTAESHCKEG-----DQP-----ERVQPIASSTLIHSDLTSVYGTVMNR 387  
Qy 444 SLAPVGTGSKLKKIRVDGPRGNALQYETVQVY-----DQGVLRDMAPSKD 490  
Db 388 TVLFLGTGQQLLKVL---GENLTSNCPVIEYKEETPVYFKLVDPDV-----K 435  
Qy 491 HEOLYIMSEQLTRVPVESCQYQSCGECIGSGDPHCGVCLHNTCTRKERCERSKEPRR 550  
Db 436 NIYILTAGKEVRIRVANCNKHKSCSECLTADPHCGWCHSLQRTTFQDC----- 487  
Qy 551 FASEMKQCVALTYPNNISVSQYNVLLVLETYNVPELSAGVNCCTFDLSEMDGLVVGNI 610  
Db 488 -----VHSENLE-----NWLDISG----- 502  
Qy 611 QCVSPAKEVPRILITENGDDHHVVLQIQLSKSETGMTASTSFVFNCSVHNSCL-SCVESP 669  
Db 503 -----AKCPKI-----QITRSKKEKTTVMVGSF-----SPRSHCKMVKNVDS 542  
Qy 670 YRCHWCYKRVHCTHDPKTCSTQEGRVKLPDCCQLLRVDKILVPVVIKPTILKAKNLPQ 729  
Db 543 -----RELK-----QNKSQ 551



Qy	730	PSQGRGYECILNIGSEORVPALRNFSSVQCONTSYSEYEGMEINNLVELTVVNV--G	787
Db	552	PNR-----TCTCSI-----PTRYATKDVSVNVVWFSGS-----WNLSD	585
Qy	788	HFNIDNPAQNKVHLKYGAMRESGLCLKADPDACGWCQGPQOCTLRQHCFAQESQWLE	847
Db	586	RNFNTN-----CSSLKE-CPACVET-----GCAWCKSARRC-----	615
Qy	848	LSGAKSKCTNPRITEIPVTGPREGGTKVIRGENLGLBRDIASHVKVAGVECSPLVDG	907
Db	616	-----IHFFTA-----CDP-----S	625
Qy	908	YIPAEQIVCEM-----GEAKPSQAHGVEICVAVCRPEFMARSSQLYTFMTLTLSDLKP	961
Db	626	DYERNOEQCPVAVEKTSGGGRPKENKG-----NRTNQALQVY-----IKSIEP	669
Qy	962	SRGPMSCGTQTTITGTHNLNAGSNV-VVMFGKQPC-----LFHRRSPSYIVCNVTSDEV	1014
Db	670	QKVSTLGSKNVITGANFTRASNTITLTKGTSTCDKDVIOVSHVLDNTHMKFSLPSRK-	728
Qy	1015	LEMK-VSVQVDRAKIHQDLVFQYVEDPTIVRIEPEWSIVSGNTPIAVWGTHLDLIONPOI	1073
Db	729	-EMKDVCIOFDGNCSSVGLSYIALPHCSLIIPATTWISGGQNTIMMGRNFDVIDN--L	785
Qy	1074	RAKHGGKEHINICEVLENATEMTCOAPALAGPHQSDLTERPEEFGILDNVOSLLILNK	1133
Db	786	IISHELKGNINVSCEYCATYCGFLAPSL-----KSSKVRTNVTVKLRVQD	830
Qy	1134	T-----NFTYVNPVFEAFGPSGILELKPQTPILKGNLIPPVAGGNVKLNTVLVGEK	1188
Db	831	TYLDCGTLOYREDPRFTGYR-----VESEVTELEVKIQ-----KENDFNISKK	875
Qy	1189	PCVTVT-----SDVQLLCSNLI-----GHHKVMARVGGMEVYS	1222
Db	876	DIEITLPHGNGQLNCFENITRNQDLTTLICKIKGTASTIANSSKVRVKGNLNLE--	933
Qy	1223	PGMYVIAPDS-PLSLPAIVSAVAGGLIIFIAVLIAVKRKGRESLTLKRLQMOWDNL	1281
Db	934	---LYVQESVPSWTYFLIVLPV---LLVIVIPAAVGVTRKSKKE--LSRKQSQ-QLELL	984
Qy	1282	ESRVALECKEAFABLOTTIDHELTSDLGAG-IPFLDYRTVTMRVLPP--GIEDHPVLRLD	1338
Db	985	ESELRKEIRDFABELQDKLDV---VDSFGTVPLDYKHFALRTFFPESGGFTHIETDM	1041
Qy	1339	EVPGYORBEVKGKLEFA--QLINKVFLISFIRLESORFSMRDRGNVASLIMTVLOS	1396
Db	1042	---HNRDANDKNESLTALDALICNKSFLTVIHTLEKQNFVSKDRCLFASFLITALQT	1097
Qy	1397	KLEYATDVLKOLLADLIDKNLESKHPKLLLRTERESVAEKMLTNWFTFLYKFLKECAGE	1456
Db	1098	KLVLTSILEVLTDLMEQC--SNQPKMLMRTERESVVEKLLTNWMSVCLSGFLRETVE	1155
Qy	1457	PLSLFCAIKOOMEKGPDAITGEARYSLSEDKLIROQIDYKTLVLSV---SPDNANSP	1513
Db	1156	PFYLLVTTLNQKNGPVDVITCKALYTLNEDWLLMQVPBFSTVALNVVFEKIPENESAD	1215
Qy	1514	---EVPVKILNCDDITQVKEKILDAIFKNVPCSHRPKAADMDLEWRQSGARMILQDEDI	1570
Db	1216	VCRNISVNVLCDDITGOAKEKIFQAFLSKNGSPYGLQNEIGLEQLMGTRQKELLIDSS	1275
Qy	1571	TTKIENDWKLRLTIAHYQVPGSVVALYSKQVTAYNVNNSTVSRTSASKYENMIRTGS	1630
Db	1276	SVILEDGTIKLNTIGHYBISNGSTIKV-----FKKIANTFSD	1312
Qy	1631	PDSLRSRTPMITPOLESQVGMWHLVKNHEHQDQKEGRGSK--MVSEIYLTRLIATKGTIL	1688
Db	1313	VEYSDDDCHLLLPDSEA---FQDVQGRH-----RGKHFKVKEMYLTKLLSTKVAI	1361
Qy	1689	QKFVDDLPETTFSTAHRSALPLAIKYNWDFLDQADKHGHDPHVHTWKSNCCLPLRFW	1748
Db	1362	HSVLEKLFERSIWSLEN--SRAPPAIKYFPDFLDAQENKKITDPPDVVHINKTNSLPLRFW	1419

RESULT 6

US-09-459-066-2  
; Sequence 2, Application US/09459066  
; Patent No. 6187909  
; GENERAL INFORMATION:  
; APPLICANT: Spriggs, Melanie  
; TITLE OF INVENTION: VIRAL ENCODED SEMAPHORIN PROTEIN  
; NUMBER OF SEQUENCES: 10  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Janis C. Henry  
; STREET: 51 University St.  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: US  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: MS-DOS/Windows 95  
; SOFTWARE: Word for Windows 95, 7.0a  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/459,066  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/958,598  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Henry, Janis C  
; REGISTRATION NUMBER: 34,347  
; REFERENCE/DOCKET NUMBER: 2631  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206)470-4189  
; TELEFAX: (206)233-0644  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1568 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-09-459-066-2

Query Match 13.5%; Score 1349; DB 3; Length 1568;  
Best Local Similarity 24.8%; Pred. No. 1e-111;  
Matches 480; Conservative 291; Mismatches 591; Indels 576; Gaps 74;

Qy	72	YKLSDDLKVLVTHETGPDENKCYPRIVQTCNEPLTTT-----NNVNMKLLIDYK	123
Db	70	YSLSHSLSLYRDQAG-----NCTFVSLAPPARPGSSFSK-LLLPYR	113
Qy	124	ENR-----LIACGSLYQGIKLLKLEDLFKLGEYPYHKEHYLSGV-----NESGSVGV	172
Db	114	EGAAGLGGLLTGWTDFRGACEVRPLGNL-----SRNSLRNGTEVVVSCHPQOSTAGV	165
Qy	173	IVSYSNLDDKLFIA-----TAVDGKPEYPTISSRKLTKNS	208
Db	166	VTR-AGNNRWTLAVNAATVLPETASRCNPAASHDTAIAKDKTEGSLATQELGRLK	224
Qy	209	EADGMFAYVHDEFV-ASMIKIPSTFTTIIPDFIYVYVFGSSGNFVFLTLQPEKVSPP	267

Db 225 LCEGAGSLHFVDAFLWNGSIYFP-----YYPNYTSG-----AATGWSMARIA 268  
QY 268 GSTTKEQVYTSKLVRLCKEDTAFNSYVTVPIGCRSGVY-YRLLQAAVLSKAGAVLRTLL 326  
Db 269 QST-----EVLFGQ--QASLDGCHGHPDGRRLLSLSSLEA-----302  
QY 327 GVHPDDDLFTVFS--KGQKMKSLDESALCIFLTKQINDRIKERLQSCVGRGGLDLA 384  
Db 303-----LDVWAGVFSAAAGEQERRSPYTTALCLFMSIQAAR-----VS 344  
QY 385 W-LKVDPICPSALLTIDNFCGLDMNAPLGVSDMVRGIPVFTEDRDMTSMVIAVYKNH 443  
Db 345 WDFKTAESHCKEG-----DQP-----ERVQPIASSTLIHSLDTSVYGVYVMNR 387  
QY 444 SLAFVGTSGKLVKIRVDGPRGNALQYETVOV-----DGPVLRDMARSD 490  
Db 398 TVLFLGTGGQLLVIL-----GENLTSNCPVIVEIKEETPVFKLVDPDV-----K 435  
QY 491 HEQLYIMBEROLTRVPVBSQOYQSGCLSGDPHCGMCHVHNTCTRKERCERSKPRR 550  
Db 436 NIYIYLTAGVRRIRVANCKHSCSECLTATDPHCGWCHSLQRCCTFGQDC-----487  
QY 551 FASEMKQCVRLTVPHNNISVSQYNVLLVETVNVPELSAGVNCYCFEDLSEDLGLVVGNI 610  
Db 488-----VHSENLE-----NWLDISG-----502  
QY 611 QCYSPAAREVPRITENGDDHHVYQLQKSKETGMTFASTVFYVNCVHNSCL-SCVESP 669  
Db 503-----AKCPKI-----QIIRSSKERTVTVMGSP-----SPRHSCKMVKVNDSS 542  
QY 670 YCHWKVYHVCTHDPKTCSPQGRVKLPEDCPQLLRVDKLVLPVEVVKPITLAKNLPQ 729  
Db 543-----REL-----ONKQ 551  
QY 730 POSGQGVCEILNIQGEORVPALRFNSSVOCNTSYSEGMENLNPVELTVVW--G 787  
Db 552 PNR-----TCTCSI-----PRTATYKDVSVVNVMSFGS-----WNLSD 585  
QY 788 HNNINPAQNVKLVKGMRESGLCLKADPDPAFCGCGQPGQCTLRQHPAGESQWLE 847  
Db 586 RENFTN-----CSSLKE-CPACVET-----GCWCKSARRC-----615  
QY 848 LSGAKSCNPRITBIIPVTPGREGTKVTIRGENLGLFEDRIASHVKGVECSPLVDG 907  
Db 616-----IHPTA-----CDP-----S 625  
QY 908 YIPASQIVCEM-----GBAKPSQHAGFVEICVAVCRPEFMARSSQLYFMTLLSLDLKP 961  
Db 626 DYERNOEQCPVAVEKTSGGGRPKENK-----NRTNQALQVEY-----IKSTEP 669  
QY 962 SRGPMGGTQVITITGNLGNAGNV-VVMFGKQPC-----LFHRSPPSVIVCNTTSSDEV 1014  
Db 670 QKVSTLGNVIVTGANFRASNITWILKGTCTCDKDVIOVSHVNDTHMKSFLSSRK- 728  
QY 1015 LEMK-VSVQVDRAKIHQDLVQYVEDPTIVRIEPMWSIVSGNTPIAVMGTHLDLQNPQI 1073  
Db 729 -EMKDVICIFDGCNCSVSGLSYALPHCSLIFFATTWISGQNTMGRNPDVIDN--L 785  
QY 1074 RAKHGGKEHINICEVLANATEMTCQAPALGALPDHQSDLTREPEEGFILDNVQSLILNK 1133  
Db 786 IISHELGNINSEYCAVYCGFLAPSL-----KSKVATNVTVKLRVDQ 830  
QY 1134 T-----NFTYFNPVPEAFGSPGILELKPGTIILKGNLIPPVAGGNVKNLYTVLUGEK 1188  
Db 831 TVLDCGTLOVREDPRTGYR-----VESEVDTELEVKIQ-----KENDNFNISK 875  
QY 1189 PCTVTV---SDVQLCESNLI-----GRHKVAVRGVMEYS 1222  
Db 876 DIEITLFGHNGOLNCSFNITRNQDLTILCKIKIKTASTIANSSKKVRKLGKLE-- 933  
QY 1223 PGWVYIAPDS-PLSLPAIVSIAVAGLLIIFIVAVLIAVKKRSRSDLTCLKQOMDNL 1281

Db 934 ---LYVEQESVPSTWYFLIVLPV---LLVIVIFAAVGVTRHKSKE--LSRKQSQ-QLELL 984  
QY 1282 ESRVALECKEAPAELOTDIHELTSOLDGAG-IPFLDYRTYTVRVLFP--GIEDHPVLRDL 1338  
Db 985 ESELRKEIRGDAELQMDKLDV---VDSFGTVFFLDYKGFALRTFFPESGGTHLFTEDM 1041  
QY 1339 EVFGYQERVERKGLKFA--QLNNKVFLLSFIRLESQSRFSMRDRGNVSLIMTVLOS 1396  
Db 1042 ---HNRDANDKNESLTALDALICNKSFLVTVIHTLEKQKNFSKDRCLFASFLTIALQT 1097  
QY 1397 KLEYATDVLLKOLLADILDKNLSKQHPKLLLRTESSVAEMKLTNNWTFPFLYKFLKECAGE 1456  
Db 1098 KLVYLSILLEVLRDLMEOC--SNMOPKLMURKTESVVEKLLTNMMSVCLSFRLRTVGE 1155  
QY 1457 PLFSLFCAIKQKMEKGPIDAITGEARYSLSEDKLRQQIDYKTLVLSCV---SPDNANBP 1513  
Db 1156 PFYLLVTTLNQINKGPDVITCKALYTLNEDWLLWQVPEFSTVALNVVFEKIPENESAD 1215  
QY 1514 ---EVPKILNCDTIQVKEKILDAIFKNVPCSHRPAADMDLEWFGSGARMILQDEDI 1570  
Db 1216 VCRNISVNVLDCTIGQAKEKIFQAFLSKNGSPYGLQNEIGLELQMGTRQKELLIDSS 1275  
QY 1571 TTKIENDWKRNLTAHYQVDPDGSVALVSKQVTAYNVANNSTVSRTSASKYENMIRYGS 1630  
Db 1276 SVLEDDGITKNTIGHVEISNGSTIKV-----FKKIANFTSD 1312  
QY 1631 POSLRGRTMITDLESQVMKMHVKNHEHGOKEGDRGSK--MVSEIYLTRLLATKGTLL 1688  
Db 1313 VEYSDHCHLILPDSEA---FQDVQGRH-----RGKHFKPKVEMLYTLKLSKVAI 1361  
QY 1689 QKPVDDLFEITFHTAHRGSGALPLAIKYMDFDLDEQADKHGIDHPHVRHTWKSNCPLRFW 1748  
Db 1362 HSVLEKLFBSIWLPN--SRAPFAIKYFFDLDAQAKNKITDPDVVHIWKNLSLPLRFW 1419  
QY 1749 VNMKNPQVFDIHKNSITDACLSSVVAQTFMOSCSTSEHRLGKDSPSNKLKYAKOIPSYK 1808  
Db 1420 VNLKNPQVFDIKTTPHIDGCLSVIAQAFMDAFSLTEOOLGKEAPTNNKLLYAKDIPTYK 1479  
QY 1809 NWERYSDIGKMPALSDODMAYLAEQSRMHMNEFTMSALSEIYSYVKYSEIILGPL 1868  
Db 1480 EEVSKYKALRDPPLSSSEMEEFLLQESKKNENEFNEEVALTEIYKIVYKVFDEILNKL 1539  
QY 1869 DHD---DQCGKQKLAYKL 1883  
Db 1540 ERERGLEEAQQLLHVKV 1557

RESULT 7  
US-09-459-065-2  
; Sequence 2, Application US/09459065  
; Patent No. 6562949  
; GENERAL INFORMATION:  
; APPLICANT: Spriggs, Melanie  
; TITLE OF INVENTION: VIRAL ENCODED SEMAPHORIN PROTEIN  
; TITLE OF INVENTION: RECEPTOR DNA AND POLYPEPTIDES  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Janis C. Henry  
; STREET: 51 University St.  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: US  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: MS-DOS/Windows 95  
; SOFTWARE: Word for Windows 95, 7.0a  
; CURRENT APPLICATION DATA: US/09/459,065  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: 08/958,598
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Henry, Janis C
; REGISTRATION NUMBER: 34,347
; REFERENCE/DOCKET NUMBER: 2631
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)470-4189
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS
; LENGTH: 1568 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-459-065-2

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Query Match	13.5%	Score 1349	DB 4	Length 1568
Best Local Similarity	24.8%	Pred. No. 1e-111		
Matches	Conservative 291	Mismatches 591	Indels 576	Gaps 74
Qy	72	YKLSDDLKVLVTHETGPDENPKCYPRIQVTCNEPLTT-----NNVMKMLLDYK	123	
Db	70	YSEHLSRLYRDQAG-----NCTEPVSLAPPAPRPGSFSK-LLPYR	113	
Qy	124	ENR-----LIACOSLYQGICKLRLLEDLFLKLGEPYHKHLYLGSV-----NESGSVFG	172	
Db	114	EGAAGLGGLLTGTWDFRGACEVRPLGNL-----SRNSLRNGTEWSCHPOGSTAGV	165	
Qy	173	IVSVSNLDDKLFIA-----TAVDGEFVFPPISSRKLTKNS	208	
Db	166	YIR-AGRNNRWYLAATAATYVLPETASRCNPAASDHDITALKDTGRSLATQELGRLK	224	
Qy	209	EADGMFAKFHDEFV-ASMIKIPSDTFTIIPDFIYYVYGSSGNFVFFTLQPEMVSPP	267	
Db	225	LCEGAGSLHFVDAFLWNGSIYFP-----YYPNYTSG---AATGWSMARIA	268	
Qy	268	GSTTKGEQVYTSKLVRCKEDAFNSYVEVPIGERSGVE-VRLLOAAYLKAGAVLGRTL	326	
Db	269	QST-----EVLFGQ--QASLDCGHGPDGRLLLSLSSLVEA-----	302	
Qy	327	GVHPDDDLLFTVES--KQOKRMKLSDESALCIILKQINDRIKERLQSCVYRGSGTDLDA	384	
Db	303	-----LDVWAGVFSAAGEGGERSPPTTLCFLPFMSIQARAK-----VS	344	
Qy	385	W-LKVYKOTPCSSALLITIDNFCGLDMNAPLGVSWMVIRGIPVFTEDRDMTSVIAVYKQH	443	
Db	345	WDFKTAESHCKEG-----DQP-----ERVQPIASSTLIHSDLSVTYGVVMNR	387	
Qy	444	SLAFVGTSGSKLKIYVDGPRGNALQYETQVW-----DGPVLRDMAPSKD	490	
Db	388	TVLFJGTGDLKVL-----GENLTSNCEPVIYEKETPFVFKYLVDPDV-----K	435	
Qy	491	HEQLYIMBEROLTRVPVBSGQYQSCGCLSGDPHCGWCVLHNTCTRKERCERSKEPRR	550	
Db	436	NIYYILTAGVRRIRVANCCHKKSCSCLTATDPHCGWCCHLQRCITQGC-----	487	
Qy	551	FASEMKQCVRLTVHPNNISVSQYNVLLVLETYNVPELSAGVNCFTFEDLSEMDGLVVGQI	610	
Db	498	-----VHSENLE-----NMLDISG-----	502	
Qy	611	QCYSAPAAKEVPRIITENGHHVVOQLKSKETGMTFASTSFVYNCVSVHNSCL-SCVESP	669	
Db	503	-----AKCKPXI-----QIRSSKEKTTVTWVGSF-----SPHSHKCMVKQNDSS	542	
Qy	670	YRCHWCKVRHVCTHDPKTKCSFOGGRVKLPEDCPQLLRVDKILVPVEVIKPTLKAKNLPQ	729	
Db	543	-----RELK-----	551	
Qy	730	POSGORGECEILINIQSGEORVPALRPNSSVQCNQTSYSYEGMEINNLPELTVVMN--G	787	
Db	552	PNR-----TCTCSI-----PTATYKDVSVVNMVFSFG-----WNLSD	585	

Qy	788	HNENIDPAGKVHLYCKGMBRES	CGLCLKADPDFACGKCGPGCOTLRHQHCPAQESOWLE	847
Db	586	RNFNTN	---CSSLKE-CPACVET---GCAWCKGARRC---	615
Qy	848	LSGAKSKCTNPRITEII	IVTGPREGGTVKIRGENGLGLEPRDIASHVKVAGVECSPLVDG	907
Db	616	-----	IHPFTA-----CDP-----S	625
Qy	908	YIPAEQIVCEM	-----GEAKPSOHAGFVEICVACRPEFWMARSSQLYYFWTLTUSDLPK	961
Db	626	DYERNOEQCPVA	VEKTSGGGRPKENKG-----NRTNOALQVYV-----	669
Qy	962	SRGPMGGQVTVITGNLNAGSNV	-VVMFGKQPC-----LFHRSPSSYIVCVNTTSSDEV	1014
Db	670	QKVSTLGGKSNVTVTGANETFRASNI	TMIWKGTSTCDKDVIOVSHVINDTHMKFSLPSSSRK-	728
Qy	1015	LEMK-VSVQVODRAKHODLV	FOYVEDPTVIRLEPEWSIVSGNTPIAVAGTHLDLLQNPQI	1073
Db	729	-EKWDVICIOFGDGNCSVCSLSYIAL	PHCSLIFFPATWISGQNTMGRNFDVIDN--L	785
Qy	1074	RAKHGKEHINICEVNLNATEMTQ	APALALGDPHOSDLTERPEBFGFILDNVQSLLINK	1133
Db	786	IISHELKGNINSEYCAVTCYGLFAPSL	-----KSKVRTNVTVKLRVQD	830
Qy	1134	T-----NFTYYPNPVEAFPGSPG	ILELKPGTPIILKGNLIPPVAGGNVKLNTYVLVGEK	1188
Db	831	TYLDCGTQYREDPFTGYR	---VESEVDTELVKIQ-----KENDNFENISCK	875
Qy	1189	PCVTVV	---SDVOLCESPNLI-----GRHKVMARVCGMEYS	1222
Db	876	DIBITLPHGENGQALNCSFENIR	NODLTTLCKIKGIKTASTIANSSKKVRVKLGLE--	933
Qy	1223	PGWVIYAPDS-PLSLPAIYSIAVAG	GLLIIFTVAVLIAVKRSRSDLTLEKLOQMOMNL	1281
Db	934	---LYVEQSVSPSTWYFLVLPV	--LLVIVIFAAGVTRHSKE--LSRKQSQ-QLELL	984
Qy	1282	ESRVALECKEAPABLQTDIHELT	SDLDGAG-IPFDLYRTYTRVULFP--GIEDHPVLRL	1338
Db	985	ESELRKEIRDGAELQMDKLDV	---VDSEGTVPFLDYKHFAULTFPFESGGTHIPTEDM	1041
Qy	1339	EVPGYQERVEKGLKFLFA--Q	LIINNKFVLLSFIRTLESQRSFMSRDRGNVASLIMTVLOS	1396
Db	1042	---HNRDANDKNESLTALDALI	CNKSFLVTVHTLEKQKNFSVKDRCLFASFLLTALQT	1097
Qy	1397	KLEYATDVLKOLLADLIDKNLES	KHPKPLLLRRTESVAEKMLTNWTFLLYKFLKECAGE	1456
Db	1098	KLVLTAISILEVTRDLMEQC--	SNMOPKMLRTERSVVEKLITNMWSVCLSGFLRRTVEG	1155
Qy	1457	PLFSLFCAIKQOMEKPIDAITGE	ARYSISEDKLIRQQIDYKTLVLSCV---SPDNANSP	1513
Db	1156	PFYLLTTLNQINKNGPVDVIT	CALYTLNEDWLLWQVPEFSTVALNVVFEKIPENESAD	1215
Qy	1514	---EVPKILNCOTITQVEKILDA	LFPKVPCHRPKAADMLEWPGQSGARMLOQEDI	1570
Db	1216	VCNINSVNLJDCDTIOAKEKIF	QFQFLSKNGSPYGLOLNEIGLELOMGTRQKELLIDSS	1275
Qy	1571	TTKIENDKRLNTLAHVQPDG	SWALVSKQVTAYNAVNNSTVSRTSASKYENMIRYTG	1630
Db	1276	SVILEDGIKTLNIGHVEISNG	TIKV-----FKKIANFTSD	1312
Qy	1631	PDLSRSTRPMTIDLES	GVKOWHLVKXHBHGDQKEDGRGSK--MVSEIYLTLLATKGTLL	1688
Db	1313	VEYSDDDCHILPLDSEA----	FQDVQGXH-----RGKHKPKVEMYLTKLLSTKVAI	1361
Qy	1689	QKFVDDLDFETIFSTAHRG	SALPLAIKMYMDFDLDEQADKHGIDHPHYRHTKWSNCLPLRFW	1748
Db	1362	HSVLEKLFRSIWSLPN--SR	APPFAIKYFDFDLQAENKKITDPDVVHVWKTNSLPLRFW	1419
Qy	1749	VNMKPNQFVFDTHKNSITDACL	SVNAQOFMDCSCSTSEHRLGKDSFNKLLYAKDIPSYK	1808
Db	1420	VNLRPNQFVFDIXKTPHID	GCILSVTAQAQMFDAFSLTEOOLGKEAPTNKLLYAKDIPITYK	1479
Qy	1809	NWVERYSDYDCKMPAIDSDQ	DMNAYLABQCSRMHNFENTWSALSEIYSYGVKYEELGPL	1868

Db 1480 EVKSYKAIADLPPLSSSEMEFLTQSKKHENEFEVALTEIYKIVKFIENLKL 1539  
Qy 1869 DHD---DQGGKQKAYKL 1883  
Db 1540 ERERGLEEAQKQLLHVKV 1557  
RESULT 8  
US-09-345-473E-24  
; Sequence 24, Application US/09345473E  
; Patent No. 6558903  
; GENERAL INFORMATION:  
; APPLICANT: Hodge, Martin  
; TITLE OF INVENTION: No. 6558903el Kinases and Uses Thereof  
; FILE REFERENCE: 35800/183781  
; CURRENT APPLICATION NUMBER: US/09/345,473E  
; CURRENT FILING DATE: 1999-06-30  
; NUMBER OF SEQ ID NOS: 62  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 24  
; LENGTH: 1404  
; TYPE: PRT  
; ORGANISM: Gallus gallus  
US-09-345-473E-24

Query Match 5.4%; Score 538.5; DB 4; Length 1404;  
Best Local Similarity 20.3%; Pred. No. 1.6e-38;  
Matches 349; Conservative 223; Mismatches 548; Indels 599; Gaps 76;  
Qy 10 CLLSHLLMVGSGSTLLFR-----QAPLSQKQSFVTF-----RGEPAEGFNLVUDE 58  
Db 5 CLVCLLLLL-----APSLQAGAWQCRRIPIFSFTRNFSVYPTLPSLDAGSPVQ---NIAVFP 58  
Qy 59 RTGHTYLGAVNRIYKLSDDLKVLVTHETGPDENPKCYPRIVQTCNEPLATTNNVKNML 118  
Db 59 DPTTFVAVRNILVVDPELRSLRVLTGTSAP-CEICRLCPAAVDAPGEDVDNVL 117  
Qy 119 LIDYKENLIIAGSLYQGIKLLRLE-----DLFK-LGEPYHKHEHYLSGVN 164  
Db 118 LLDPEVPELYSGTARRGLCYLHLDVRGSEVTIASTRCLYSAAANSPVNCPCVASPLG 177  
Qy 165 ESGSVFVGVIVSYNLDLKLFIATAVDGK--PYEP-TJSSKLTKNSEADGMEAVVFHDE 221  
Db 178 STATVVA-----DRYASFYLGSTVNSVVAARYSPRSVSVRL--KGRDQ-FADPFL-- 227  
Qy 222 FVASMIKIPSDFTTIIPDFD-----IYVYGFSSGNFVFLTLQPMVSPGSGTTKEQYTT 277  
Db 228 -----SLTVLPHYQDVPIHYVHSFTDGDHVLTVQPEF-----PGSST-----FH 269  
Qy 278 SKLVRLCKEDTAFNSYVEVPICG-----ERSGVE-----YRLQRAYLSKAGAV 321  
Db 270 TRLVRLSAHEPELRRYREIVLDCRYESKRRRRRGAEEETERDVAINVLQAAHAARPGAR 329  
Qy 322 LGRTLGVHPDDLLFTVFSKQKRWKMSLDESALCIFILOKQINDRIKERLOSQYRGEGLT 381  
Db 330 LARDLIGDGTETVLFQGAFAESHPEBPAPQHNSAVCAFFPLRLNQAIREGMDKC----- 382  
Qy 382 DLAWLKVDI PCSSALLTIDNFCGLDMNAPLGVDMDVRGIFVFTEDRDMTSVIATYVK 441  
Db 383 -----CG-----TGOTLKRGLAFFOPOQ-----YC 403  
Qy 442 NLSLAPVGTGSKLIRVDGPRGNALQYETVQVDPGVLDMAFSKDHEOLYIMSERQ 501  
Db 404 PHS-----VNLSAPVNTSCWD-----Q 421  
Qy 502 LTRVPVBSGQVQSGCEGLSGDPRGCGWCVLNTCTRKERCBSRPRFASSEMKCQVRL 561  
Db 422 PTLVPAAS-----H-----KV 432  
Qy 562 TVHPNNISVQYNVLLVLETYNVPELSAGVNCFTFEDLSMDGLVGNQIQCYSPAKEVP 621  
Db 433 DLENGLSGTLTISIFVVLQNV-----TVAHLGTAQGRVL----- 468

Qy 622 RIITENGDDHHVQVLQKSKETGMTASTSFVFNCSVHNSCLSVESPYRCHWKYRHYC 681  
Db 469 QMVLQRSSSYVVAL-----TNF----- 485  
Qy 682 THDPKTCSPQEGRVKLPEDCPQLLRVDKILVPEVIKPIITLAKNLPQPSQGRGYECIL 741  
Db 486 -----SLGEPGLVQHATGLQHS--LL 505  
Qy 742 NIOGSEQRVPALRFNSSVQCCNTSYSEGMENNLVELTVVWNGHFNIDNPAQNKHVL 801  
Db 506 FAAGTK-----VMRVNVTGPGR-----HFS----- 526  
Qy 802 YKCGAMRESGLCLKADPDFACWCQCGQCTLRQHCPAQESQWLSLGAKSCKTNPRT 861  
Db 527 -----ICDRCLRAERFMGCGWC--GNG-CIRHHEC--AGFWVQ-----DSCP-PVLT 567  
Qy 862 EIIPVTGPREGKTVTIRGENLGLPR-----DIASH-----VKVAGVECSPLVD--G 907  
Db 568 DFHPRGAPLRGQTRVTL-----CGMTFSPDPDTAHSLSLFPYRVAYGSRSCVTLDES 623  
Qy 908 YIP-----AEQIVCEMGEAKPSOAHGFVEICVAVCRPEFMAR-----SSQL--YVF 951  
Db 624 YRPLPTFRKDFVDVLVLCVLEPGEPAVAGPADVLNVTESAGTSRPRVQSGSTLSGFVF 683  
Qy 952 MTLTSLDLKPSRPMGSGTQVITITGNLGNAGNVVVMFKQPCLFHRRSPS-----YIVCN 1007  
Db 684 VEPHISTLHPSFGPGGGTILMSLYGTHLSAGSMRVTINGSECLLDGQ--PSEGDGEIRCT 742  
Qy 1008 TTGSDEVLEMKVSQVODRAKHQDLVQVVEPTIVRIEPMISVSGNTPPIAVMGTHL 1067  
Db 743 APATSLGAAPVALWIDGEEFLAPLPEFRDPDSVLTVVPCSY--GGSTLILGTHLDS 800  
Qy 1068 IONPQIRAK--HGGKEHINICEVLNATE-MTCOAPALALGPDHQSULTERPEBFGILDN 1124  
Db 801 VYRAKIQFGGGGKTEATECEGPQPNWLLCRSPAPPI-----EIKVPGNLSVLLDG 854  
Qy 1125 VQSLILINKTNFYNNPVPFEAPGPG--ILELKGTPPIILKGKILPPVAGGNVKNLYTV 1183  
Db 855 AADRNLFP--RLRYFPQPMFSGQGRYQLKPGDNEIKVNLGDSVAG--CMNITM 908  
Qy 1184 LVGKEPCTVTSVDQLLCESPNLI-----GRHKMARVGVGMEYSPGVYIAPDSPLPAI 1239  
Db 909 TVGGRDCHPNVKNVTCRVPDVLTPAGAPQICVNGDCQALGLV--LPASSLDMAA-- 965  
Qy 1240 VSTAVAG--LLIIFIVAVLIAYK-RKSR-----ESDLTKRLQMOMDNL 1281  
Db 966 -SLALGTGVTFLVCCVLAALVLEWRWRKRGLENLELVHPRIEHPITQR--PNVDYR 1022  
Qy 1282 ESRVLECKEAPAELOTDIHELTSDDLGDAG-----IPFL-----DYR----- 1318  
Db 1023 EVQV-LPVADSPGLARPHAFASAGADAAGGSPVPLRTTSCLEDRLPELLEVKDIL 1081  
Qy 1319 -----TYTMVRL-----PPGIEDHVLRLD-----EVPGRQERV- 1348  
Db 1082 IPBERLITHRSVIRGHHFGSVYHGTMDPLLGNLHCAVKSRLHRTDLEVEBFLREGIL 1141  
Qy 1349 -----BKGLKLAQLINNKVFLLSFIRTLB----- 1373  
Db 1142 MKSFHHQVLSLIGVCLPRHGLPLVLPYMRHGDLRHFIQAQERSPTVKELIGLQVAL 1201  
Qy 1374 -----SORSFMRD-----RGNVASLIMTVLOSKELEYATDVL-KOLLADLIDKNLESKNHPK 1424  
Db 1202 GMEYLAQCKFVHRDLAARNCMLDETITVKVADFGARDVFGKEYY-----SIRQHRHAK 1255  
Qy 1425 LLRL--RTESVAEKMLTN---W-FTFLYKFLKECAGEPLFLFLCAIKQOMKEGPIDAI 1477  
Db 1256 LPVKWMALESLOQKFTTKSDVWSFGVLMWELLTRGA-----SYPEVDPYDM- 1303  
Qy 1478 TGEARYSLSDKLIROQIDYKTL---VLSCVSPDNANSP 1513  
Db 1304 ---ARYLLRGRRLPQPQPCPDITLYGVMLSCWAPTPERP 1339

Db 593 QOGLGVFCWS 603

RESULT 10

US-09-077-940A-4  
; Sequence 4, Application US/09077940A  
; Patent No. 6576441  
; GENERAL INFORMATION:  
; APPLICANT: KIMURA, Toru et al.  
; TITLE OF INVENTION: NOVEL SEMAPHORIN Z AND GENE ENCODING THE SAME  
; FILE REFERENCE: 0020-4426P  
; CURRENT APPLICATION NUMBER: US/09/077,940A  
; CURRENT FILING DATE: 1998-06-05  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 4  
; LENGTH: 888  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-077-940A-4

Query Match 2.6%; Score 263; DB 4; Length 888;  
Best Local Similarity 22.7%; Pred. No. 5.7e-14;  
Matches 144; Conservative 90; Mismatches 208; Indels 192; Gaps 34;  
QY 11 LLSHLLMVGMGSSLLTRQAPILSOKORSFVTF-----RGEPAEGFNHLVVD--- 57  
Db 13 LLLLLLLIG-GAHLFPEDPPPLSVAPRDYLNHYFVVGSGPGLRTPAEGADDLNIQRLV 71  
QY 58 --ERTGHIYLGAVNRIYKL-----SSDLKV--LVTHETGPDNDPKCYPRIVQTCNEP 107  
Db 72 RVNET--LFIGDRNLXVLELPTSTELAYQKLTWRSNPSDINVCRMKGQEGECR-- 127  
QY 108 LTTNNVNMMLLDYKENRLIACGS-IYQIGICKLLRLLEDLPKGE-----PYHKEH 158  
Db 128 ---NFVKVLLLRD--ESTLFCVCGSNAFNVCANYSIDTLQPVGDNISGMARCYDPKH 180  
QY 159 YLSGVNESGVFGVIVG-----YSNLDLKLFIATAVDGKPEYPTTSSRKLTKNSE 209  
Db 181 ANVALFSDGMLFTATVDFLAIDAVIYRSLGDR-----PTLRVTK----- 220  
QY 210 ADGMFAVYHDFEVSAMIKIPSDFTTIPDFIYVYVFGSGNFPVYPLTLQPMVSPGS 269  
Db 221 -----HD---SKWKEP-----YFVHAVEMGSHVYFFREIAM-----EF 252  
QY 270 TTKEQVYTSKLVRCKSDTA-----FNSVVEVPICGERSG---VEYRLQAAVLSK 317  
Db 253 NYLEKVVSVRVARVCKNDVGSFVLEKQWTSFLKRLNCSVPGDSHFYFNVLQAV--- 308  
QY 318 AGAVLGRTLGVHPDDLLFTVFSKGQRKMKSLDESALCIFIILKQINDRIKERLQSCYRG 377  
Db 309 TGWV---SLGGRP---VVLAVFS---TPSNSIPGSAVCAFDLTQVAAVFEGR---FRE 354  
QY 378 EGTLDLAWLKYD--IP-----CSSALLTIDDNFCGLDMNA---PLGVSDMVRGIPVPT 426  
Db 355 QKSPESITVTPVEDQVPRPRPGCCAA-----PGMQYNASSALPDDIILNFVKTFLMD 406  
QY 427 ED-----RDRMTSVIAYV---YKNHSLAFVGTGSKGLKIRV-----D 461  
Db 407 EAVFSLGHAPWILRLTLARHQLTRVAVDVGAGPWGNTQVFLGSEAGTVLFLVRPNASTS 466  
QY 462 GPRGNALQYETVQVDP-----GPVLRDMAFSKDHEQLYINSEQLTVPVYESC 510  
Db 467 GTSGLSVFLEBEFYRDRGCRPGGGETGQRLLSLELDAASGGLLAAFPCCVVRVPVARC 526  
511 QYQSC-GECLGSDPHCGW-----CVLHNTCTR 538  
527 QYSGCKMKNCIGSDPYCGWAPDGCIFLSPGTR 560

RESULT 11

US-09-077-940A-2  
; Sequence 2, Application US/09077940A

RESULT 9

US-08-556-422A-4  
; Sequence 4, Application US/08556422A  
; Patent No. 6576754  
; GENERAL INFORMATION:  
; APPLICANT: HALL, Kathryn T.  
; APPLICANT: FREEMAN, Gordon J.  
; APPLICANT: SCHULTZE, Joachim L.  
; APPLICANT: BOUSSIOTIS, Vassiliki  
; APPLICANT: NADLER, Lee M.  
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING CD100 MOLECULES  
; FILE REFERENCE: DFN-005CPA2  
; CURRENT APPLICATION NUMBER: US/08/556,422A  
; CURRENT FILING DATE: 1995-11-09  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 607  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-08-556-422A-4

Query Match 3.1%; Score 308; DB 4; Length 607;  
Best Local Similarity 21.5%; Pred. No. 2.4e-18;  
Matches 144; Conservative 110; Mismatches 257; Indels 160; Gaps 29;  
QY 36 KQSFVTFRGEPAEGFNHLVVDERTGHIYLGAVNRIYKLSLDKVLVTHE-----TGPDE 90  
Db 1 EERLIRKFEAENISNTALLSQDGKTLVYGAREALFALNSNLSFLPGGEYQELLWSADA 60  
QY 91 DNEPKCYPRIVQTCN---EPLTTNNVNMMLLDYKENRLIACG-SLYQIGICKLLRLLED 145  
Db 61 DRK-----QCCSPKGDPRKDCQYIKILL-PLNSSHLITCGTAASPLCAVIHIAS 111  
QY 146 LFKLGPYPYHKEHYLGVNESGVFGVIVSYNSLD-----DKLFIATA--VDGKPEY 195  
Db 112 -FTLAQ-----DEAGNVI-----LEDGKGCPDPNFKSTALVWDG--EL 148  
QY 196 F-----PTSSRKLTKNSEADGMFAVYHDFEVSAMIKIPSDFTTIPDFIY 244  
Db 149 ITGTVSFQGNDAFARSOSRRTKESSLNLWQDPAFVASATSPESLSPGDDDDKIYF 208  
QY 245 VYGFSSGNFYFILTQPEMVSPGSTTKEQVYTSKLVRCKEDA-----FNSVVEV 296  
Db 209 FSETQGEPEFF-----ENTIVSRVARVCKGEGGERVLQQRWTSFLKA 252  
QY 297 PICER--SGVEYRLQAAVLSKAGAVLGRTLGVHPDD--DLLFTVFSKGQRKMKSLD 351  
Db 253 QLLCSCRDDGFPFNVLQDVF-----TLNPNQDWRKTLISIGVFTSQWHR--GTTE 300  
QY 352 ESALCIPILKQINDRIKERLQSCYRGEGTLDLAW-LKVKDIPCSSALLTIDDNFCGLDMN 410  
Db 301 GSALCVFTM--ND-VQXAFDGLYKKVNETQCYWYETHTQVTPRPGACITNSABERKIN 356  
QY 411 APLGVSD-----MYRGIPVFTEDRDRMTSVIAY---YKNHSLAFVGTGKS 452  
Db 357 SSLQLPDRVLNFKDHPFLMDGQVRSRLLLQPRARYQVAVHRVPGHSTYDVLFLGTGD 416  
QY 453 GKLKICRVDPGRGNALQYETVQVDPGPVLRDMAFSKDHEQLYIMSEROLTRVPVYESCGQ 512  
Db 417 GRLLKAVTLSSRVHII--EELQIFPQGPQVONILLDSHGGLLYASSHSGVGVQVFNCSL 474  
QY 513 YQSCGECCLGSDPHCGW-----CVLHNT-----CTXKERCERSKBPFRFA 552  
Db 475 YPTCGDCLLARDPYCAWTGACRSLASLYOPDLASRPWTQDIEGASVKELCNKSYYKARFL 534  
QY 553 SEMKQCVRLTVPHNNISVSQYNVLLVLET-----YNPVLSAGVNCCTFELSEMDGLVGN 608  
Db 535 VPGKPCQVQIQNTVNTLACPLLSNLATLWVHGAPVNASASCRV--LPTGDLILLVGS 592  
609 Q-----IQCVS 614

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; Patent No. 6576441
; GENERAL INFORMATION:
; APPLICANT: KIMURA, Toru et al.
; TITLE OF INVENTION: NOVEL SEMAPHORIN Z AND GENE ENCODING THE SAME
; FILE REFERENCE: 0020-4426P
; CURRENT APPLICATION NUMBER: US/09/077,940A
; CURRENT FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 2
; LENGTH: 887
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; US-09-077-940A-2

Query Match      2.4%; Score 244.5; DB 4; Length 887;
Best Local Similarity 22.2%; Pred. No. 2.7e-12;
Matches 141; Conservative 86; Mismatches 206; Indels 203; Gaps 34;

Qy 8 WT-----CLLSHLLMVGMSSSTLLTROPAPLSQKQSFVTF-----RGEPAE 49
Db 2 WTPRAPPPAPALLFLLLLRVTGHLFPDEPPPLSVAPRDYLSHYVPVGVGSGPGLTAP 61
Qy 50 GFNHLVVD-----ERTGHIYLGAVNRIYKL-----SSDLKV--LVTHETGFDENPKCY 96
Db 62 GAEDLNIOQLRVLRNRT--LFIGDRNLQVLEPSTSTELRYQKLTWRSNPSD----- 113
Qy 97 PPRIVQTC-----NEPLTTNNVNMKLLIDYKENRLIACGS-LYQGIKLLLEDLFLKGE 151
Db 114 ----IDVCRMKQGECECNFVKVLLRD--ESTLFCVGSNAFNICANYSMDTLQLLGD 167
Qy 152 -----PYHKHEHLSGWSGSGVFGVIVS-----YSNLDDKLFIATAVDGKPE 194
Db 168 NISGMARCYDPK-HANVALFSDGMLFATVTDLDAIDAVIYSLGDR----- 214
Qy 195 YPFTTSSRLTKNSEADGMFAVFDHDFVASMIKIPSDTFTIIPFDIYVYVGSNGFV 254
Db 215 --PTLRTVK-----HD--SKWKEP-----YFVHAVEWGSHV 242
Qy 255 YFLTLQPMVSPGSGTTEQVYTSKVLRLCKEDTA-----FNSVVEVPIGCSRG- 304
Db 243 YFFPREIM-----EFNYLEKVVSVRVCKNDVGSPPVLEKQWTSFLKARLNCVPGD 298
Qy 305 --VEYRLQAAVLSKAGAVLGTGLVHPDDLLFTVFSKGQKRMKSLDESALCIFILKQ 362
Db 299 SHFYFNLQAV---TGWV---SLGGRP---VILAVFS---TPSNSIPGSVAVCAFDMMQ 344
Qy 363 INDRIKERLQSCYRGSTGLDLAWLYKD--IP-----CSSALLTIDDNFCGLDMNAPLGV 415
Db 345 VAAVFEGR-----FREQKSPESITWTFVDEQVPRPRPGCCAA-----PGMYNASNAL 392
Qy 416 SD-----MVRGIP-----VFEDRDRMTSVIAYV-----YKNHSLAFVGTKS 452
Db 393 PDEILNFVKTHPLMDEAVPSLGHSPWIVRLIRHQLTRVAVDVAGPWNQITIVELGSEV 452
Qy 453 GKLLKI-----RVDGPRGNALQYETVQVVDP-----GPVLRDMAFSKDHEQL 494
Db 453 GTVLKFLVKNASVSGTGTGSIFFLEFETPRDRCGRSSAGEWGQRLLSLELDAASGGL 512
Qy 495 YIMSERQLTRVPVSESCQYQSC--GECILGSDPHCGW 529
Db 513 LAAFPRCVAVPVARCOLYSGCMKNCIGSQDPYCGW 548

RESULT 12
US-09-653-274-4
; Sequence 4, Application US/09653274
; Patent No. 6635742
; GENERAL INFORMATION:
; APPLICANT: Boyle, Bryan J
; APPLICANT: Yeung, George Y
; APPLICANT: Arterburn, Matthew C
; APPLICANT: Mize, Nancy K

; Patent No. 6576441
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Dmanac, Radoje T
; TITLE OF INVENTION: Methods and Maaterials Relating to Semaphorin-Like
; FILE REFERENCE: HYS-23
; CURRENT APPLICATION NUMBER: US/09/653,274
; CURRENT FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-10
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 4
; LENGTH: 1086
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-653-274-4

Query Match      2.3%; Score 228; DB 4; Length 1086;
Best Local Similarity 19.9%; Pred. No. 1.2e-10;
Matches 123; Conservative 107; Mismatches 219; Indels 168; Gaps 31;

Qy 10 CLLSHLLMVGMSSSTLLTROPAPLS-----QKQSFVTFRGEPAEAGFNHLVVD-----ERT 60
Db 7 CAVILLMVSQLRAVSPDEDEPLNTVDYHSQYVFRGRPSGNSQHRDLDFQLMLKIR 66
Qy 61 GHIYLGAVNRIYKLSDDLKVLVTHETGPD-----EDNPKC--YPPRIVQTCNEPLTT 110
Db 67 DTLYIAGRDQYIV--NINEMPKTEVIPNKKLTWRSRQDQRENCAMKGRKHDECHNFI-- 122
Qy 111 TNNVNMKLLIDYKENRLIACG-SLYQGIKLLLEDLFLKGEFYHKHEHLSGV----- 163
Db 123 -----KVFPNRDEMVFCVGNFNAFPMCRYRLSTLEYDGER-----ISGLARCPFD 169
Qy 164 --NESGVSFVGVSYNSLDDKLFIATAVDGKPEVFTTISRKLTKNSEADGMFAVYVPHDE 221
Db 170 ARQTNVALFA-----DGKLYSATVAD-----FLASDAVIYRSMGDSALRTI--K 212
Qy 222 FVAMIKIPSDTFTIIPFDIYVYVGSNGFVYFLTLQPMVSPGSGTTEQVYTSKLV 281
Db 213 YDSKWKEP-----HFLHATEYGNVYVFFFE---IAVEHNHNLGKAVY--SRVA 256
Qy 282 RLCKEDTA-----FNSVVEVPIGCSRG-----VEYRLQAAVLSKAGAVLGR 325
Db 257 RICKNDMGSGQGVLEKHTWTFKARLNCVPGDPFFVDFVLSITDIQINGIPTVVG-- 314
Qy 326 LGVHPDDLLFTVFSKGQKRMKSLDESALCIFILKQINDRIKERLQSCYRGSTGLDLAW 385
Db 315 -----VFTT-----QLNSIPGSVAVCAFSMDIDIEKVFGR-----FKEQKTPDSVW 354
Qy 386 LKVKD--IP-----CSSALL-----TID--DNFCGLDMNAPLGVSDM--VRGIPVTE 427
Db 355 TAVPEDKVPKPRPGCCAKHGLAEAYKTSIDFPDETLSFIKSHPLMDSAVPIADEPFTK 414
Qy 428 D--RDRMTSV---IAVYKNSHLAFVGTSGKLLKI-----RVDG 462
Db 415 TRVRYRLTATSDHSAGPYQNYTVIFVGEAGMVLKVLAKTSPFSLNDSVLLEBEIAYNH 474
Qy 463 PRGNALQYETVQVVDPGVLRDMAFSKDHEHLSQYIMSERQLTRVPVSESCQYQSCGE-CLG 521
Db 475 AKCSAENEEDKKVI-----SLQDKDHALYVAFVAFSCIIIRIFLSCRYGCKKSCIA 527
Qy 522 SGDPCGWCVLHNTCTR 538
Db 528 SRDPYCGW-LSQSGGR 543

RESULT 13
US-08-121-713D-62
; Sequence 62, Application US/08121713D
; Patent No. 5639856
; GENERAL INFORMATION:
; APPLICANT: Goodman, Corey S.
```

Qy		53	HUVDETHIYJGAVNRIYKLSDDLKVLTHTHETGPDEDPKCVPPIRIVQTNCPELTTTN	112
Dd		72	HMNEDRDT--LYVGAMDVFRV--NLQNISSSNCNRDAIN-----LEPTRDDVVSCV	119
Qy		113	NVNKKLLIDYKENRLIACGSIIYQGICKLLRLLEDIFKLGEPVHKKEHY-----LSGVNESG	167
Dd		120	SKGKSQIFDCK-NHVRIQSDMQ-----DRLYVCGTNAHNPKDVIVIANULTHPRE	171
Qy		168	SVFGEVIYS-----YSNLDDLKFIATAV---DGKPEYPFTTISRRLTKRNSEADGMFAYVPH	219
Dd		172	YVIGVGLGIACPYPDLDN---STAIVWENGNGPGLPYSGTNAEBFKRAD---TWIER	224
Qy		220	DEFVASMIKPSPDRFTIIPDFDI-----YYVGFSSGNFYVFLTLQP--EMWSPPGSTT	271
Dd		225	TDLNTSAKRLXYEKFRTLYKYDSKWLDKPNFVGSFDIGEYVYFFRETAVEYIN-----C	279
Qy		272	KEQVYTSLVRLCCKEDTA-----FNSYVEVEPIGBERSG---VEYRLLQAAYLSKAGA	320
Dd		280	GKAYV-SRIARVCKDVCGKNLLAHNWATYLKARLNCISISEFPFYNEIGSVY-----	332
Qy		321	VLGRTLGHVPDDDLLTFVFSKGQRKMKSDELSCALCIPILKOI---NDRIKERLQSCYR	376
Dd		333	-----OLPSDKSRFFATFT---TSTNGLIGSAVCSFHINEIOAAFNKGFEQSSES---	379
Qy		377	GEGTLDIAWLAKVD--IPCSSALLTIDDNFCGLDMNAPLGVSMDMVRGTP-----	423
Dd		380	-----NSAWLPVLNSRPPEPRPGTCNDT-----SNLPDTVLNTRISHPLMDKANVHEHN	429
Qy		424	-----VFTE---DRDRMTSVIAYYKNHS-LAFGTKSGKULKIRVGDGFRGNAL-QY	470
Dd		430	NPVYXKRDLVFTKLWDKIR---IDILOSBYIVYVYGTNLGRYIKIYOYVRNAGESISKL	485

Query Match 2.3%; Score 227; DB 1; Length 724;  
Best Local Similarity 20.4%; Pred. No. 6.9e-11;  
Matches 147; Conservative 118; Mismatches 260; Indels 196; Gaps 36;

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QY 53 HLVDERTGHIYLGAVNRYYKLSLKLVLVTHETGPDENPKCYPPIVQTCNEPLTTN 112
DB 72 HNNEDRDT--LYVGAMDRVRV--NLQNISSNCRDAIN-----LEPTRDDVVSCV 119
QY 113 NVNKMILLIDYKENRLIACGLYOGICKLLELDLFLKLBEPYHKEHY-----LSGVNESC 167
DB 120 SKGSKQIFDCK--NHRVVIQSDQG-----DRLYVCGTNAHNPCKDYVIYANLTHLPSE 171
QY 168 SVFEGVIVS-----YSNLDKLFATAV---DGKPEYFPTISSRKLTKNSEADGMFAYVPH 219
DB 172 YVIGVGLGIAKCPYDPLDN---STAIVYENGNGPGLPGLYSGTNAEFTKAD---TVIFR 224
QY 220 DEFVASMIPKPSDTPIIIPDFI-----YVYGFSSGNFVYFLTLQP---EMVSPPGSTT 271
DB 225 TDLYNTSAKLEYKFKRLKYDSKWLDPKPNFVGSFDIGEYVYFFRETAVEYIN-----C 279
QY 272 KEQVYTSKLVRLCKEDTA-----FNSYVEVPIGERSG---VEYRLLQAAAYLSKAGA 320
DB 280 GKAVY--SRIARVCKKDVGGKMLLAHNWATYILKARLNCISGEBFFPYFNEIQSVY----- 332
QY 321 VLGRTLGVHPPDDLLFTVFSKGQKRMKSLDESALCIFILKQI-----NDRIKERLQSCYR 376
DB 333 -----QLPSDKSRFFATFT-----TSTNGLIGSAVCSFHINEIQAAFNGKFEQSSS--- 379
QY 377 GEGTLDLAWLKVD--IPCSSALLTIDNFCGLDMNAPLGVSDMVRGIP----- 423
DB 380 -----NSAWLPVLSRVPRPGTCVNDT-----SNLPTVLNFIIRSHPLMDKAVNHEHN 429
QY 424 -----VFTE---DRDRMTSVIAYVYKNSHLAFVGTGSKGLKIRVDGPRGNAL-QY 470
DB 430 NPVYKRDVLVFTKLVDKIR-----IDLNQEVIVYVGTNLGRIYKIVQYENGESLSKL 485
QY 471 ETQVQVDPGVLRDMAFKDHQOLYIMSERQLTRVPVESCQ-QYQSCGECGLSGDPHCGW 529
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QY 530 CVLHNTCTRKER-----CERSKEPRFASMKQCVRLTVHPNNISVSQYNVL 576
DB 544 DKEANTCRPYELDLQDVANETSIDCSSVLKKIIVVYQSVHLGCF----- 591
QY 577 LVLETYNVPELSAGVNCFTFEDLSEMDGLVVGNGIQCYSPAKEVPRIITENGHHVQLQ 636
DB 592 -----VKIPVLKNEQVTHHSKDKGRY---EIR-YSPTK-----YIETTERGLVVVS 636
QY 637 LKSKETQMTFASTSFVFNCSVHNSCLSCVESPVYRCHWKYR-----HVTCHDPKTCSPQ 691
DB 637 VNEADGGR-----YDCHLGSL-----CSYNTVDAHRTCPNKNNDYQ 676
QY 692 E 692
DB 677 K 677

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RESULT 15

US-09-060-692-62

Sequence 62, Application US/09060692

Patent No. 5935865

GENERAL INFORMATION:

APPLICANT: Goodman, Corey S.

APPLICANT: Kolodkin, Alex L.

APPLICANT: Matthes, David R.

APPLICANT: Bentley, David R.

APPLICANT: O'Connor, Timothy

TITLE OF INVENTION: The Semaphorin Gene Family

NUMBER OF SEQUENCES: 100

CORRESPONDENCE ADDRESS:

ADDRESS: SCIENCE & TECHNOLOGY LAW GROUP

STREET: 268 Bush Street, Suite 3200

CITY: San Francisco

STATE: CA

COUNTRY: USA

ZIP: 94104

COMPUTER READABLE FORM:

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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent'n Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/060.692
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/121.713
FILING DATE: 13-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Oeman, Richard A.
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: B94-002-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
TELEX:
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 724 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-060-692-62

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Query Match 2.3%; Score 227; DB 2; Length 724;

Best Local Similarity 20.4%; Pred. No. 6.9e-11;

Matches 147; Conservative 118; Mismatches 260; Indels 196; Gaps 36;

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QY 53 HLVDERTGHIYLGAVNRYYKLSLKLVLVTHETGPDENPKCYPPIVQTCNEPLTTN 112
DB 72 HNNEDRDT--LYVGAMDRVRV--NLQNISSNCRDAIN-----LEPTRDDVVSCV 119
QY 113 NVNKMILLIDYKENRLIACGLYOGICKLLELDLFLKLBEPYHKEHY-----LSGVNESC 167
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QY 168 SVFEGVIVS-----YSNLDKLFATAV---DGKPEYFPTISSRKLTKNSEADGMFAYVPH 219
DB 172 YVIGVGLGIAKCPYDPLDN---STAIVYENGNGPGLPGLYSGTNAEFTKAD---TVIFR 224
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DB 430 NPVYKRDVLVFTKLVDKIR-----IDLNQEVIVYVGTNLGRIYKIVQYENGESLSKL 485
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DB 486 LDIFEVAPNEAIQVMEISQTRKSLYIGTDHRIKQIDLAMCNRYYDNCRCV--RDPYCGW 543
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DB 544 DKEANTCRPYELDLQDVANETSIDCSSVLKKIIVVYQSVHLGCF----- 591
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DB 592 -----VKIPVLKNEQVTHHSKDKGRY---EIR-YSPTK-----YIETTERGLVVVS 636
QY 637 LKSKETQMTFASTSFVFNCSVHNSCLSCVESPVYRCHWKYR-----HVTCHDPKTCSPQ 691
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QY 692 E 692  
Db 677 K 677

Search completed: May 25, 2004, 04:26:25  
Job time : 44 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 25, 2004, 03:50:55 ; Search time 82 Seconds  
(without alignments)  
6449.214 Million cell updates/sec

Title: US-09-964-956-13

Perfect score: 9990

Sequence: 1 MKAFPNWNTCLSHLMVGM.....QKLYKLEQVITLMSLDNK 1896

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1149313 seqs, 278921704 residues

Total number of hits satisfying chosen parameters: 1149313

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
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- 18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	9979	99.9	1894	16	US-10-451-010-9
3	6782	67.9	1963	12	US-09-964-956-43
4	6393.5	64.0	1905	12	US-09-964-956-44
5	6357	63.6	1896	12	US-10-312-352-34
6	6337	63.4	1894	12	US-10-087-684-81
7	6337	63.4	1894	12	US-10-218-779-81
8	6267.5	62.7	1925	12	US-10-087-684-32
9	6267.5	62.7	1925	12	US-10-218-779-32
10	5994	60.0	1871	12	US-09-964-956-42
11	5988	59.9	1871	12	US-10-087-684-84
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13	5847.5	58.5	1754	12	US-10-087-684-82
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15	3386.5	33.9	813	12	US-09-964-956-45

# ALIGNMENTS

## RESULT 1

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; Sequence 13, Application US/09964956
; Publication No. US20040043926A1
; GENERAL INFORMATION:
; APPLICANT: Gerlach, Valerie L
; APPLICANT: MacDougall, John R
; APPLICANT: Smithson, Glennda
; APPLICANT: Millet, Isabelle
; APPLICANT: Stone, David
; APPLICANT: Gunther, Erik
; APPLICANT: Ellerman, Karen
; APPLICANT: Alsobrook II, John P
; APPLICANT: Lepley, Denise M
; APPLICANT: Burgess, Catherine E
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Leach, Martin D
; APPLICANT: Shimkets, Richard A
; TITLE OF INVENTION: No. US20040043926A1el Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-124
; CURRENT APPLICATION NUMBER: US/09/964,956
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/235,631
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/235,633
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/235,808
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/236,064
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/236,065
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/236,066
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/236,135

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16	2708	27.1	593	12	US-09-964-956-46	Sequence 46, Appl
17	2565	25.7	1849	12	US-10-276-774-2188	Sequence 2188, Ap
18	2471	24.7	1992	12	US-10-276-774-2079	Sequence 2079, Ap
19	2385.5	23.9	1892	12	US-10-087-192-1944	Sequence 1944, Ap
20	184	18.2	344	15	US-10-108-260A-3245	Sequence 3245, Ap
21	1609.5	16.1	1806	15	US-10-369-493-5622	Sequence 5622, Ap
22	1573.5	15.8	362	12	US-10-276-774-2123	Sequence 2123, Ap
23	1351.5	13.5	552	9	US-09-909-320-170	Sequence 170, App
24	1351.5	13.5	552	9	US-09-909-088B-170	Sequence 170, App
25	1351.5	13.5	552	9	US-09-905-291A-170	Sequence 170, App
26	1351.5	13.5	552	9	US-09-902-853-170	Sequence 170, App
27	1351.5	13.5	552	9	US-09-907-824-170	Sequence 170, App
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37	1351.5	13.5	552	10	US-09-906-786-170	Sequence 170, App
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39	1351.5	13.5	552	10	US-09-906-700-170	Sequence 170, App
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43	1351.5	13.5	552	10	US-09-904-119-170	Sequence 170, App
44	1351.5	13.5	552	10	US-09-904-956-170	Sequence 170, App
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; PRIOR FILING DATE: 2000-09-28  
; PRIOR APPLICATION NUMBER: 60/237,434  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/238,321  
; PRIOR FILING DATE: 2000-10-05  
; PRIOR APPLICATION NUMBER: 60/238,399  
; PRIOR FILING DATE: 2000-10-06  
; PRIOR APPLICATION NUMBER: 60/238,396  
; PRIOR FILING DATE: 2000-10-06  
; PRIOR APPLICATION NUMBER: 60/276,667  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/294,823  
; PRIOR FILING DATE: 2001-05-31  
; PRIOR APPLICATION NUMBER: 60/304,868  
; PRIOR FILING DATE: 2001-07-12  
; NUMBER OF SEQ ID NOS: 127  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 13  
; LENGTH: 1896  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-964-956-13

Query Match 100.0%; Score 9990; DB 12; Length 1896;  
Best Local Similarity 100.0%; Pred No. 0;  
Matches 1896; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 361 KQINDRIKERLQSCYRGEGLDLAWLKVDI PCSSALLITIDNFCGLDMNAPLGVSDMVR 420  
DB 361 KQINDRIKERLQSCYRGEGLDLAWLKVDI PCSSALLITIDNFCGLDMNAPLGVSDMVR 420  
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DB 1441 WFTFLLYKFLKECAGEPLSLFCAIKQOMKGPIDAITGEARYSLSDKLIROQIDYKTL 1500  
QY 1501 VLSCVSPDNANSPEVPVKILNCDTITOVKEKILDAIFKNVPCSHRPKAADMDLEWRQSG 1560  
DB 1501 VLSCVSPDNANSPEVPVKILNCDTITOVKEKILDAIFKNVPCSHRPKAADMDLEWRQSG 1560  
QY 1561 ARMTLQDEDIITTKIENDWKRLNTLAHYQVPDGSVALVSKQVAYNAVNNSTVSRTSASK 1620  
DB 1561 ARMTLQDEDIITTKIENDWKRLNTLAHYQVPDGSVALVSKQVAYNAVNNSTVSRTSASK 1620  
QY 1621 YENMIRYTGSPDSLSRSTPMITPDLESQVKNWHLVKQHEHGDQKEGDRGSKMWSEIYLTR 1680  
DB 1621 YENMIRYTGSPDSLSRSTPMITPDLESQVKNWHLVKQHEHGDQKEGDRGSKMWSEIYLTR 1680  
QY 1681 LLATKGTLOKQVDDLFETIISTAHGSGALPLAIKYMFDLDEQADKHGIDHPVHRHTWKS 1740  
DB 1681 LLATKGTLOKQVDDLFETIISTAHGSGALPLAIKYMFDLDEQADKHGIDHPVHRHTWKS 1740  
QY 1741 NCLPLRFWNNMKNPQFVFDIHKNSITDACLSSVVAQTFMDSCTSEHRLGKDSPNKLLY 1800  
DB 1741 NCLPLRFWNNMKNPQFVFDIHKNSITDACLSSVVAQTFMDSCTSEHRLGKDSPNKLLY 1800

QY 1801 AKDIPSYKNWERYYSYDYGKMPAISDQDMNAYLAEQSMHNEFTMSALSEIFSYGKY 1860  
DB 1801 AKDIPSYKNWERYYSYDYGKMPAISDQDMNAYLAEQSMHNEFTMSALSEIFSYGKY 1860  
QY 1861 SEELGPHDDQCKQKAYKLQVITLMSLDSNK 1896  
DB 1861 SEELGPHDDQCKQKAYKLQVITLMSLDSNK 1896

RESULT 2

US-10-451-010-9  
; Sequence 9, Application US/10451010  
; Publication No. US20040082761A1  
; GENERAL INFORMATION:  
; APPLICANT: INCYTE GENOMICS, INC.  
; APPLICANT: DUGGAN, Brendan M.  
; APPLICANT: XU, Yuming  
; APPLICANT: LEE, Ernestine A.  
; APPLICANT: LEE, Sally  
; APPLICANT: LU, Dyung Aina M.  
; APPLICANT: WARREN, Bridget A.  
; APPLICANT: YUE, Henry  
; APPLICANT: GIETZEN, Kimberly J.  
; APPLICANT: HONCHELL, Cynthia D.  
; APPLICANT: BURFORD, Neil  
; APPLICANT: BAUGHN, Mariah R.  
; APPLICANT: TANG, Y. Tom  
; APPLICANT: JACKSON, Jennifer L.  
; APPLICANT: GANDHI, Ameena R.  
; APPLICANT: KALLICK, Deborah A.  
; APPLICANT: BANDMAN, Olga  
; APPLICANT: GRAUL, Richard C.  
; APPLICANT: CHAWLA, Narinder K.  
; APPLICANT: LU, Yan  
; APPLICANT: RAMKUMAR, Jayalaxmi  
; APPLICANT: YAO, Monique G.  
; APPLICANT: LAL, Preeti G.  
; TITLE OF INVENTION: CELL ADHESION PROTEINS  
; FILE REFERENCE: PF-0867 USN  
; CURRENT APPLICATION NUMBER: US/10/451,010  
; CURRENT FILING DATE: 2003-06-17  
; PRIOR APPLICATION NUMBER: PCT/US01/49206  
; PRIOR FILING DATE: 2001-12-18  
; PRIOR APPLICATION NUMBER: US 60/256,542  
; PRIOR FILING DATE: 2000-12-18  
; PRIOR APPLICATION NUMBER: US 60/259,604  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: US 60/260,101  
; PRIOR FILING DATE: 2001-01-05  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PERL Program  
; SEQ ID NO 9  
; LENGTH: 1894  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No: 7156379CD1  
US-10-451-010-9

Query Match 99.9%; Score 9979; DB 16; Length 1894;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1894; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKAMPNNWTCLLSHLLWVGWGSSTLLTRQAPLSQKQSFVTFRGEPAEGFNHLVVDERT 60  
DB 1 MKAMPNNWTCLLSHLLWVGWGSSTLLTRQAPLSQKQSFVTFRGEPAEGFNHLVVDERT 60  
QY 61 GHYIYGAUNRIYKLSDDLKVLVTHETGPDENPKYPRIVQTCNEPLTTNNVNMKLLI 120  
DB 61 GHYIYGAUNRIYKLSDDLKVLVTHETGPDENPKYPRIVQTCNEPLTTNNVNMKLLI 120

QY 121 DYKENELIACGSLYQGIICKLLEDLFKLGEPEYHKHEHYLSCVNESGSGVFGVIVSYNLD 180  
DB 121 DYKENELIACGSLYQGIICKLLEDLFKLGEPEYHKHEHYLSCVNESGSGVFGVIVSYNLD 180  
QY 181 DKLFATAVDGPPEYPTTSSRKLTKNSADGKFAVYHDEFFVASMIKIPSTFTTIIIDP 240  
DB 181 DKLFATAVDGPPEYPTTSSRKLTKNSADGKFAVYHDEFFVASMIKIPSTFTTIIIDP 240  
QY 241 DIYVYVFGSSGNFVYFLTLQPEMVSPGGSTTKKQVYVTSKLVRLCKEDTAFNSVVEPIGC 300  
DB 241 DIYVYVFGSSGNFVYFLTLQPEMVSPGGSTTKKQVYVTSKLVRLCKEDTAFNSVVEPIGC 300  
QY 301 ERSGVEYRLLOAYLSKAGAVLGRILGVHPDDDLFTFVSKGQKRMKSLDLSALCIFIL 360  
DB 301 ERSGVEYRLLOAYLSKAGAVLGRILGVHPDDDLFTFVSKGQKRMKSLDLSALCIFIL 360  
QY 361 KOINDRIKERLOSRYGEGTLDLAMLKVKDI PCSSALLITIDNFCGLDNNAPLGVSDMYR 420  
DB 361 KOINDRIKERLOSRYGEGTLDLAMLKVKDI PCSSALLITIDNFCGLDNNAPLGVSDMYR 420  
QY 421 GIPVFTEDRMTSVIAYVYKHSLAFVGTGKGLKKIRVDGPRGNALQYETVQVVDGP 480  
DB 421 GIPVFTEDRMTSVIAYVYKHSLAFVGTGKGLKKIRVDGPRGNALQYETVQVVDGP 480  
QY 481 VLKDMAPSKDHEQLYIMSRQLTRVPEVSCGQVQSCGECGLGSGDPHCGVCLHNTCTRKE 540  
DB 481 VLKDMAPSKDHEQLYIMSRQLTRVPEVSCGQVQSCGECGLGSGDPHCGVCLHNTCTRKE 540  
QY 541 RCERSKEPRRFASMEKQCVRLTVHPNNISVSQVNVLLVLETYNVPELSAGVNCFTFEDLSE 600  
DB 541 RCERSKEPRRFASMEKQCVRLTVHPNNISVSQVNVLLVLETYNVPELSAGVNCFTFEDLSE 600  
QY 601 MDGLVVGNOIQCVSPAACEVPRITITENGHHVVLQQLKSKETGTMTPASTSFVYNCVSVN 660  
DB 601 MDGLVVGNOIQCVSPAACEVPRITITENGHHVVLQQLKSKETGTMTPASTSFVYNCVSVN 660  
QY 661 SCLSCVESPYRCHWKYRHVCTHDPKTCFQEGRVKLPEDCPQLLAVDKILVPEVEIKPI 720  
DB 661 SCLSCVESPYRCHWKYRHVCTHDPKTCFQEGRVKLPEDCPQLLAVDKILVPEVEIKPI 720  
QY 721 TLKAKNLPQOSQRCQYECILNIQSGEORVPALRENSVQCVQNTSYSEGMEINNLVPE 780  
DB 721 TLKAKNLPQOSQRCQYECILNIQSGEORVPALRENSVQCVQNTSYSEGMEINNLVPE 780  
QY 781 LTVVWNGHFNIDNPAQNKVHLKCGAMRESGCLKADPDFACGWCQGGQCTLRQHCFA 840  
DB 781 LTVVWNGHFNIDNPAQNKVHLKCGAMRESGCLKADPDFACGWCQGGQCTLRQHCFA 840  
QY 841 QESQWLELSGAKSKCTNPRITEIIPVTPREGGKTIRGENLGLFRIASHVKVAGVE 900  
DB 841 QESQWLELSGAKSKCTNPRITEIIPVTPREGGKTIRGENLGLFRIASHVKVAGVE 900  
QY 901 CSPLVVDGYTPAEQIVCEMGEAKPSQAGFVEICVAVCRPEFMARSSQLYFMTLTLSDLK 960  
DB 901 CSPLVVDGYTPAEQIVCEMGEAKPSQAGFVEICVAVCRPEFMARSSQLYFMTLTLSDLK 960  
QY 961 PSRGPMSGGTQVTITGTNLMAGSNVVMFGKQPCLFHRRSPSYIVCNTSSDVLKMKVS 1020  
DB 961 PSRGPMSGGTQVTITGTNLMAGSNVVMFGKQPCLFHRRSPSYIVCNTSSDVLKMKVS 1020  
QY 1021 VQVDRAKIHODLVQVVEDPTIVIRIBPEWSIVSGNTPIAVWGTHLDLQNPQIRAKHGK 1080  
DB 1021 VQVDRAKIHODLVQVVEDPTIVIRIBPEWSIVSGNTPIAVWGTHLDLQNPQIRAKHGK 1080  
QY 1081 EHINI CEVLNATEMTQAPALAGPHQSDLTERPEEFGFILDNVQSLILANKNTFTYYP 1140  
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QY 1141 NPVFEAPGPSGILLEKPGTPIILKGNLIPPVAGGNVKLNYTVLVGKPCCTVTVSDVQLL 1200  
DB 1141 NPVFEAPGPSGILLEKPGTPIILKGNLIPPVAGGNVKLNYTVLVGKPCCTVTVSDVQLL 1200  
QY 1201 CESFNLTGRHKWAVRGMEYSFGWYIAPDSPSLPAIVSIAGAGLLIIFIVAVLIAY 1260

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1201 CESFNLIGHKVNARVGGMEYSGMWYIAPDSPLSLPAIVSAVAGGLLIIFIVAVLIAY 1260
1261 XKRSRESLTLKRLQMDNLESRVALECKEAEAEQTDIHELTSDDLQAGIPFLDYRTY 1320
1261 XKRSRESLTLKRLQMDNLESRVALECKEAEAEQTDIHELTSDDLQAGIPFLDYRTY 1320
1261 XKRSRESLTLKRLQMDNLESRVALECKEAEAEQTDIHELTSDDLQAGIPFLDYRTY 1320
1321 TMRVLPFGIEDHEDVLEDPVPGVQRORVEKGLKFAQLLNKVFLLSFRTLESORSFSM 1380
1321 TMRVLPFGIEDHEDVLEDPVPGVQRORVEKGLKFAQLLNKVFLLSFRTLESORSFSM 1380
1381 RDRGNVASLIMTVLQSKLEAVATDLVQLLADLIDKNLESKNHPKLLIRRTESVAEKMLTN 1440
1381 RDRGNVASLIMTVLQSKLEAVATDLVQLLADLIDKNLESKNHPKLLIRRTESVAEKMLTN 1440
1441 WFTFLYKFKLKECAGELPSLFCALIKQOEKGPIDAITGEARYSLEDKLIHQOIDYKTL 1500
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1501 VLSVSPDNANSPEVPVKILNCDTITQVKEKILDAIFKNVPCSHRPKAADMLEWRQSG 1560
1501 VLSVSPDNANSPEVPVKILNCDTITQVKEKILDAIFKNVPCSHRPKAADMLEWRQSG 1560
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1621 YENMIRYTGSPDSLRGTPMITPDLSSGVKQWHLVKNHEHGDQKEDGRGKMWSEIYLTR 1680
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1741 NCLPLRFVWNMIKNPQVFDIHNKSTIDACLSSVVAOTFMDSCSTSHRLGKDSPSNKLAY 1800
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1801 AKDIPSKNMYRYSDIGKMPAISQDDMNAYLAEQSRMHMFNTMSALSIFSVGKY 1860
1801 AKDIPSKNMYRYSDIGKMPAISQDDMNAYLAEQSRMHMFNTMSALSIFSVGKY 1860
1861 SEELGLDHDHDDCGKQKAYKLEOVITLMSLDS 1894
1861 SEELGLDHDHDDCGKQKAYKLEOVITLMSLDS 1894

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RESULT 3

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US-09-964-956-43
; Sequence 43, Application US/09964956
; Publication No. US20040043926A1
; GENERAL INFORMATION:
; APPLICANT: Gerlach, Valerie L
; APPLICANT: MacDougall, John R
; APPLICANT: Smithson, Glennda
; APPLICANT: Millet, Isabelle
; APPLICANT: Stone, David
; APPLICANT: Gunther, Erik
; APPLICANT: Ellerman, Karen
; APPLICANT: Grosse, William M
; APPLICANT: Alsobrook II, John P
; APPLICANT: Lepley, Denise M
; APPLICANT: Burgess, Catherine E
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Leach, Martin D
; APPLICANT: Shimkets, Richard A
; TITLE OF INVENTION: No. US20040043926A1e1 Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-124
; CURRENT APPLICATION NUMBER: US/09/964,956
; CURRENT FILING DATE: 2001-09-26

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; PRIOR APPLICATION NUMBER: 60/235,631
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/235,633
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/235,808
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/236,064
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/236,065
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/236,066
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/236,135
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 60/237,434
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/238,321
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: 60/238,399
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,396
; PRIOR FILING DATE: 2000-10-06
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/294,823
; PRIOR FILING DATE: 2001-05-31
; PRIOR APPLICATION NUMBER: 60/304,868
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 43
; LENGTH: 1963
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-964-956-43

Query Match 67.9%; Score 6782; DB 12; Length 1963;
Besc Local Similarity 66.9%; Pred. No. 0;
Matches 1278; Conservative 238; Mismatches 350; Indels 44; Gaps 9;

QY 23 STLLTROPAPLSQKOR-----SFVTFRGEPAE- 49
DB 60 SELLT--AAPLSMEQRWPRALEVDRSVVLLSVVWLLAPPAAQMPQSTFHSERNRW 117
QY 50 GFNHLVVDERTGHIYLGAVNRIYKLSDDLKVLVYTHETGDEDPNPKYPPRTVQTCNEPLT 109
DB 118 TFNHLTVHQGTGAVYVGAINRVYKLTGNLTQIQAHTKGPEDNKSCTPPLIVQPCSEVLT 177
QY 110 TTNVNMKLLIDYKENRLIACGLYQIGICKLLRLLEDLFKLGEPYHKEHYLSGVNBSGSV 169
DB 178 LTNVNMKLLIIDYSENRLIACGLYQYGVCKLLRLDLDLFILVEPSHKEHYLSVNKTGTM 237
QY 170 FGVIVSYNLDLKLPIATAVDGKPEYPTTSSRKLTKNSEADGMFAVYHDEFVAMIKI 229
DB 238 YGVIVRSEGEDGKLFICTAVDQKQDYPTLSSRKLPRDPRESSAMLDYELHSDYFVSSLIKI 297
QY 230 PSDTFTTIPDFDIYVYVGFSSGNFVYFLTLQPEMVSPG---STTKQVYVTSKLVRLCKE 286
DB 298 PSDTIALVSHEDIFYYIGFASGGFYFLTVQPE--TEGVAINAGDLFYTSRIVRLCKD 355
QY 287 DTAFNSYVEVPIGERSGVEYRLLQAAAYLSKAGAVLQRTLGVDHDDLLFTVFSKGQKQK 346
DB 356 DPKFHSYVSLPFGCTRAGVEYRLLQAAAYLAKPGDSLAAAFNITSQDDVLFALFSGKQKQY 415
QY 347 MKSLDESALCIFILKQINDRIKQLQSCYRCEGLFDLAWLKVKDIPCSSALLTIDDDNFCG 406
DB 416 HHPDDSSALCAFFIRAINLQIKRLQSCYQEGNLELNLWLLGKDVQCTKAPVPIDDDNFCG 475
QY 407 LDMNAPLGSDMVNRGIPVFTEDRMTSVIAYVYVYKNSHSLAFVGTYSKGLKKIRVDGPRGN 466
DB 476 LDIINQPLGGSTPVEGLATLTITTSRDMTSVASVYVYNGYSVVFVGTYSKGLKKIRADGPPHG 535
QY 467 ALQYETVQVW--DPGVLREDMAFSKDHQELIYMSRQLTRVPEVSGQYQSGCEGLSGDP 525

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Db 536 GVQYEMSVLKGSPILRDMFAFSDQRYLYMSRQVTRVPVSECEQYTTCEGLSSGDP 595  
QY 526 HCGKCVLHNTCTKXERBERSKEPERPASEMKQCVRLTWHNNISVSQYVLLVLETVNP 585  
Db 596 HCGKCVLHNTCTKXERBERSKEPERPASEMKQCVRLTWHNNISVSQYVLLVLETVNP 655  
QY 586 ELSAGVNTCTFBDLSEMDGLVGNQIQCYSPAKEVPRITENGDDHVVQQLKSKETGMT 645  
Db 656 DLSAGIACAFGNLTVEQVSGSVQICISPGKQDP-VIPLDQDWFGLEQLQSKETGKI 714  
QY 646 PASTSFVFNYSVNSCLSVESYRCHCKYKRVCHDPTKCSFOGRVKLPEDCPOLL 705  
Db 715 FVSTEFKYNCSAHLCLSCVNSAFRCHCKYKRVCHDPTKCSFOGRVKLPEDCPOLL 774  
QY 706 RVDKILVPEVVKPITLAKNLPQFQSGQRYGECILNIQSGEORVPALRNFSSVQOQNT 765  
Db 775 PTEBILIPVGEVKPITLAKNLPQFQSGQRYGECILNIQSGEORVPALRNFSSVQOQNT 834  
QY 766 SYSEGMENINLPVELTVMNGHFNIDNPAQKVKHLYKCGAMRESGLCLKADPDFACGW 825  
Db 835 SYQYDGMDSINLAVFVVMNGFNIDNPAQKVKHLYKCGAMRESGLCLKADPDFACGW 894  
QY 826 CQGPQCTLRQCPAQESQWLELSGAKSKCTNPRITEIPVTGREGGKTVTIRGENLGL 885  
Db 895 CSGERRCTLRQCTLRQCPAQESQWLELSGAKSKCTNPRITEIPVTGREGGKTVTIRGENLGL 954  
QY 886 BPRDIASHVAVGECSPUDGYIPABOIVCEMGEAKPSQAGFVETVAVCRPEFMARS 945  
Db 955 DFSEIAHVQVAGVCTPLPGEYIAEOIVCEMGEALVGTTSVGRVLCIGCEKPEFTKS 1014  
QY 946 SOLYFMTLTLSLKPSPGMSGGQVITITGNLGNAGSNVVMFGKQPCLPFRHSPSPVIV 1005  
Db 1015 HQQYTFNPSVLSNPIGPPSGGTMVITGHYLGAGSSVAVYLGNTCEFYGRSMSEIV 1074  
QY 1006 C-NTTSEDEVEMKVSQVDRAKIHQDLVQFVEDPTVIRTEPKSVISGNTPTAVGWTH 1064  
Db 1075 CVSPSSNGLGFPVSVSDRAHVDNLQFIEDPRVQRTEPWSIASGHTPTITGFN 1134  
QY 1065 LDLIQNPQIRAKHGKHEINICEVLNATEMTQAPALAGDPHQSDLTTERPEEGFILDN 1124  
Db 1135 LDVQEPRIKRVKNGESVNVCKVNTTILCLAPSLTDYRPGDVTVERDEDFGVFNN 1194  
QY 1125 VQSLILNKNTFYYPNVFEAFSPGSGILEKPGTPPIILKGNLIPPVAGNVKLYNTVL 1184  
Db 1195 VQSLILYNDTKFYYPNTPFELLSPGLDQKPGSPPIILKGNLCPASGG-AKLYNTVL 1253  
QY 1185 VGEKCTVSDVOLLCSNPILGRKQMARVGGMEYSPGMYIAPDSPLSIPATVSTAV 1244  
Db 1254 IGETPCAVTSETOLLCEPNLTGQKVMVHVGGMVFPSPGVSIVSDSLTLPALVSTAA 1313  
QY 1245 AGGLLIIFTVAVLIAKRSRESDLTLKRLQMDNLSRVALECKEAFELQTDIHBLT 1304  
Db 1314 GGSLLLIIVILVIAKRSRENDLTLKRLQMDNLSRVALECKEAFELQTDIHBLT 1373  
QY 1305 SOLDGAIFPLDYRTVMVLPFGIEDHPLVLDLEVPYGRVQREKGLKFAQLINNVF 1364  
Db 1374 SLDLSGIFPLDYRTVMVLPFGIEDHPLVLDLEVPYGRVQREKGLKFAQLINNVF 1433  
QY 1365 LLSFRTLSQSFMSRDRGNVASLIMTVLQSKLEVATDVLKQMLADLDKNLESKNHPK 1424  
Db 1434 LUTFTLTLQSFMSRDRGNVASLIMTVLQSKLEVATDVLKQMLADLDKNLESKNHPK 1493  
QY 1425 LLRRTESVAEKMLTNWFTFLYKFKECAGPLSLFCAIKQOQKEGPIDAITGEARYS 1484  
Db 1494 LLRRTESVAEKMLTNWFTFLYKFKECAGPLSLFCAIKQOQKEGPIDAITGEARYS 1553  
QY 1485 LSEDKLIROQIDYKTLVLSVCPDANSPEVPVKILNCPTITQVKEKILDAIFKNVPCSH 1544  
Db 1554 LSEDKLIROQIDYKTLVLSVCPDANSPEVPVKILNCPTITQVKEKILDAIFKNVPCSH 1613  
QY 1545 RPKAADMDLEWRQSGARMLOQEDDITTKIENDWKLNTLAHYQVDPGSSWALVSKQVTA 1604

Db 1614 RPRVMDLEWRQSGARMLOQEDDITTKIENDWKLNTLAHYQVDPGSSWALVSKQVTA 1673  
QY 1605 YNAVNNSTVRSASKEYENMIYRTGSPDLRSRTPMITPDLESYGVMWHLVKHHEHGDQK 1664  
Db 1674 YNPASASISRTSISRYDSSFRYTCGSPDLRSRAPMITPDLESYGVMWHLVKHHEHGDQK 1733  
QY 1665 EDRGSKVSEIYLRLLATKATGTLQKFDVDDLPETTFSTAHGSAALPLAKYMFDFLDEQA 1724  
Db 1734 EDRGSKVSEIYLRLLATKATGTLQKFDVDDLPETTFSTAHGSAALPLAKYMFDFLDEQA 1793  
QY 1725 DXGHGHDPRVHTWKSNCPLPLRFVWNNIKNPQFVPIHKNISITDACLVSVAQTFWDCSCT 1784  
Db 1794 DRHSIHDTVHTWKSNCPLPLRFVWNNIKNPQFVPIHKNISITDACLVSVAQTFWDCSCT 1853  
QY 1785 SEHRLGKDSFNKLYAKDIPSKYKVVRYISDIGNKPAISDQDNAYLAEGSRHMHNEF 1844  
Db 1854 SEHRLGKDSFNKLYAKDIPSKYKVVRYISDIGNKPAISDQDNAYLAEGSRHMHNEF 1913  
QY 1845 NTMSALSEIFSVYGVKSEIILGPDHDDOCCGKQKLAKEQVITLMSLDS 1894  
Db 1914 NMLSALNEIYSVYKSEIILGPDHDDOCCGKQKLAKEQVITLMSLDS 1963

RESULT 4  
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; Sequence 44, Application US/09964956  
; Publication No. US20040043926A1  
; GENERAL INFORMATION:  
; APPLICANT: Gerlach, Valerie L  
; APPLICANT: MacDougall, John R  
; APPLICANT: Smithson, Glenda  
; APPLICANT: Millet, Isabelle  
; APPLICANT: Stone, David  
; APPLICANT: Gunther, Erik  
; APPLICANT: Ellerman, Karen  
; APPLICANT: Grosse, William M  
; APPLICANT: Alsobrook II, John P  
; APPLICANT: Lepley, Denise M  
; APPLICANT: Burgess, Catherine E  
; APPLICANT: Padigar, Muralidhara  
; APPLICANT: Kekuda, Ramesh  
; APPLICANT: Seytek, Kimberly A  
; APPLICANT: Leach, Martin D  
; APPLICANT: Shimkets, Richard A  
; TITLE OF INVENTION: No. US20040043926A1e1 Proteins and Nucleic Acids Encoding Same  
; FILE REFERENCE: 21402-124  
; CURRENT APPLICATION NUMBER: US/09/964,956  
; PRIOR FILING DATE: 2001-09-26  
; PRIOR APPLICATION NUMBER: 60/235,631  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: 60/235,633  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: 60/235,808  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: 60/236,064  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: 60/236,065  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: 60/236,066  
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; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/238,321  
; PRIOR FILING DATE: 2000-10-05  
; PRIOR APPLICATION NUMBER: 60/238,399  
; PRIOR FILING DATE: 2000-10-06  
; PRIOR APPLICATION NUMBER: 60/238,396  
; PRIOR FILING DATE: 2000-10-06  
; PRIOR APPLICATION NUMBER: 60/276,667  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/294,823

; PRIOR FILING DATE: 2001-05-31  
 ; PRIOR APPLICATION NUMBER: 60/304,868  
 ; PRIOR FILING DATE: 2001-07-12  
 ; NUMBER OF SEQ ID NOS: 127  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 44  
 ; LENGTH: 1905  
 ; TYPE: PRI  
 ; ORGANISM: Xenopus laevis  
 ; US-09-964-956-44

Query Match 64.0%; Score 6393.5; DB 12; Length 1905;  
 Best Local Similarity 63.7%; Pred. No. 0;  
 Matches 1222; Conservative 245; Mismatches 396; Indels 55; Gaps 13;

QY	6	NNWTCLLSHLLMVGMSSTLLTRQAPLPSQKQBSFVTFRGEPAAGNHLVDBERTGHYIL	65
DB	14	WTELVLLGSIATGDGS-----PKDFRTFTGSD-WSLTHLVHVKHTGEVYV	58
QY	66	GAVNRYIKLSSDLKLVLTHTGDEPNKCPYPIVQTCNEPLTNNVKNMLLIDYKEN	125
DB	59	CAINRYIKLNNLTATHVTGVEDNEKCPYPPSQSCPHGLITNNVKNMLLIDYSDN	118
QY	126	RLIACGSXYGICIKLLRLDLFKLGPYHKHLYSLGVNESGVFVIVSYGNLDDKLP	185
DB	119	RLIACGSASQICQFLRLDLFLKLGSPHHRKHEHLYSLGVNESGTMGVIEVNPQNKL	178
QY	186	ATAVDGPEYEPITSSRKLTNKEADGMFAVVFHDFEASMIKIPISDTFTIIPDPIYV	245
DB	179	GTIDGKSEYFPILSSRKLTNENAEVGFVQDFEVSQKIPISDTLSKPTFDPIYV	238
QY	246	YGFSSGNFVYFLTLQ--PEMVSPPGSTTKQVQVTSKLVRLCKEDTAFNSYVEVPIG	303
DB	239	YSFSEQFVYVYTLQLDTQLTSP--DSTGEQFTSKIVRLCVDDPKFSYVEVPIG	296
QY	304	GVEYRLLOAYLSKAGAVLRTLVGHVDDLLFTVSKGOKKMSLDESALCIFLTKOI	363
DB	297	GVEYRLLOAYLSKAGAVLRTLVGHVDDLLFTVSKGOKKMSLDESALCIFLTKOI	356
QY	364	NDRIKERLQSCYRGEGLDLAWLKVDIPCSSALLTIDDFCGLDNMNAPLGSDMVRGIP	423
DB	357	KDKIKERLQSCYRGEGLDLAWLKVDIPCSSALLTIDDFCGLDNMNAPLGSDMVRGIP	416
QY	424	VFTEDRDMTSVIAVYKNSHLAFVGTGSKLKIIRVDGPRGNA---LQYETVQVVDGP	480
DB	417	LFLDKEDMTSVAAYDYGHTVWFAGTGRVKKILVDLSASSSHLVQYENVVHEGNA	476
QY	481	VLDRMAFSKDEQLYIMSEROLTRVPVSVESQCGYQSCGECILGSGDPHCGWCVLHNTCTRKE	540
DB	477	ILRLDLVLSPEQYIYAMTEKQVTRVPVSVESQCGYQSCGECILGSGDPHCGWCVLHNTCTRKE	536
QY	541	RCERSKSPRRFASAKOCVRLTVHPNNISVQYVNLVLTNYVPELSAGVNCPTFDLSE	600
DB	537	KCERADELHRTSDQRCVQLTVHPKNIISVTVSEVPMVLQANVPDLSAGVNCSPEDFTE	596
QY	601	MDGLVVGNIQCYSPAAKEVPRIITENGDDHVVQLKSKETGTMFTASTGTFVYVNCVHN	660
DB	597	MEGRILDKIYCTSPSAKEVPIYRGGDKXVVKLYLKSKEGKGFASVDFVYVNCVHQ	656
QY	661	SCLCSVESPYRCHCKYRHTVTHDPKTCSPQEGRVKLPEDCPQLLRVDKILVPVETKPI	720
DB	657	SCLCSVNGSFPCHCKYRHTVTHDPKTCSPQEGRVKLPEDCPQLLRVDKILVPVETKPI	716
QY	721	TLKAKNLPQSGGQRYECLINIOGSEORVPALAFNSVQONTYSYEGMEINNLVPE	780
DB	717	TLTAKNLPQSGGQRYECLINIOGSEORVPALAFNSVQONTYSYEGMEINNLVPE	776
QY	781	LTVMVNGHFNIDNPANQKHLVYKCGAMPESCGCLCKADDPFACQWCGQPGQCTLRQCPA	840
DB	777	LSVMVNGHFNIDNPANQKHLVYKCGAMPESCGCLCKADDPFACQWCGQPGQCTLRQCPA	836
QY	841	QESOWLELSGAKSCKNTNRIETIIPVTGPRGGIKVITIRGENLGLERDIAHVKVAGVE	900

DB	837	LENPMWHAASANSRCDTPKILTKLPETPGPQGGTRLTITGENLGLAFEDIRFGVRVGHVM	896
QY	901	CSPLVDGYIPABQIVCEMGEA-KPSQAGAVEICVAVCRPEFMARSQLYYFWTLTSLDL	959
DB	897	CVPVESEYISAEQIVCEINDAGTRVHEAQVEVCVXDCSQDYRAISPKSFTFVLPFNRV	956
QY	960	KPSRGMSSGGTQVTTITGNLNAGSNVVMFGKOPCLFHRHRSYVIVCNITSSDELEMKV	1019
DB	957	TPSRGPLSGGTWISIEGNYLNAGSDVSAIGGRPCMFSEWETAKEIRCKTPQGPSTGAEI	1016
QY	1020	SVQVDRAKHODLV-FOYVEDPTIVRIEPEWSIVGNTPIAVWGTHTLHLNQLQIRAKHG	1078
DB	1017	QILINRATMNNSEVHYNYTDPVTKIEPEWSIASGOTPLIVTGMNLATIKPKIRAKYG	1076
QY	1079	GKEHINICEVLNATEMTCQAPAL--ALGPDHQSDLTERPEEFGLIDNVSLLILNKTN	1135
DB	1077	DVEKENCTLINDTMTVCLAPSDNPLRSPENDC---RPDEIGFINDVHALLIVNTTS	1133
QY	1136	FTYYPNVFEAFPGSGILELKPPTIILKGNLPIPPVAGNVKLYNIVLVEKPCCTVVS	1195
DB	1134	FLYYPDPVFEPLTAGSNLELKPSPILIKGRNLI-PAAPGNFRNLNYTLVIGDTPCALTVS	1192
QY	1196	DVQLLCSPNLIGRHKVMARVGMVSPGMVYAPDSPLSIPAIVSAVAGGLIIIFIVA	1255
DB	1193	ETQLLCSPNLTGQHKVTIKAGFEYSPGTLOIYSDSLTLPAIIGGGGGGLLIIII	1252
QY	1256	VLIAYKRSRESDLTLKQLQMDNLESVALECKEAPAELOTDIHELTSDLGAGIPFL	1315
DB	1253	VLIAYKRSRDAKTLKQLQMDNLESVALECKEAPAELOTDIHELTSDLGAGIPFL	1312
QY	1316	DYRYTTRVLPFGIEDHPVLDLEVPQVQREVEKGLKPAQLNNKVELLSFRTLESQ	1375
DB	1313	EYRYTTRVLPFGIEDHPVLDLEVPQVQREVEKGLKPAQLNNKVELLSFRTLESQ	1368
QY	1376	RSFMRDRGNVASLMTVLQSKLEYATDVLKQLADLIDKNLESKNHPKLLRRTESVAE	1435
DB	1369	RSFMRDRGNVASLMTALQEMEYATGVLKQLADLIDKNLESKNHPKLLRRTESVAE	1428
QY	1436	KMLTNWFTFLYKLEKCEGEPFLSCAIKQOEKGPIDAITGEARYSISEDKLROOI	1495
DB	1429	KMLTNWFTFLYKLEKCEGEPFLSCAIKQOEKGPIDAITGEARYSISEDKLROOI	1488
QY	1496	DYKTL-----VLSCVSPDNANSPEVPVKILNCDDITITQVKEKILDAI	1536
DB	1489	DYKTLPCADDVGLSDESCCRSPQTLNCVNPENENAPEIPVKVLCDDITITQVKEKILDAI	1548
QY	1537	FQVPCSHRPAKADMDLEWRGSGARMILQDEDTTKIENDWKRLNTLAHYQVDPGSVA	1596
DB	1549	YKGVFYSORPKAGMDLEWRGSGARMILQDEDTTKIENDWKRLNTLAHYQVDPGSVA	1608
QY	1597	LVSKQVTAYNVNNSTVSRITGASKYENMIRVTGSPDSLSRSTPMITPDLESQVMMHLVK	1656
DB	1609	LVPKONSAYNLSNSTFTK-SLSRYESMLRTASSPDSLSRSTPMITPDLESQVMMHLVK	1667
QY	1657	NHEHGDQKEDRGSKVSEIYILTRLLATKGLTQKFDVDDLFTIFSTAHRSALPLAIKYM	1716
DB	1668	NHDHLDQKEDRGSKVSEIYILTRLLATKGLTQKFDVDDLFTIFSTAHRSALPLAIKYM	1727
QY	1717	FDLDEQADKGIHDPHVRHTWKSCLPLRFVWNNIKNPQFVDFIHKSITDACLSSVVAQ	1776
DB	1728	FDLDEQADKGIHDPHVRHTWKSCLPLRFVWNNIKNPQFVDFIHKSITDACLSSVVAQ	1787
QY	1777	TFMDCSTSEHRLKXDSFNKLLYAKDIPSYKQWVERYYSDIGKMPAISQDMNAYLAEO	1836
DB	1788	TFMDCSTSEHRLKXDSFNKLLYAKDIPSYKQWVERYYSDIGKMPAISQDMNAYLAEO	1847
QY	1837	SRMHNENFMTGMSALFEISYVCKYSEIILGPLDHDQCKOKLAVKLEQVITMSLDS	1894
DB	1848	SRLHSQFNSMSALHEIYSITTKYRDEILTALEKQARRQLRSKLEQVIDTMAQSS	1905

RESULT 5  
 US-10-312-352-34

Sequence 34, Application US/10312352  
Publication No. US20040053824A1  
GENERAL INFORMATION:  
APPLICANT: INCYTE GENOMICS, INC.; TANG, Y. Tom  
APPLICANT: YUE, Henry; AZIMZAI, Yalda  
APPLICANT: HE, Ann; BATRA, Sajeev  
APPLICANT: LO, Terence P.; NGUYEN, Dammitel B.  
APPLICANT: BURRILL, John D.; MARCUS, Gregory A.  
APPLICANT: ZINGLER, Kurt A.; GANDHI, Ameena R.  
APPLICANT: LAI, Preeti G.; KEARNEY, Liam  
APPLICANT: BURFORD, Neil; YAO, Monique G.  
APPLICANT: CHAWLA, Narinder K.; ELLIOT, Vicki S.  
APPLICANT: ARVIZU, Chandra S.; KHAN, Farrah A.  
APPLICANT: BAUGHN, Mariah R.; HAFALIA, April, J.A.  
APPLICANT: POLICKY, Jennifer L.; AU-YOUNG, Janice K.  
APPLICANT: LU, Yan; BOROMSKY, Mark L.  
APPLICANT: LU, Dying Aina M.; RAMKUMAR, Jayalaxmi  
APPLICANT: YANG, Junning; GURURAJAN, Rajagopal  
APPLICANT: WARREN, Bridget A.; GIETZEN, Kimberly J.  
APPLICANT: XU, Yuming; KALLICK, Deborah A.  
APPLICANT: LEE, Ernestine A.; THANGAVELU, Kavitha  
APPLICANT: DELEGANE, Angelo M.; LEE, Sally  
TITLE OF INVENTION: EXTRACELLULAR MATRIX AND CELL ADHESION MOLECULES  
FILE REFERENCE: PP-0794 USN  
CURRENT APPLICATION NUMBER: US/10/312,352  
CURRENT FILING DATE: 2002-12-18  
PRIOR APPLICATION NUMBER: PCT/US01/21067  
PRIOR FILING DATE: 2001-06-29  
PRIOR APPLICATION NUMBER: US 60/215,454  
PRIOR FILING DATE: 2000-06-30  
PRIOR APPLICATION NUMBER: US 60/219,462  
PRIOR FILING DATE: 2000-07-18  
PRIOR APPLICATION NUMBER: US 60/240,111  
PRIOR FILING DATE: 2000-10-12  
PRIOR APPLICATION NUMBER: US 60/240,106  
PRIOR FILING DATE: 2000-10-12  
PRIOR APPLICATION NUMBER: US 60/244,021  
PRIOR FILING DATE: 2000-10-27  
PRIOR APPLICATION NUMBER: US 60/248,887  
PRIOR FILING DATE: 2000-11-14  
PRIOR APPLICATION NUMBER: US 60/249,570  
PRIOR FILING DATE: 2000-11-16  
NUMBER OF SEQ ID NOS: 72  
SOFTWARE: PERL Program  
SEQ ID NO 34  
LENGTH: 1896  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc feature  
OTHER INFORMATION: Incyte ID No. US20040053824A1 7204554CD1  
US-10-312-352-34

Query Match 63.6%; Score 6357; DB 12; Length 1896;  
Best Local Similarity 64.0%; Pred. No. 0;  
Matches 1213; Conservative 258; Mismatches 401; Indels 22; Gaps 13;

Qy 11 LLSHLLMVGMSSTLLTQAPLSQKRSFVTERGEPAEGFNHVLVDERTGHIYLGAVNR 70  
Db 15 LLLLLLPGMAEAGL---PRAGGSQPPFTFSASD-WGLTHLVVHEQTGEVTVGAVNR 70  
Qy 71 IYKSSDLKVLVTHETGDEPNKCYPPRIYQTCNEPLTTNNYKMLIDYKENRLIAC 130  
Db 71 IYKLSGNLTLLRAHVTGPVEDNEKCYPPPSVQSCPHGLGSTDNVKKLLLDYAANRLAC 130  
Qy 131 GSLVQIGCKLRLDLFKLGPYHKKHYLGSVNESGSVFGVIYS--YSNLDLKLFTATA 188  
Db 131 GSASQGIQCFRLDDLLFKLGPYHKKHYLGSVNESGSVFGVIYS--YSNLDLKLFTATA 190  
Qy 189 VDGPEYPTTSSRLKTKNSADGMFAVVFHDEFVASMIPKIPSTFTIIPDFDIYVYGF 248  
Db 191 IDGKSEYPTTSSRLKTKNSADGMFAVVFHDEFVASMIPKIPSTFTIIPDFDIYVYGF 250

Qy 249 SSGNFVYFLTLQ--PEMVSPGSGTTKEQVYTSKLVRLCKEDTAENFSYVEVPICBRSQVE 306  
Db 251 RSEQFYVYTLTQLDQLTSP--DAAGEHFFTSKIVRLCVDDPKFYSYVEFFPGCEQAGVE 308  
Qy 307 YRLQAAYLSKAGAVLGLTGVHPDDLLFTVFSQGRKMKSLDESALCIFILKQINDR 366  
Db 309 YRLVQDAVLSRPGRALAHQGLAEDVLTFFAQQGNKVRKPPRESALCLFTLRAIKEK 368  
Qy 367 IKERLQSCYRGEGTDLAWLKVKDIPCSALLTIDNFCGLDMNAPLGVSDMVRGIPVFT 426  
Db 369 IKERLQSCYRGEGTDLAWLKVKDIPCSALLTIDNFCGLDMNAPLGVSDMVRGIPVFT 428  
Qy 427 EDRDMTYSIAYVYKNSHSLAFVGTSGKMKIRVD--GPRGN-ALQYETVQVVDGPPVLR 483  
Db 429 DKDDGLTAVAAYDYRGRTVWFAGTSGRIRKILVLSNPPGGRPALAYSVVAQEGSPILR 488  
Qy 484 DNAPSKDHEQLYMSERQLTRVPSVSCGYQSCGICSGDHPCHCWCVLHNTCTKERCE 543  
Db 489 DLVLSNHOYLYAMTEKQVTRVPSVSCGYQSCGICSGDHPCHCWCVLHNTCTKERCE 548  
Qy 544 RSKEPRRFASBMKQCVRLTVHPNNISVSQYNVLLVLETYNVPELSAGVNCCTFEDISEMDG 603  
Db 549 RADEPQRFADLLQCVLTQVQPRNVSVTMSQVPLVLAQWNPVPLDSAGVNCSEFDETES 608  
Qy 604 LVVGNQIQCYSPAAREVPRITTEGDDHVVQLQSKKETMTFASTSFVYNCVSNVNSCL 663  
Db 609 VLEDGRHCRSPSAREVAPITRGQGDQDQVVKLYLKSKEKTKKFAVDFVYNCVSNVNSCL 668  
Qy 664 SCVESPYRCHWKYRHVCTHDPKTSFQGRVVKLPEDCPQLLRVDKILVPEVVIKPIITK 723  
Db 669 SCVNGSPFCHWKYRHVCTHDPKTSFQGRVVKLPEDCPQLLRVDKILVPEVVIKPIITK 728  
Qy 724 AKNLPQSGQRYGECILNIQSGEORVPALRPNSSVQCNQTSYSGMEINNLVELTV 783  
Db 729 AKNLPQSGQRYGECILNIQSGEORVPALRPNSSVQCNQTSYSGMEINNLVELTV 788  
Qy 784 VVNGHENIDNPAQNVHLKCGAMRESGLCLKADPDACGWCQCGOCTLROHQAQ-E 842  
Db 789 VVNGHENIDNPAQNVHLKCGAMRESGLCLKADPDACGWCQCGOCTLROHQAQ-E 848  
Qy 843 SOWLELSGAKSKCTNPRITEIIPVTPRGEGTKVTIRGENLGLERDIAHVKVAGVGS 902  
Db 849 ASWMHARHGSRRCTDPKILKSPETGPRQGGTTLTGTENLGLERDIAHVKVAGVGS 908  
Qy 903 PLVDGYIPAEQIVCEMGEAKPSQ-HAGFVEICVAVCRPEFMARSQLYVFMTLTSLDLP 961  
Db 909 PVESEYISAEQIVCEMGEAKPSQ-HAGFVEICVAVCRPEFMARSQLYVFMTLTSLDLP 968  
Qy 962 SRGPMSSGGTQVTTITGTLNAGSNVVMFGKQPCLFHRRSPSYIVCNTSSSDEVLEMKSV 1021  
Db 969 SRGPMSSGGTQVTTITGTLNAGSNVVMFGKQPCLFHRRSPSYIVCNTSSSDEVLEMKSV 1028  
Qy 1022 QVDRAKI-HQDLVQYVEDPTIVREPWSIVSGNTPAVMGTHLDLIONPOIRAKHGK 1080  
Db 1029 NINRAQLTPREKYNNTEDFTILRIDPEWSINSGGTLLTGTNTLATVREPRIRAKYGI 1088  
Qy 1081 EHNICEVLNATEMTQAPALALPDHQSGLTERPEEFQFILDNQSLLILNKTFTYYP 1140  
Db 1089 ERENGCLVNDITMVCRAFSVANPVRSPELGERDELGFVMDNVRSLVLNSTFLYYP 1148  
Qy 1141 NPVEAFAGSGILELKPPTIILKGNLIPVAVGNVKNLYTVLVEKECTTVSDVQLL 1200  
Db 1149 DPVLEPLSPGLLELKPSSPLIKGNLIPVAVGNVKNLYTVLVEKECTTVSDVQLL 1207  
Qy 1201 CSEPNLGRHKVMARVGMGMEYSPGMVYIAPDPSLPAIVSIAVAGGLIIIFVAVLIAY 1260  
Db 1208 CEAPNLTGQKVTVRAGGFEFGTLOVYSDLLTLPALVIGGGGGLLLIVAVLIAY 1267  
Qy 1261 KRKRSRSDTLKRLQMDNLSRVALECKEFAELQTDIHELTSLDGAGIPFLDYRTY 1320  
Db 1268 KRKRSRSDTLKRLQMDNLSRVALECKEFAELQTDIHELTSLDGAGIPFLDYRTY 1327  
Qy 1321 TTRVLPFGIEDHVPGLDLEVPGRQVRVEKGLKLAFLINNKVFLISFRTLESQRSFSM 1380





Db 1791 KDSPNKLLYAKDIPNYKSWERYADIAKMPAISDQDMSAYLAEQSRHLHSQFMSMAL 1850  
QY 1851 SBEISYVGVKSEELPLDHDQCKQKQKAYLKEQVITLMSLDS 1894  
Db 1851 HEIYSYIAKYDEILVALEKDEQARRQSRKSLKEQVDTMALSS 1894

RESULT 7

US-10-218-779-81  
; Sequence 81, Application US/10218779  
; Publication No. US2004002922A1  
; GENERAL INFORMATION:  
; APPLICANT: Edinger, Shlomit  
; APPLICANT: MacDougall, John  
; APPLICANT: Millet, Isabelle  
; APPLICANT: Ellerman, Karen  
; APPLICANT: Stone, David  
; APPLICANT: Gerlach, Valerie  
; APPLICANT: Grosse, William  
; APPLICANT: Alsobrook II, John  
; APPLICANT: Lepley, Denise  
; APPLICANT: Rieger, Daniel  
; APPLICANT: Burgess, Catherine  
; APPLICANT: Casman, Stacie  
; APPLICANT: Spytek, Kimberly  
; APPLICANT: Boldog, Ferenc  
; APPLICANT: Li, Li  
; APPLICANT: Padigaru, Muralidhara  
; APPLICANT: Mishra, Vishnu  
; APPLICANT: Patturajan, Meera  
; APPLICANT: Shenoy, Suresh  
; APPLICANT: Rastelli, Luca  
; APPLICANT: Tchernev, Velizar  
; APPLICANT: Vernet, Corine  
; APPLICANT: Zerhusen, Bryan  
; APPLICANT: Malyankar, Uriel  
; APPLICANT: Guo, Xiaojia  
; APPLICANT: Miller, Charles  
; APPLICANT: Gangolli, Bsha  
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same  
; FILE REFERENCE: 21402-214  
; CURRENT APPLICATION NUMBER: US/10/218,779  
; CURRENT FILING DATE: 2002-08-14  
; PRIOR APPLICATION NUMBER: 60/253,834  
; PRIOR FILING DATE: 2000-11-29  
; PRIOR APPLICATION NUMBER: 60/250,-926  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: 60/264,180  
; PRIOR FILING DATE: 2001-01-25  
; PRIOR APPLICATION NUMBER: 60/313,656  
; PRIOR FILING DATE: 2001-08-20  
; PRIOR APPLICATION NUMBER: 60/327,456  
; PRIOR FILING DATE: 2001-10-05  
; NUMBER OF SEQ ID NOS: 216  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 81  
; LENGTH: 1894  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-218-779-81

Query Match 63.4%; Score 6337; DB 12; Length 1894;  
Best Local Similarity 63.5%; Pred. No. 0;  
Matches 1209; Conservative 267; Mismatches 408; Indels 20; Gaps 13;  
QY 1 MKAMPNWTCLSHLLMVGMSSTLLTROPAPLSQKRSFVTFRGEPAGFNHLYVDERT 60  
Db 1 MPLPPLSSRTLLLLLLLRGVWIAISSPPAGIG-PQPAFTFVASD-WGLTHLVVHEQT 58  
QY 61 GHYLVGNVRIYKLSDDLKVLVTHETGPDNDPKCYPPRIVOTCNPLTTNNNNKMLLI 120  
Db 59 GEYVGNVRIYKLSGNLTLLRAHVTGPDNEKCYPPSPVQSCPHGLGSTDNNKLLLL 118

Db 717 VGWVKPTTLAARNLPQSQGQGYECFLHIFGSPARVATLRFNSSLQCNSSYSYEGND 776  
QY 774 INNLPELTVVWNGHFNPAQKVHLYKCGAMRESCGLCKLADPDPAFCGWCGQPGQCT 833  
Db 777 VSDLPVNLVWVWNGFNVDNPQNIQAHLYKCPALRQSCGLCKLADPRFECGMCVAERCS 836  
QY 834 LRHCPCABE-SQWLELGAOKSCTNPRITEIIPVTPGREGGTVKTINGENGLFEDFIAS 892  
Db 837 LRHCPCADSPASWMAHGHSSRCTDPKILKLSPETGPRQGGTLTITGENGLRFDVRL 896  
QY 893 HVKAVGECPLVDGYIPAEQIVCEMGEAKPSQ-HAGFVEICVACRPEFMASSOLYXF 951  
Db 897 GVHVGVKVCSPVSEYISAQIVCEIGDASTLRAHDALVEVCVDCSLHYRALSPPKFTF 956  
QY 952 MTULTSLDKPSRPMGSGTQVTTGTNMLNAGSNVVMFGKQPCLFHRRSPSYIVCMTSS 1011  
Db 957 VTPFTFVSPSRGLSGGTWIGIEGSHNAGSDVAVSIGRPGCSFWSRNSREIRCLTPPG 1016  
QY 1012 DEVLEKVSQVODRAKI-HDPLFQVYVEDPTIVRIEPEMSIVSGTPIAVMGTHLDLION 1070  
Db 1017 HTPOSAPIVININRAQUSNFEKVNYYETDPTILKIDFEMWINSGGTLLITVTGNLATRE 1076  
QY 1071 PQIRAKHGKHEHINICEVLNATEMTQAPALALGPDHQSOLTERPEFEGFILDNVQSLLI 1130  
Db 1077 PRIARAKGGERENSCVYNDTWTVCRASTGDNPKRSPPELGERPDSIGFIMDNVRLTV 1136  
QY 1131 LKNTNFTYVNPVPEAGPSGILEKPGCTPIILKGNLIIPVAGNVKLVNLYVLGKPC 1190  
Db 1137 LNSSFYVDFVLEPDSPTLLEKSPSSPILKGRNLLFP-APGNRLNYYTLLIGSTPC 1195  
QY 1191 TVTVSDVQLLCEPNLGRHKVAVRGMEYSPGMVYIAPDSPLSLPAIVSIYAVAGLLI 1250  
Db 1196 ILTVSETQLLCEAPNLATGQHKVTVRAGGFEPSCMLQVYSDSLTLLPAIVIGIGGGGLL 1255  
QY 1251 IFIVAVLIAYKRSRDLTKRLQMDNLESVALECKEAPAELOTDHELTSDLDGA 1310  
Db 1256 LVIIVAVLIAYKRSRDLTKRLQMDNLESVALECKEAPAELOTDHELTSDLDGA 1315  
QY 1311 GIPELDRTYMRVLPFGIEDHPVLRDLEVPYQERVKELKFAQLINNKVFLSFFIR 1370  
Db 1316 GIPELDRTYMRVLPFGIEDHPVLEKMEV---QANVKSLLTFFGQLLKKGHLLTFFIR 1371  
QY 1371 TLESQSFMSDRGNVASLIMTVLQSKLEYATDVLKOLLADIDKNLESKNHPKLLRRT 1430  
Db 1372 TLEAQSFSMDRGNVASLIMTALQGEYATGVLKQLLSLIEKNLESKNHPKLLRRT 1431  
QY 1431 ESWAEKMLTNFTLLYKFLKCEAGEPLFLFCALQOMEKGPIDAITGEARYSLSDKL 1490  
Db 1432 ESWAEKMLTNFTLLYKFLKCEAGEPLFLMYCALQOMEKGPIDAITGEARYSLSDKL 1491  
QY 1491 IRQQIDYKTLVLCVSPDNANSPEVPVKILNCDDTITQVKEKILDAIFKNVPCSHRPAAD 1550  
Db 1492 IRQQIDYKTLVLCVSPDNANSPEVPVKILNCDDTITQVKEKILDAIFKNVPCSHRPAAD 1551  
QY 1551 MDLEWROSGARMILQDSDITTKIENDMKRLNTLAHYQVDPGVSVALVSKOVTAYNVNN 1610  
Db 1552 MDLEWROSGARMILQDSDITTKIENDMKRLNTLAHYQVDPGVSVALVSKOVTAYNVNN 1611  
QY 1611 STVSRATSAYENMIRYTGSPDSLSRTPMITPDLESQVKNWHLVKNHEHGDQEGDRGS 1670  
Db 1612 STFTK-SLSRYESMLRTASSPDSLSRTPMITPDLESQVKNWHLVKNHEHGDQEGDRGS 1670  
QY 1671 KMWISIYITRLLATKGTLOKFDVDDLFETIFSTAHRGSAIPALIKYMPDFLDEQADKHQIH 1730  
Db 1671 KMWISIYITRLLATKGTLOKFDVDDLFETIFSTAHRGSAIPALIKYMPDFLDEQADKHQIH 1730  
QY 1731 DPHVHTWKSNCPLRFVWVNMKNPQFVFDIHKNSITDACLSSVAQTFMDCSTSEHRLG 1790  
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QY 1791 KDSPNKLLYAKDIPSYKSWERYSDIGKMPAISDQDMSAYLAEQSRHLHSQFMSMAL 1850



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; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Guo, Xiaojia
; APPLICANT: Miller, Charles E.
; APPLICANT: Gangolli, Esha A.
; TITLE OF INVENTION: PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-214 CIP
; CURRENT APPLICATION NUMBER: US/10/087,684
; CURRENT FILING DATE: 2003-03-10
; PRIOR APPLICATION NUMBER: 60/253,834
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: 60/250,926
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: 60/264,180
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/274,194
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 60/313,656
; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: 60/327,456
; PRIOR FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 220
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 32
; LENGTH: 1925
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-087-684-32

Query Match      62.7%; Score 6267.5; DB 12; Length 1925;
Best local Similarity 63.7%; Pred. No. 0;
Matches 1214; Conservative 260; Mismatches 397; Indels 35; Gaps 23;

QY 11 LLSHLLMVGMSSTLLTRQAPLSQKRSFVTRGEPAGFNHLVVDERTGHYLGAVNR 70
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QY 71 IYKLSDDLKVLVTHGTGDEDDNPKYPPRIVOTCNEPTTTNNYNNKMLLLIKENLIAC 130
DB 89 IYKLSGNLTLLRAHYTGPVEDNEKCYPPPSVQSCPHGJGSTDNNKLLLLDYAANRLIAC 148
QY 131 GSLYOGICKLLEDLFKLGEHYKHEHYLSGVNESGVSFGVIVS--YSNLDKLFATA 188
DB 149 GSASGICQFLRLDLDLKLGEHHRKEHYLSVQEGASWAGVLIAGPPGQGOAKLFVGT 208
QY 189 VDGKPEYPTTSRKLTKNSEADGMPAYVHFDEFVASMIKIPSDFTTPIIDFYIYVGF 248
DB 209 IDGKSEYFPTLSRRLMANEEDADMFGFYQDEFVSSQLKIPSDTLSKFPAPFDIYVYSF 268
QY 249 SSGNFVYFLTLQ--PEWVSPGSGTTKEQVYTSKLVRLCKEDTAFNSYVEVPICBSRGVE 306
DB 269 RSEQFYVYTLQLDQLTSP--DAAGEHFTTSKIYRLCVDDPKFYSYVEFPICGEOAGVE 326
QY 307 YRLQAAVLSKAGAVLGRTLGVHPDDLLFTVFSKGQRKMKSLDESALCIPILKQINDR 366
DB 327 YRLVQDAYLSRPGRALAHQGLAEDEDLVTFVFAQGNKRVKPPKESALCLFTRAIKEK 386
QY 367 IKERLQSCYRGEGTLDLMLVKVDIPCSALLTIDNFCGLDMNAPLGVSDMVRGIPVFT 426
DB 387 IKERLQSCYRGEGKUSLPWLLNKLGCINSPILQIDDDFCGQDFNPLGQTVTIEGTPLV 446
QY 427 EDRDRMTSVIAYYKNHSLAFVGTSGKLKIRVD--GPRGN-ALQYETVQVVDPEPVL 483
DB 447 DXDDGLTAAVAYDGRCTRVFAGTSRGRIRKILVDLSNPGGRPALAYESVVAQEGSPIL 506
QY 484 DNAFSKDHQLYIMSERQLTRVPVSCGQYSCGCEGLSGDPCGHCVCVLIHNTCTKERCE 543
DB 507 DLVLSNPHOYLAMTEKQVTRVPEVSCVQYTSCEJCLGSRDPHCGVCVLIHNSMCSRRDACE 566
QY 544 RSKEPRERFASMKQCVRLTVHPNNISQVNV--LLVLETYNYPFELSAGVNCVTFDELSEMD 602
DB 567 RADEPQFRADLLQCQVLTQVPRNVSVTMSQFVLVQLQANVVDLSAGVNCSEFDEPTESE 626
QY 603 GLVVGNIQIQCYSAPAKEVPRII--TENGHDHVVLQQLKSKETGTMFASTSFVYNCVSH- 659

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DB 627 SVLEDRGIRHCRSPAREVAPITRGGQEGDORVVKLYLKSKEGKPFASVDFVYNCVHQ 686
QY 660 NSCLSCVESPYRCHWKCKYRHVCTHDPKTCSPQGRVKLPEDPCQLLRVDVKILVPEVVKP 719
DB 687 SSCLSCVNGSFPCHWKCKYRHVCTHNVADCAFLGVRVNVSEDCQILPSPQIYVPGVWKP 746
QY 720 ITLKAKNLPQOSGQGVYECIINIQSEORVPAALFNSSVOCQNTSYEGMEINNLV 779
DB 747 ITLAARNLPQOSGQGVYECIINIQSEORVPAALFNSSVOCQNTSYEGMEINNLV 806
QY 780 ELTVVWNGHFNIDNPAQNKHLYKCAWMBESGCLKADPDACGWCQCGQOCTLRHQPC 839
DB 807 NLSVWVNGNFVIDNPQNIQAHLYKCPALRESGCLCLKADPRFECGCVARERCSLHCA 866
QY 840 AQ-ESOWLELSGAKSKCTNPRITEIIPVTGPRGGTKVTIRGENLGLERDITASHVKVAG 898
DB 867 ADTPASWMEARHGSSRCTDPKILKJSPETGPGQGTRLITGENLGLERDITASHVKVAG 926
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QY 1315 LDYRTYTMRYLFPFIEDHPVLRDLVPGYRQERVEKGLKLAQILNNKVPFLSFIRTL 1374
DB 1345 LDYRTYAMRVLPFGIEDHPVLEKMEV---QANVEKSLTLFGQLTKGHFLTFTLEA 1400
QY 1375 QRSFSDRGVNASLIMTVLOSLEYATDVLKOLLADLIDKNLESKNHPKLLLR--TESV 1433
DB 1401 QRSFSDRGVNASLIMTVLOSLEYATDVLKOLLADLIDKNLESKNHPKLLLR--TESV 1460
QY 1434 AEKMLTNWFTLLYKFLKECAGBPLFSLFCAIKQOMKEGPIDAITGEARYSLSEDKLIRQ 1493
DB 1461 AEKMLTNWFTLLYKFLKECAGBPLFSLFCAIKQOMKEGPIDAITGEARYSLSEDKLIRQ 1520
QY 1494 QIDYKTLVSCVSPDNANSPEVVKILNCCTITQVKEKILDAIFKNVPCSHRKAADM 1553
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QY 1554 EWROSGARILQDEDTITTKIENDWKRINTLAHYQVDPDGSVVALVSKQVYATYAVNNSTV 1613
DB 1581 EWROSGARILQDEDTITTKIENDWKRINTLAHYQVDPDGSVVALVSKQVYATYAVNNSTV 1640
QY 1614 SRTSASKYENMRYTGSPPSLRTRTPMITPDLESQVGMWHLVQHEHGDQKEDGRGSKM 1673
DB 1641 TK-SLSRYESMLRTASSPDSLRSTRTPMITPDLESQVGMWHLVQHEHGDQKEDGRGSKM 1699
QY 1674 SEIYLTLLATK-GTLQKFDVDDLFTETIFSTAHRGSLPLAIKYMFPDPLDQADKGHDP 1732

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 Db 1760 DVHRTWKSNC-SPLRFVWNNIKNPQFVFDIHKNSITDACLSSVVAQTFMDSCTSEHKLCK 1819  
 Qy 1792 DSSNKLLYAKDIPSKYKWE-RYSDIGKMPAISQDKNAYLAQSRWHMNEFNTMSAL 1850  
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 Qy 1851 SEIFSVMGKYSSE--IIGPLDHDHDDQCKQKLAAYKLEQVITLMSLDS 1894  
 Db 1880 HEIVSYITKYKDEVOILAALKEQBARQRLRSKLEQVVDTMALSS 1925

RESULT 9

US-10-218-779-32  
 ; Sequence 32, Application US/10218779  
 ; Publication No. US20040029222A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Edinger, Shlomit  
 ; APPLICANT: MacDougall, John  
 ; APPLICANT: Millet, Isabelle  
 ; APPLICANT: Ellerman, Karen  
 ; APPLICANT: Stone, David  
 ; APPLICANT: Gerlach, Valerie  
 ; APPLICANT: Grosche, William  
 ; APPLICANT: Alsobrook II, John  
 ; APPLICANT: Lepley, Denise  
 ; APPLICANT: Rieger, Daniel  
 ; APPLICANT: Burgess, Catherine  
 ; APPLICANT: Casman, Stacie  
 ; APPLICANT: Spytek, Kimberly  
 ; APPLICANT: Boldog, Ferenc  
 ; APPLICANT: Li, Li  
 ; APPLICANT: Padigan, Muralidhara  
 ; APPLICANT: Mishra, Vishnu  
 ; APPLICANT: Patturajan, Meera  
 ; APPLICANT: Shenoy, Suresh  
 ; APPLICANT: Rastelli, Luca  
 ; APPLICANT: Tchernev, Velizar  
 ; APPLICANT: Vernet, Corine  
 ; APPLICANT: Zerhusen, Bryan  
 ; APPLICANT: Malyankar, Uriel  
 ; APPLICANT: Guo, Xiaojia  
 ; APPLICANT: Miller, Charles  
 ; APPLICANT: Gangoli, Esha  
 ; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same  
 ; FILE REFERENCE: 21402-214  
 ; CURRENT APPLICATION NUMBER: US/10/218,779  
 ; CURRENT FILING DATE: 2002-08-14  
 ; PRIOR APPLICATION NUMBER: 60/253,834  
 ; PRIOR FILING DATE: 2000-11-29  
 ; PRIOR APPLICATION NUMBER: 60/250,-926  
 ; PRIOR FILING DATE: 2000-11-30  
 ; PRIOR APPLICATION NUMBER: 60/264,180  
 ; PRIOR FILING DATE: 2001-01-25  
 ; PRIOR APPLICATION NUMBER: 60/313,656  
 ; PRIOR FILING DATE: 2001-08-20  
 ; PRIOR APPLICATION NUMBER: 60/327,456  
 ; PRIOR FILING DATE: 2001-10-05  
 ; NUMBER OF SEQ ID NOS: 216  
 ; SOFTWARE: Patent In Ver. 2.1  
 ; SEQ ID NO 32  
 ; LENGTH: 1925  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-218-779-32

Query Match 62.7%; Score 6267.5; DB 12; Length 1925;  
 Best Local Similarity 63.7%; Pred. No. 0;  
 Matches 1214; Conservative 260; Mismatches 397; Indels 35; Gaps 23;

Qy 11 LLSHLLMVGMSSGSLTLTROAPAPLSQKQSFVTRGEPAGFNHLVVDERTGHYLGAVNR 70  
 Db 33 LLLLLPGLMABEAGL--PRAGGSGPPFRTFSASD-WGLTHLVVHEQGEVTVGAVNR 88  
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 Db 89 IYKSSGNLTURAHVTGVEDNEKCYPPSVQSCPHGLGSDNNVNNKLLIDYAAANRLIAC 148  
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 Qy 189 VDGKEVEYPTISSRKLTKNSEADOMPAYVHDEVASMIKIPSTFTIIPDFDIYVYVGF 248  
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Qy 1195 SDVOLLCEPNLIGRHKMARVGEVSPGMVYIAPDSPLSLPAIVAGGLLIIFIV 1254  
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Qy 1614 SRTSASKYENMIRVTGSPDSLSRSTPMITPDLGSKVWHLVQNHEDQKEGDRGSKMV 1673  
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Qy 1674 SEIYLTRLLATK-GTLQKFVDDLPETTFSTAHRSALPLAIKYMFDFLDEQADKHGHP 1732  
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Qy 1733 HVRHTWKNC-LPRFWNNMINKQFVFDIHNKSITDACLSSVAQTQWDCSTSEHLGK 1791  
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Qy 1792 DSPSKLLYAKDIPSYKNWVE-RYVSDIGKMPAISDQDMNAYLAEQSRMHNENFTWSAL 1850  
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Qy 1851 SEIFSYGKXSEE--ILGPLDHDQCGKQKLAYKLEQVITLMSLDS 1894  
Db 1880 HEIYSYITKXKDEVOILAALKEDEQARRQLRSKLEQVVDTWALSS 1925

RESULT 10  
US-09-964-956-42  
; Sequence 42, Application US/09964956  
; Publication No. US20040043926A1  
; GENERAL INFORMATION:  
; APPLICANT: Gerlach, Valerie L  
; APPLICANT: MacDougall, John R  
; APPLICANT: Smithson, Glenda  
; APPLICANT: Millet, Isabelle  
; APPLICANT: Stone, David  
; APPLICANT: Gunther, Erik  
; APPLICANT: Ellerman, Karen  
; APPLICANT: Grosse, William M  
; APPLICANT: Alsbrook II, John P  
; APPLICANT: Lepley, Denise M  
; APPLICANT: Burgess, Catherine E  
; APPLICANT: Padigaru, Muralidhara

; APPLICANT: Kekuda, Ramesh  
; APPLICANT: Spytek, Kimberly A  
; APPLICANT: Leach, Martin D  
; APPLICANT: Shimkets, Richard A  
; TITLE OF INVENTION: No. US20040043926A1el Proteins and Nucleic Acids Encoding Same  
; FILE REFERENCE: 21402-124  
; CURRENT APPLICATION NUMBER: US/09/964,956  
; PRIOR FILING DATE: 2001-09-26  
; PRIOR APPLICATION NUMBER: 60/235,631  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: 60/235,633  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: 60/235,808  
; PRIOR FILING DATE: 2000-09-27  
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; PRIOR APPLICATION NUMBER: 60/236,135  
; PRIOR FILING DATE: 2000-09-28  
; PRIOR APPLICATION NUMBER: 60/237,434  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/238,321  
; PRIOR FILING DATE: 2000-10-05  
; PRIOR APPLICATION NUMBER: 60/238,399  
; PRIOR FILING DATE: 2000-10-06  
; PRIOR APPLICATION NUMBER: 60/238,396  
; PRIOR FILING DATE: 2000-10-06  
; PRIOR APPLICATION NUMBER: 60/276,667  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/294,823  
; PRIOR FILING DATE: 2001-05-31  
; PRIOR APPLICATION NUMBER: 60/304,868  
; PRIOR FILING DATE: 2001-07-12  
; NUMBER OF SEQ ID NOS: 127  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 42  
; LENGTH: 1871  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-09-964-956-42

Query Match 60.0%; Score 5994; DB 12; Length 1871;  
Best Local Similarity 60.0%; Pred. No. 0;  
Matches 1133; Conservative 295; Mismatches 435; Indels 26; Gaps 13;

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Qy 130 CGSLYQIGICKLJLELDLFLKGEPIYKHEHYLGVNKGSGVFGVIVSYNSLDDKLFATAV 189  
Db 112 CGSIWQIGICQFLRLDDFLKLGEPHHRKHEHYLGAOEFDPSMAGVIVEQGGPSKLFVGTAV 171  
Qy 190 DGKPEYFPTISRKLTNKEADGMFAVPHDFVFAVMKIPSDTFTIIPDFDIYYVYGF 249  
Db 172 DGKSEYFPTLSRKLTSDSDSADMFLSVYQDEFVSSQIKIPSDTSLYPAFADIYYIGFV 231  
Qy 250 SGNFVYFLFLOPMWSPPGSTTKEQVYTSKLVRCKEDTAFNSYVEVPICGERSGYEYRL 309  
Db 232 SASFVYFLTLQDQTQTLTDTAGEKFTSKIVRMCAGDSEFYSEYFPGCWRGVEYRL 291  
Qy 310 LQAAVLSKAGAVLGRTLGVHPDDDLFTVFSKGQKRMKSLDESALCITILKQINDRIKE 369  
Db 292 VQSAHLAKPGLLAQALGVPADEDLVFTIFSQQGQKRAFPPTQTLCLTSLNNAHRR 351  
Qy 370 RLQSCVRGEGTDLAWLKVKVDIPCSSALLTIDDNFCGLDMNAPLGVSDMVRGIPVFTEDR 429

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QY 1506 SPDNANSPFVVKILNCOTITOVKEKILDAIFKNVPCSHRPAKADMDLEWRQSGARMIL 1565  
Db 1484 CPNEGSAQFVKVNLNDSITQAKDLDTVYKIGIPYSQRPKADMDLEWRQSGARMIL 1543  
QY 1566 QDEITTKIENDWKRLNLAHYQVPGDGVVALYKQVTAYNVANNSTVSRSTASKYENMI 1625  
Db 1544 QDEVTTKIECDWKLNSLAHYQVTDGSLVALVPKQVSAYNMANSFTFTR-SLSRYESLL 1602  
QY 1626 RYTGSPDLSRTPMTITPDLESQVGMHLVKNHEHGDQKEDRGSKVSEIYITRLLATK 1585  
Db 1603 RTASSPDLASRAEMITPDQETGKLMHLVKNHHDHADHREGDRGSKVSEIYITRLLATK 1662  
QY 1686 GTLKQFVDDLPETITFSTAHRGSALPLAIKYMFDLDEQADKHGHDHPRHHTWKSNCPL 1745  
Db 1663 GTLKQFVDDLPETITFSTAHRGSALPLAIKYMFDLDEQADKHGHDHPRHHTWKSNCPL 1722  
QY 1746 RFWNMKNPQVFDIHNKSITDACL SVQAQTFMDSCTSEHRLGKDSPNKLLIYAKDIP 1805  
Db 1723 RFWNMKNPQVFDIHNKSITDACL SVQAQTFMDSCTSEHRLGKDSPNKLLIYAKDIP 1782  
QY 1806 SYKMWZRYSDICKMPAISDQDMNVALBQSRMHMNEFTMSALSIFSVGKYSEIL 1865  
Db 1783 NYKSWERYRDIAMASISDQDMNVALBQSRMHMNEFTMSALSIFSVGKYSEIL 1842  
QY 1866 GPLDHDQCGKQKLAAYKLEQVITLMSLDS 1894  
Db 1843 TALDRDASCRKHKLQKLEQIISLVSDS 1871

RESULT 11  
US-10-087-684-84  
; Sequence 84, Application US/10087684  
; Publication No. US20040029116A1  
; GENERAL INFORMATION:  
; APPLICANT: Edinger, Shlomit R.  
; APPLICANT: MacDougall, John R.  
; APPLICANT: Millet, Isabelle  
; APPLICANT: Ellerman, Karen  
; APPLICANT: Stone, David J.  
; APPLICANT: Grosse, William M.  
; APPLICANT: Lepley, Denise M.  
; APPLICANT: Rieger, Daniel K.  
; APPLICANT: Burgess, Catherine E.  
; APPLICANT: Casman, Stacie, J.  
; APPLICANT: Spytek, Kimberly A.  
; APPLICANT: Boldog, Ferenc L.  
; APPLICANT: Li, Li  
; APPLICANT: Padigaru, Muralidhara  
; APPLICANT: Mishra, Vishnu  
; APPLICANT: Shenoy, Suresh G.  
; APPLICANT: Rastelli, Luca  
; APPLICANT: Tchernev, Velizar T.  
; APPLICANT: Vernet, Corine A.M.  
; APPLICANT: Zethusen, Bryan D.  
; APPLICANT: Malyankar, Uriel M.  
; APPLICANT: Guo, Xiaojia  
; APPLICANT: Miller, Charles E.  
; APPLICANT: Gangolli, Bsha A.  
; TITLE OF INVENTION: PROTEINS AND NUCLEIC ACIDS ENCODING SAME  
; FILE REFERENCE: 21402-214 CIP  
; CURRENT APPLICATION NUMBER: US/10/087,684  
; CURRENT FILING DATE: 2003-03-10  
; PRIOR APPLICATION NUMBER: 60/253,834  
; PRIOR FILING DATE: 2000-11-29  
; PRIOR APPLICATION NUMBER: 60/250,926  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: 60/264,180  
; PRIOR FILING DATE: 2001-01-25  
; PRIOR APPLICATION NUMBER: 60/274,194  
; PRIOR FILING DATE: 2001-03-08  
; PRIOR APPLICATION NUMBER: 60/313,656

Db 352 RIOSVRGEGTLALFWLNLKELSCINTPQINGNFCGLVNLQPLGLHVGIEGLPLADST 411  
QY 430 DRMTSVIAYVXNHSALFVGTGSKGLKIRVDGPRGNALQYETQVVDVDPGVLRLDWFASK 489  
Db 412 DGMASVAAAYTRQHSVVFVIGTRSGSLKVRVDGFQ-DAHLYETVPVVDGSPILRDLLFSP 470  
QY 490 DHEQLYMSRQILTRVPVSCGYQSGCEGLSGDHPHCWCVLHNTCTEKERCESEKPR 549  
Db 471 DHRHITLSEKQVQSPVETCEQYQSCAACLGGSDHPHCWCVLHNTCTEKERCESEKPR 530  
QY 550 RFASEMKQCVRLTVHPNNISVSQYNVLLVLETYNPELSAGVNCVCTFEDISEMDG-LVWGN 608  
Db 531 GFABEELS KCVVRVNNVSVTSPGVQLTVTLHNVFDLSAGVSCAPEAAAEAVLLPSG 590  
QY 609 QIOCYSPAAKEVPRITITENGDDHVVOLQKSTGMTFASTSFVFNCSVHNSCULSCVSES 668  
Db 591 ELLCPSPSLOELRALTRGHATTVRLQLLSKETGVRFAADPFVFNCSVLSQSCMSCVGS 650  
QY 669 PYRCHWKYRHVTHDPKTCSEFQGRVGLPEDCPQLLRVDKILVPEVIEKIPITLAKANLP 728  
Db 651 PYRCHWKYRHVTHDPKTCSEFQGRVGLPEDCPQLLRVDKILVPEVIEKIPITLAKANLP 710  
QY 729 QPQSGQGRYECILNIQSGEORVPALRFNSSVOCNTSYSEGEINNLVPLTVVWNGH 788  
Db 711 QPQSGQGRYECILNIQSGEORVPALRFNSSVOCNTSYSEGEINNLVPLTVVWNGH 770  
QY 789 FNIDNPAQNKHLYKGCAMRESGCLCLKADDPFACGCGQPGCTILRQCPAQESQWLEL 848  
Db 771 FPIDKPPSPRALLYKQWAPRSCGLCLKADDPFACGCGQPGCTILRQCPAQESQWLEL 830  
QY 849 SGAKSKCTNPRITETIPVTPGREGTKVIRGENGLGLEDPRDIASHVYKAGVCECPLVDQY 908  
Db 831 SQXGTRCSHPRIITQIHLVPGKGGTRVTVIGNLGLLREVG--LRVAGVRCNSIPASV 888  
QY 909 IPAEQIVCEMGEA-KPSQAHGAFVEICVAVCRPFMARSSQLYYFMTLTLSDLKPSRGPMS 967  
Db 889 ISAEIVCEMEESLVSPPPGVELCVGDSADFRQSEQVSVFVTFDQVSPSRGPAS 948  
QY 968 GTQVITITGNLHAGSVVNVFQKQPCQLFHRSPSVIVC-NTTSSDEVLEMKVSVQVDR 1026  
Db 949 GGTRLTISGSLDAGSRVTVVDRSECFVRDRAKAVICISPLSTLGPSPQAPITLADRA 1008  
QY 1027 KIHQ-DLAVFOVDRPTVIRTEPWSIVSGNTPVAVMGTHLDLQNPQIRAKHGKHEINI 1085  
Db 1009 NISPSGLIYITQDPTVIRLEPWSIINGSTATVSGTHLLTVQEPVRVAKYGIETWT 1068  
QY 1086 CEVLNATEMTQAPALAGDPHQSDLTERPEEFGLDNVQSLILINKNTFTYYPNPVFE 1145  
Db 1069 CQVINDTAMLCAPGIFLGRPQRAQGEHPDEFGLLDHVTQARSINRSSTYYPDPSPFE 1128  
QY 1146 AFGSGILELKPPTIILKGNLIPPVAGGNVNLVTLVGEKPCVTTVSDVOLLCESPN 1205  
Db 1129 PLGSGVLDVPGSHVVKGNLIPAAAGSS-RUNYTLVIGGQPCSLTVSDTQLLCSFS 1187  
QY 1206 LIGRHKVMARVGMESPGMYIAPDSPLSLPAIVSIAVAGGLIIFIVAVLIAYKRKR 1265  
Db 1188 QTGRQPVVVLVGLLEFWLGLTHISAERALTLPAMMGLAAGGLLLAITAVLVAYKRKTQ 1247  
QY 1266 ESDTLKELQOMNLESRALECKEAPAELOTDIHELTSDDLQAGTFLPDYTYMVRVL 1325  
Db 1248 DADTLKRLQOMNLESRALECKEAPAELOTDIHELTSDDLQAGTFLPDYTYMVRVL 1307  
QY 1326 FPGIEDHPVLRLDLEVPVQERVEKGLKFLAQLINKNVFLLSIRTLSESQSFESMRDRGN 1385  
Db 1308 FPGIEAPVLELDTQ---PNVEKALRLFQLLHSAFVLTFTHTLEAQSSFSMRDRGT 1363  
QY 1386 VASLIMTVLQSLKYATDVLKOLLADLIDKNLESKNHPKLLIRRTESVAEKMLTNMFTFL 1445  
Db 1364 VASLIMTVLQSLKYATDVLKOLLADLIDKNLESKNHPKLLIRRTESVAEKMLTNMFTFL 1423  
QY 1446 LYKFLKBCAGEPLFLYCAIKQQMEKGPIDAITGEARYSLSEDKLIRQIDYKTLVLSCV 1505



; PRIOR FILING DATE: 2001-08-20  
 ; PRIOR APPLICATION NUMBER: 60/327,456  
 ; PRIOR FILING DATE: 2001-10-05  
 ; NUMBER OF SEQ ID NOS: 220  
 ; SOFTWARE: CuraSeqList version 0.1  
 ; SEQ ID NO 84  
 ; LENGTH: 1871  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: misc feature  
 ; LOCATION: (380)..(380)  
 ; OTHER INFORMATION: Wherein Xaa may be any naturally occurring amino acid  
 US-10-087-684-84

Query Match 59.9%; Score 5988; DB 12; Length 1871;  
 Best Local Similarity 60.0%; Pred. No. 0;  
 Matches 1133; Conservative 293; Mismatches 437; Indels 26; Gaps 13;

QY 10 CLLSHLLVMGSSLLTRQAPLSQKORSFVTFRGEPAEGFNHLVVDERTGHVYLGAVN 69  
 DB 5 CULLL-LFLVAGGA--LGNRP-----RAFV-----TDTTLTHLAVHRTGEVFGAVN 51  
 QY 70 RYKLSDLKVLVTHETGPDENPKYPPRIVQTCNEBELTTNNVNMMLLDYKENRLIA 129  
 DB 52 RVFKLAPNLTELRAHVTGPVEDNARCYPSPMRVCAHRLAPVDNINKLLLDIYAARLVA 111  
 QY 130 CGSLYGGICKLRLDLKLPYHKKHXYLGSVNESGVFGVIVSYNLDKLFATAV 189  
 DB 112 CGSIWGGICQFURLDDLFKLGEHPHKKHYLSGAQEPDSMAGVIVEQQGSKLFGVATV 171  
 QY 190 DGKPYFPTISSRKLTQKSEADMFAYVFBHDFVASKIKIPSDTFTIIPDPIYVYGF 249  
 DB 172 DGKSEYFPTLSSRKLLSDSDAMFSLVYQDEFVSSQIKIPSDTSLVLPALDIYVYGFV 231  
 QY 250 SGNFYFYLQPEMVSPPGSTTKEQVYTSKLVRLCKEDTAFNSYVEVPIGERSGVYRL 309  
 DB 232 SASFYFYLQDQTQTLDTAGEKFTSKIVRMCAQSEFYSYVEFPFGCSWRGEYRL 291  
 QY 310 LQAAYLSKAGVGLRTGLVHPDDLLFTVFSKGQRKMKSLDESALCIFILKQINDRIKE 369  
 DB 292 VQSAHLAPGLLQAALGVPADEVDLFIIFSOGQRNASPPRQTILCLFTLSINAHIR 351  
 QY 370 RIQSCYRGEGTLDLAWLKVDIIPCSALLTIDNFCGLDMAPLGVSDMVRGIPVFTEDR 429  
 DB 352 RIQSCYRGEGTLLPWLNLKLPFCINTPXQINGNFCGLVNLQGLHVEGLPLADST 411  
 QY 430 DRMTSVIAYVKNHSLAFVGTSGKLKIRVDGPRGNALQVETVQVDPGVLRLDMPSK 489  
 DB 412 DGMASVAAYTRQSHVVFITRSGSLKVRVDGFO--DAHLVETVPVVDGSPILRDLFSP 470  
 QY 490 DHEQLYMSEBRLTRVPVSECGQYSCGECGLSGDPHCGWCVLHNTCTRKERCERSKEPR 549  
 DB 471 DHRHLYLSEKQVQLPVETCEQYQSCAACLGSGDPHCGWCVLRHRCREGACLGASAPH 530  
 QY 550 REASEMKQCVRLTVHPNNISVQYVLLVLEYNYPVLSAGVNCYTFEDLSEMDG-LVYGN 608  
 DB 531 GRAEELSKCVQRVRPNVSVSPGVQLTVTLHNPDLISAGVSCAFEAANEAVLLPSG 590  
 QY 609 QICQSPAAKEVPRITENGDDHHVQLQKSKSETGMTFASTGFVFNCSVHNSCLSCVES 668  
 DB 591 ELLCSPSLQELRALTRGHGATRTVRLQLLSKETGVRFAGADVFVFNCSVLQSCMCSVGS 650  
 QY 669 PYRCHWCKYRNVCTHDPKTCSEQEGRYKLPECPQLLRVDKLLVPEVIKPTLKAKNLP 728  
 DB 651 PYPCWCKYRNVCTHDPKTCSEQEGRYKLPECPQLLRVDKLLVPEVIKPTLKAKNLP 710  
 QY 729 PQSQGQRYGECILNIQGSQRYPALRFNNSVQCQNTSYSEYGEINNLPLBELTVVWNGH 788  
 DB 711 PQSQGQRYGECVVRVQGRQYRPAVRFNNSVQCQNASYSYGEDEHGTDLDFSVVWDG 770  
 QY 789 FNIDNPAQNKVHLKYCGAMRESGLCLKADDPFACGWCQPGQCTLRQHCPAQESQWLEL 848

DB 771 FPIDKPPSPRALLYKCAQORPSCGLCLKADPRFNGCMWICSEHRCQLRTHCPAPKTNWML 830  
 QY 849 SGAKSKCTNPRITEIIPVTGREGGKVTIRGENGLGEFRDIASHVKVAGVCSPLVDQY 908  
 DB 831 SQKGTRECSHPRTQIHPLVGPKEGGTRVITVGENLGLSREVG--LRVAGVACNSIPASY 888  
 QY 909 IPAEQIVCEMGEA-KESQHAGFVIEICVACRPEFMASSQLYFWMLTSLDLKPSRGPWS 967  
 DB 889 ISAEIVCEMBESLVPSPPPGVELCVGDCSADFTQSEQVYSFVTPPTDQVSPSPGAS 948  
 QY 968 GGTQVTTITGNLGNAGSNVVMFGKQPCLFHRSPSYIVC-NTTSSDEVLEMKYVSQVQDRA 1026  
 DB 949 GGTRLTISGSLDAGSRVTVVRDSCQFVRDAKAIVCISPLSTLGPQAPITLAIDRA 1008  
 QY 1027 KIHQ-DLVQYVEDPTIVRIEPEWSIVSGNTPIAVWGLHLDLIQNPQIRAKHGGKEHINI 1085  
 DB 1009 NISSPGLIYTYQDPTVTRLEPTWSIINGSTAITVSGTHLLTVQEPRAVKRNGIETTNT 1068  
 QY 1086 CEVLNATEMTQCAPALALGPDHQSULTEPPEFGFILDNVQSLLIINKNTFTYYPNPVE 1145  
 DB 1069 CQVINDTMLCKRAGPFLGRPOPRAQGEHPDEFGLLDHVQTARSLNRSSFTYYPDPSPF 1128  
 QY 1146 AFPSGILELKPOTPIILKGNLIPPVAGNVKLVNTVVLGKPCPTVTVSDVQLLCESPN 1205  
 DB 1129 PLGPGVLDVKPGSHVVLKGNLIPAAAGSS-RLNVTVLIGQPCCSLTVSDTQLLCDSPS 1187  
 QY 1206 LIGRHKVMARVGMESYPMGYIAPDSPLSIPAIVSIAVAGGLLIIFIIVAVLIAYKRSR 1265  
 DB 1188 QTRQPPWVLVGLLEFWLGTLHLSAEALTLPAWGLAAGGGLLILAITAVLVAVKRQ 1247  
 QY 1266 ESDLTKRLQOMQNDLLESRLVALECKEAFELQTDIHELTSDDLQDAGIPFLDRTYTMVRL 1325  
 DB 1248 DADRTLKRLQLQOMDNLESRLVALECKEAFELQTDINELTNHMDVQIPFLDRTYTMVRL 1307  
 QY 1326 FPGIEDHPVLRLDEVPGYRQERVEKGLKLPFAQLINKNKFLSPIRLESQRSFMSDRGN 1385  
 DB 1308 FPGIEAHPVLELUTP-----PNVEKALRLFGQLHSAFVLFIHILEAQSSFSMDRGT 1363  
 QY 1386 VASLIMTVLOSLEYATDVLKQLLADLIDKNLESKNHPKLLLRTRTSVEAKMLTNFTFL 1445  
 DB 1364 VASLIMTVLOSLEYATDVLKQLLADLIDKNLESKNHPKLLLRTRTSVEAKMLTNFTFL 1423  
 QY 1446 LYKFLKECAGEPLFSIFCAIKQOMEGPIDAITGEARYSISEDKLIRQOQIDYKTLVLCV 1505  
 DB 1424 LHPLKECAGEPLFLYICAIKQOMEGPIDAITGEARYSISEDKLIRQOQIDYKTLVLCV 1483  
 QY 1506 SPDNANSPYVPVKILNCITITQVKEKILDAIFKNVFCSHRPKAAADMLEWRQSGARMIL 1565  
 DB 1484 CPNEGSAQVPVKVNLCDSTIQAKDKLDTVYKGIPIVQSQRPKAEDMDLEWRQGRMTRIL 1543  
 QY 1566 QDEDITTKIENDWKRLTLAHYOVPDGSVVALYSKQVTAYNVNNSTVSTSAKYENMI 1625  
 DB 1544 QDEDVTTKIECDWKRLNSLAHYQVTDGSLVALYPKQVSAYNNMANSFTFTR-SLSRYESLL 1602  
 QY 1626 RYTGSPDLSRSRTPMITPDLESQVWHLVKNHEHGDQKEGDRGSKVSVIYLITLLIATK 1685  
 DB 1603 RTASSPDSLRSRAPMTTPDQETGTLKHLVKNHHDHREGDRGSKVSVIYLITLLIATK 1662  
 QY 1686 GTLQKQVDDLFETIFSTAHRSALPLAIKTMFPFLDEQADKHGHIHPHVTWKSNCLPL 1745  
 DB 1663 GTLQKQVDDLFETIFSTAHRSALPLAIKTMFPFLDEQADKHGHIHPHVTWKSNCLPL 1722  
 QY 1746 RFWNMILKNPQVDFDIHKNISITDACLISVVAQTPMDCSTSEHRLGKDSPSNKLLIYAKDIP 1805  
 DB 1723 RFWNMILKNPQVDFDIHKNISITDACLISVVAQTPMDCSTSEHRLGKDSPSNKLLIYAKDIP 1782  
 QY 1806 SYKNWERYYSIDGKMPALSDQDMAYLAEQSRHNMNFMTMSALSEIFSVYOKYSEIL 1865  
 DB 1783 NYKSWERYYSIDGKMPALSDQDMAYLAEQSRHNMNFMTMSALSEIFSVYOKYSEIL 1842  
 QY 1866 GPLDHDQCCGKQKLAYLEQVITLMSLDS 1894  
 DB 1843 TALDRASCRKHKLRQKLEQIISLVSSDS 1871



RESULT 12

US-10-218-779-84

; Sequence 84, Application US/10218779

; Publication No. US20040029222A1

; GENERAL INFORMATION:

; APPLICANT: Edinger, Shlomit  
; APPLICANT: MacDougall, John  
; APPLICANT: Millet, Isabelle  
; APPLICANT: Ellerman, Karen  
; APPLICANT: Stone, David  
; APPLICANT: Gerlach, Valerie  
; APPLICANT: Grosse, William  
; APPLICANT: Alsobrook II, John  
; APPLICANT: Lepley, Denise  
; APPLICANT: Rieger, Daniel  
; APPLICANT: Burgess, Catherine  
; APPLICANT: Casman, Stacie  
; APPLICANT: Spytek, Kimberly  
; APPLICANT: Boldog, Ferenc  
; APPLICANT: Li, Li  
; APPLICANT: Padigaru, Muralidhara  
; APPLICANT: Mishra, Vishnu  
; APPLICANT: Patturajan, Meera  
; APPLICANT: Shenoy, Suresh  
; APPLICANT: Rastelli, Luca  
; APPLICANT: Tchernev, Velizar  
; APPLICANT: Vernet, Corine  
; APPLICANT: Zerhusen, Bryan  
; APPLICANT: Malyankar, Uriel  
; APPLICANT: Guo, Xiaojia  
; APPLICANT: Miller, Charles  
; APPLICANT: Gangoli, Esha  
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same  
; FILE REFERENCE: 21402-214  
; CURRENT FILING DATE: 2002-08-14  
; PRIOR APPLICATION NUMBER: 60/253,834  
; PRIOR FILING DATE: 2000-11-29  
; PRIOR APPLICATION NUMBER: 60/250,-926  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: 60/264,180  
; PRIOR FILING DATE: 2001-01-25  
; PRIOR APPLICATION NUMBER: 60/313,656  
; PRIOR FILING DATE: 2001-08-20  
; PRIOR APPLICATION NUMBER: 60/327,456  
; PRIOR FILING DATE: 2001-10-05  
; NUMBER OF SEQ ID NOS: 216  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 84

; LENGTH: 1871

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: VARIANT

; LOCATION: (380)

; OTHER INFORMATION: Wherein Xaa is any amino acid.

US-10-218-779-84

Query Match 59.9%; Score 5988; DB 12; Length 1871;

Best Local Similarity 60.0%; Pred. No. 0;

Matches 1133; Conservative 293; Mismatches 437; Indels 26; Gaps 13;

Qy	10	CLLSHLLMVGMSSTLLTROPAPLSQKRSFVIFRGEPAEGFNHLVVDERTGHYLGAVN	69
Db	5	CLLL-LFLAVGGA--LGNRF-----RAFVV-----TDITLTHLAVHRVTGEVFGAVN	51
Qy	70	RIYKSSDLKVLVTHETGPEBDNPKYPPRIVOTCNELPTTNNVKKLLIDYKENRLIA	129
Db	52	RVFKLAPNLTELRAHVTGPEVDNARCYPPPSMRVCAHRLAPVDNINKLLIDYAARLVA	111
Qy	130	CGSLYQGIKLLRLDLFLKLEPHVKKHEVILSGWESGVFGIVTSVNLDDKLFATAV	189

Db	112	CGSIWQICQFLRLDDLFKLGEPHRKEHYLSGAQEPDSMAGVVEQGGPSKLFVGTAV	171
Qy	190	DKPEYFPTTSRKLTNNSEADGMFAVVFHDEFVASMIKIPSDTFTTIPDFDIYVYGF	249
Db	172	DKSEYFPTLSRKLISEDSADMFSLVYQDEFVSSQIKIPSDTSLSYPALDIYIYGFV	231
Qy	250	SGNFVYFLTLQPEWVSPGSGTTEQVYTSKLVRLCKEDTAFNSVVEVPIGICRSGVYRL	309
Db	232	SASFVYFLTLQDTQQTLDTAGEKFFTSKIVMCAGDSEFSYVVEPIGCSWRGVEYRL	291
Qy	310	LQAYLSKAGAVLQRTIGVHPDDLLFTVFSKQKRMKSLDESALCIFIILKQINDRIKE	369
Db	292	VQSAHLAKPGLLAQALGVPADVDLFTIFSQGGKRAASPPRQITLCLTILSNNAHRR	351
Qy	370	RLQCYRGEGLDLAWLKVKDIPCSALLTIDDFCGLDNAPLGVSDMYRGIYFTEDR	429
Db	352	RIQCYRGEGLTALPWLNLKELPCINTPXQINGNFCGLVNLNQLGGHLHTEGLPLADST	411
Qy	430	DRMTSVIAYVYKNSHLAFVGTGSKLKKIRVDGPRGNALQYETVQVVDPPGLVLRDMSFK	489
Db	412	DGMASVAAYTYRQSHVVFVIGTRSGSLKKVRVDGQ--DAHLVETVPVVDGSPILADLLFSP	470
Qy	490	DHEQLYIMSERQLTRVPVSGQYQSGCEGLGSDPHCGMVCVLTCTRKERCERSKEPR	549
Db	471	DHRHIYLLSEKQVSLPVETCEYQSCAACLGSDPHCGMVCVLRHRCRREGACLGASAPH	530
Qy	550	RFASEMKQCVRLTVHPNNISVSQYNVLLVLETYNVPELSAGVNCCTFEDLSEMDG--LVVGN	608
Db	531	GFAEELSKCVQVRVRPNNVSVTPGVQLTVTLHNVPLDSAGVSCAFEAANEAVLLPSG	590
Qy	609	QIQCYSPAKEVPRIITENGDDHVVLQLSKETGMTFASTSFVFNCSVHNSCLSCVES	668
Db	591	ELLCPSPQLBELRALTRGHGATRTVRLQLLSKETGVRFAGADFVFNCSVLQSCMVCVS	650
Qy	669	PYRCHWKYRHCVTDPKTCFQGRVKVLPEDCDQLLRVDKILVPEVIEKIFITLAKNLP	728
Db	651	PYPCHWKYRHTCTSRPEHCSFQGRVHSPGCEPILPSGDLILPVGMQPLTLRAKULP	710
Qy	729	QPSGQRYEGILNIOGSEORVPALRPNSSVQCNYSYEGMEINNLVELTVVWNGH	788
Db	711	QPSGQRYECVVRVQGRQVRPAVRPNSSVQCNASYSYEGDEHGDTELDVFWVDGD	770
Qy	789	FNIDNPAQNVHLYKCGAMRESCGLKADPDFACGCGQPGQCTLRQHCQPAQSOMLEL	848
Db	771	FPIDKPPSFRALLYKCAQWPSGCLKADPRFCGWCISHRQCLATHCFAPNTNMHL	830
Qy	849	SGAKSKCTNPRITEIIPVTGPRGGTKVTIRGENLGLFEDRIASHVKVAGCEPLVDGY	908
Db	831	SQKTRCSHPRITQIHPVLPKGGTRVTIYGENLGLLSREVG--LRVAGVRCNSIPABY	888
Qy	909	IPAEQIVCEMGEA-KPSCHAGFVBIQVAVCRPEFMARSSQLYFMTLTLSLKPESRGPM	967
Db	889	ISAEIVCEMEESLVPSPPPVLCVDCSADPTQSEQVYSFVTFDQVSPSRGPAS	948
Qy	968	GGTQVTTITGNLNGSNVVMFGKQPCFLFHRRSYIVC--NTTSSDEVLEMKVSVQVDRA	1026
Db	949	GGTRLTISGSLDAGSRVTVTRDSECOFVARDAKAVICISPLSLTGLSPQAPITLADRA	1008
Qy	1027	KHQ--DLVFOYVEOPTVIRIEPWSIVSGNTPIAVGTHLDLIONPOLRAKHGKHEINI	1085
Db	1009	NLSSPELLIYTTQDPTVRLPTWSIIINGSTAITVSGTHLTVQEPVRAKYRIETNT	1068
Qy	1086	CEVLNATEMTQAPALALGPDHQSDLTERPEEFGFILDNVQSLILINKNTFYTPNPVFE	1145
Db	1069	CQVINDTAMLCAPGIFLGRFPQRAQGHDPDFGLLDHVTARSLNRSFTTYPDPSFE	1128
Qy	1146	APGSGIILEKPGTPIILKGNLIPPVAGGNVKNLYTVLCEKECTTVSDVOLLCESPN	1205
Db	1129	PLGPGSVLDVPGSHVILKGNLIPAAAGSS--RLNVTYVLIQGGPCSLVSTQLLDCSPS	1187
Qy	1206	LIGRHKVMARVGMGMEYSPGMVVIAPDSPLSLPATVSIAGGLLIIFIVAVLIAYKRSR	1265

Db 1188 QTGRQPVVIVGGLFMTGLTSHISAERALTLPAMMGLAAGGGLLLLAITAVLVAVYKRTQ 1247  
Qy 1266 ESDLTCLKQOMNLESRVALECKEAPAEIQTDIHETLSLDGAGPFLDRTYTRVL 1325  
Db 1248 DADRCLKQLQOMNLESRVALECKEAPAEIQTINELTNMDEVOIPFLDRTYTRVL 1307  
Qy 1326 PFGIDHEDVLDEVPQYRQERVEKGLKFAQLNNKVFLLSFRTLESQRSFMRDRGN 1385  
Db 1308 PFGIEAHFVLELDTDP----PNVEKALRFQQLHSAFVLTFTHTLEAQSSFSMRDRGT 1363  
Qy 1386 VASLIMTVLQKLEYATVVLKOLLADLIDKNLESKNHFKLLLRRTESVAEOMLNTWTFEL 1445  
Db 1364 VASLTMVALQSRDLYATGLKQLADLIEKNLESKNHFKLLLRRTESVAEOMLNTWTFEL 1423  
Qy 1446 LVKFLKECAGPFLPFCALQOMKEGPIDAITGEARYSLSEDKLIRQOIIDYKTLVLSV 1505  
Db 1424 LHKFLKECAGPFLFLLYCAIQOMKEGPIDAITGEARYSLSEDKLIRQOIIDYKTLVLCV 1493  
Qy 1506 SPDNANSEVPVKIUNCDTITQVKEKILDAIFKXVPCSHRPKAAADMDLEWQSGARMIL 1565  
Db 1484 CPENEGSAQVPVKVLCNCSITQAKDKLDTVYKIPYSQRPKAEKMDMDLEWQSGMTRIL 1543  
Qy 1566 QDEDTTKIENDWKRNLTAHVQVDPGSGVVALVSKQVTAYNVNNSTVRSASKYENMI 1625  
Db 1544 QDEDTTKIECDWKELNSLAHYQVTDGSLVALVPKQVSAYNMANSFTFTR-SLSRYESLL 1602  
Qy 1626 RYTGSPDLSRSTPMITPDLESGVKKVHVLKXNHEHGDQEGDRGSKMVSSEIYLTLLATK 1685  
Db 1603 RTASSPDSLRSAPMITPDQETGKVLHVLKXNHDHAREGDRGSKMVSSEIYLTLLATK 1662  
Qy 1686 GTLOKFVDDLEETIESTAHRSALPLAKYWFEDLDEADKHGTHDPVHRTWKSNCPL 1745  
Db 1663 GTLOKFVDDLEETIESTAHRSALPLAKYWFEDLDEADKHGTHDPVHRTWKSNCPL 1722  
Qy 1746 RFWNMINKPQVFDIHKNSITDACLVSVAQTFMDSCSTSEHRLKDSFNSKLLYAKDIP 1805  
Db 1723 RFWNVINKPQVFDIHKNSITDACLVSVAQTFMDSCSTSEHRLKDSFNSKLLYAKDIP 1782  
Qy 1806 SYKNWERYYSIDGKPAISDODMAYLAQSRMNMENFNTMSALSEIFSVYGVKSEIL 1865  
Db 1783 NYKSWERYYRDIAGVASISDQMDAYLVEQSRHLSHSDFSVLISALNELYFYVTKYRQEL 1842  
Qy 1866 GPLDHDQCGKOKLAYKLEQVITLMSLDS 1894  
Db 1843 TALDRDASCRKHKLQKLEQIISLVSSDS 1871

RESULT 13  
US-10-087-684-82  
; Sequence 82, Application US/10087684  
; Publication No. US20040029116A1  
; GENERAL INFORMATION:  
; APPLICANT: Edinger, Shlomit R.  
; APPLICANT: MacDougall, John R.  
; APPLICANT: Millet, Isabelle  
; APPLICANT: Ellerman, Karen  
; APPLICANT: Stone, David J.  
; APPLICANT: Grosse, William M.  
; APPLICANT: Lepley, Denise M.  
; APPLICANT: Rieger, Daniel K.  
; APPLICANT: Burgess, Catherine E.  
; APPLICANT: Casman, Stacie, J.  
; APPLICANT: Spytek, Kimberly A.  
; APPLICANT: Boldog, Ferenc L.  
; APPLICANT: Li, Li  
; APPLICANT: Padigaru, Muralidhara  
; APPLICANT: Mishra, Vishnu  
; APPLICANT: Shenoy, Suresh G.  
; APPLICANT: Rastelli, Luca  
; APPLICANT: Tchernev, Velizar T.  
; APPLICANT: Vernet, Corine A.M.  
; APPLICANT: Zerhusen, Bryan D.  
; APPLICANT: Malyankar, Uriel M.

; APPLICANT: Guo, Xiaojia  
; APPLICANT: Miller, Charles E.  
; APPLICANT: Gangoli, Ssha A.  
; TITLE OF INVENTION: PROTEINS AND NUCLEIC ACIDS ENCODING SAME  
; FILE REFERENCE: 21402-214 CIP  
; CURRENT APPLICATION NUMBER: US/10/087,684  
; CURRENT FILING DATE: 2003-03-10  
; PRIOR APPLICATION NUMBER: 60/253,834  
; PRIOR FILING DATE: 2000-11-29  
; PRIOR APPLICATION NUMBER: 60/250,926  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: 60/264,180  
; PRIOR FILING DATE: 2001-01-25  
; PRIOR APPLICATION NUMBER: 60/274,194  
; PRIOR FILING DATE: 2001-03-08  
; PRIOR APPLICATION NUMBER: 60/313,656  
; PRIOR FILING DATE: 2001-08-20  
; PRIOR APPLICATION NUMBER: 60/327,456  
; PRIOR FILING DATE: 2001-10-05  
; NUMBER OF SEQ ID NOS: 220  
; SOFTWARE: CuraseqList version 0.1  
; SEQ ID NO 82  
; LENGTH: 1754  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (78)..(78)  
; OTHER INFORMATION: Wherein Xaa may be any naturally occurring amino acid  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (123)..(123)  
; OTHER INFORMATION: Wherein Xaa may be any naturally occurring amino acid  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (620)..(620)  
; OTHER INFORMATION: Wherein Xaa may be any naturally occurring amino acid  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1474)..(1474)  
; OTHER INFORMATION: Wherein Xaa may be any naturally occurring amino acid  
; OTHER INFORMATION: Wherein Xaa may be any naturally occurring amino acid  
US-10-087-684-82

Query Match 58.5%; Score 5847.5; DB 12; Length 1754;  
Best Local Similarity 63.7%; Pred. No. 0;  
Matches 1114; Conservative 237; Mismatches 378; Indels 19; Gaps 12;

Qy 37 QRSFVTFRGPAGFNHLVVDERTGHYLGAVNRIYKLSDDLKVLVTHETGPDDEDPKCY 96  
Db 16 QPPFRTFSGSD-WGLTHLLVHEQTGEVYGVAVNRIYKLSGNLTLLRAHVTPGVEDNEKY 74  
Qy 97 PPRIVOTCNEPLTTNNVNNKLLIDYKENRLIACGSLYQGIKLLRLEDLFKLGEVPHKK 156  
Db 75 PPFVXQCPHGLGNTNNVNNKLLIDYKENRLIACGSLYQGIKLLRLEDLFKLGEVPHKK 134  
Qy 157 EHYLSGVNCSGVFGVIVS--YSNLDKLFATAVDGKPEYPTTISRKLTKNSEADGMF 214  
Db 135 EHYLSVVOEAGSMAGVLIAAGPPGQGAFLVGPIDGKSEYFPTLSRRLMANEEDADM 194  
Qy 215 AYVPHDFVASMUKIPSDTETIIPDDIYVYVFGSGNFVYVLTQ--PMVSPPGSTTK 272  
Db 195 GFVYQDFVSSQLKIPSDTETIIPDDIYVYVFGSGNFVYVLTQ--PMVSPPGSTTK 272  
Qy 273 EQVYTSKLVRLCKEDTAFNSYVEVPICERSGVEYELLQAAYLSKAGAVLGRITGVHPDD 332  
Db 253 EHFPTSKIVLCVDDPKFYSYVEFPFICEQAGVEYRLVQDAYLSRPGRALAHQGLADE 312  
Qy 333 DLLFTVFSKQKRNKMSLDESALCIFILKQINDRIKRLQSCYRGEGTDLANKVKDIP 392  
Db 313 DVLFTVFAQGNKRVKPKESALCLFTLRAIKERIQSCYRGEGTDLANKVKDIP 372  
Qy 393 CSSALLTIDNFCGLDMNAPLGVSDMVRGIPVTEDRDMTSTVIAYVYKNSLAFVGTGS 452

373 CINSPLQIDDDFRQDQFNQPLGGTVTTIEGTPLFVDDKDDGLTAAVAYDYRGRTVVVFAGTRS 432
453 GKLKIRVD--GPRGN-ALQVETVQVVDPPGVLRDMAPSKDHEQLYIMSRQLTRVPVES 509
433 GRIRKILVLSNPGRPALAYESVVAQEGSPILLRDLVLSNQHLYVAMTEKQYTRVPVES 492
510 CGQYQSCGECGLSDPGHGCACVLTNTCTRKERCERSKEPRPASEMKQCVRLTVHPNNIS 569
493 CVQYTSCELCGSDPGHGCACVLTNTCTRKERCERSKEPRPASEMKQCVRLTVHPNNIS 552
570 VSOYNVLVLETVNVPBLSAGVNCCTFDLSEMDGLVVGNOIQCVSPAACEVPRITENG 629
553 VTMSQVPLVQANVPDLVAGVNSCFDFTESVLEDRHICRSPSAREVAPITRQGD 612
630 HHVQLQKSKETGWTASTSFPYNSCVHNSCLCSVEPYRCHWCKYRHCVTCHDPTKTS 699
613 QRVVKLYXKSKETGWTASTSFPYNSCVHNSCLCSVEPYRCHWCKYRHCVTCHDPTKTS 672
690 FQGRVRLPDCPOLLRVDTILVPEVVKITLAKNLPQPGSQRGYECILNIQSGEOR 749
673 FLEGVNVSEDCPOLLRVDTILVPEVVKITLAKNLPQPGSQRGYECILNIQSGEOR 732
750 VPALRFNNSVQCCQNTSYSEGBEINNLVPELTVVWNGHFNINDNPAQNVHLYKCGAMRE 809
733 VTALRFNNSVQCCQNTSYSEGBEINNLVPELTVVWNGHFNINDNPAQNVHLYKCGAMRE 792
810 SCGLCKADPDFACGWCQPGQCTLRQHCAPQ--ESOMLELSGAKSKCTNPRITEIIPVTG 868
793 SCGLCKADPDFACGWCQPGQCTLRQHCAPQ--ESOMLELSGAKSKCTNPRITEIIPVTG 852
869 PREGGTVIRGENGLJEFRDIAHVKVAGVCSPLVDGYIPAEIVCEMGEAKPQO-HA 937
853 PROGGTTLITGENGLJEFRDIAHVKVAGVCSPLVDGYIPAEIVCEMGEAKPQO-HA 912
928 GFVEICVAVCRPEPMASSSQLYFMTLTLSDLPKSRGPMGGTCTVTGTGNLAGSNVYV 987
913 ALVEVCVRDCSFPYRALSPKRFPTVTFTRVSPRGLSGGTWIGIEGHLNAGSDVAV 972
988 MFGQPCFLHRRSPSYIVCNTSSDVELEMKVSVQVDRAKI-HQDLVFOVVEPTTVRIE 1046
973 SVGRPCFSFWRNSREIRCLTPQSPGSPASPIIININRAQLTNPEVKYNTEDPTILRID 1032
1047 PWSIVSGNTPVAVGTHLDLIQNPQIRAKHGKEHINICEVLNATEMTQOALALGPD 1106
1033 PWSIVSGNTPVAVGTHLDLIQNPQIRAKHGKEHINICEVLNATEMTQOALALGPD 1092
1107 HQSDLTPRBEFGFILDNVOSLJLNTFTYPPNPVFEAFPGSGILELKPPTIILKGR 1166
1093 SPPELGERPDELGFVMDNVRSLVLNSTSLYYPDPVLEPLSPTGLLELKPSPFLILKGR 1152
1167 NLIPVAGNVKLYNTVLGKPCPTVTVSDVOLLCESPNLGRHKVMARVGMGEYSPGMV 1226
1153 NLLEPP-APGNSRLNTYVLIQSTPCTLTVSSTQLLCEAPNLGQHKVTRAGGFEPFSGTL 1211
1227 YIAPDSPLSLPAIVSIAVAGGLLIIFTVAVLIAVKRSRSDTLTKELQMDNLSRVA 1286
1212 QVYSDSLTLPAIVIGIGGGGLLLVAVLIVAVLIAVKRSRDADRTLKELQMDNLSRVA 1271
1287 LECEAFABLOTDTHEITSDLDGAGIPFLDYRTYTMVLPFGIEDHPVLRDLBVPVGRQE 1346
1272 LECEAFABLOTDTHEITSDLDGAGIPFLDYRTYTMVLPFGIEDHPVLRDLBVPVGRQE 1327
1347 RVEKGLKFAQLINKKVFLLSFIETLESQSFNRDRGNVASLIMTVLQSKLEYATDVLLK 1406
1328 NVEKSLTLFGQLLTKKHFLLTFITLRAQSFNRDRGNVASLIMTVLQSKLEYATDVLLK 1387
1407 QLLADLIDKNLESKNPKLLRRRTESVAEKMLTNWFTFLYKFLKECAGEPFLSLFCAIK 1466
1388 QLLADLIDKNLESKNPKLLRRRTESVAEKMLTNWFTFLYKFLKECAGEPFLSLFCAIK 1447
1467 QQMEKGPIDAITGEARYSLSDKLIROIDYKTLVLCVSPDNANSPEVPKILNCDDTIT 1526
1448 QQMEKGPIDAITGEARYSLSDKLIROIDYKTLVLCVSPDNANSPEVPKILNCDDTIT 1507

QY 1527 QVKEKILDAIFQNVPCSHRPAKADMDLEWRQSGARMILQDEDTITTKIENDWKRLNTLAH 1586
DB 1508 QAKKLLDAAYKGVFYSQRPKADMDLEWRQSGARMILQDEDTITTKIENDWKRLNTLAH 1567
QY 1587 YQVPGSVVALVSKQVTAYNAVNSSTVSTASKYENMIRYTGSPDSLSRSTPMITPDLE 1646
DB 1568 YQVTDGSSVALVPRKTSAYNISNSSTFTK-SLSRYESMLRTASSPDSLSRSTPMITPDLE 1626
QY 1647 SCVQVHVLVXNHEHGDQKEGDRGSKVWSEIYLTLLATKGLQKQFVDDLFTFIFSTAHRG 1706
DB 1627 SGTKLHVLVXNHDHLDQREGDRGSKVWSEIYLTLLATKGLQKQFVDDLFTFIFSTAHRG 1686
QY 1707 SALPLAIKYMDFDLDEQADKHGIDHPVHTWKNCLBLRFWANMIKNPQVFDIHKNSI 1766
DB 1687 SALPLAIKYMDFDLDEQADKHGIDHPVHTWKNCLBLRFWANMIKNPQVFDIHKNSI 1746
QY 1767 TDACLSSV 1774
DB 1747 TDACLSSV 1754
RESULT 14
US-10-218-779-82
; Sequence 82, Application US/10218779
; Publication No. US20040029222A1
; GENERAL INFORMATION:
; APPLICANT: Edinger, Shlomit
; APPLICANT: MacDougall, John
; APPLICANT: Millet, Isabelle
; APPLICANT: Ellerman, Karen
; APPLICANT: Stone, David
; APPLICANT: Gerlach, Valerie
; APPLICANT: Grosse, William
; APPLICANT: Alsobrook II, John
; APPLICANT: Lepley, Denise
; APPLICANT: Rieger, Daniel
; APPLICANT: Burgesse, Catherine
; APPLICANT: Casman, Stacie
; APPLICANT: Spytek, Kimberly
; APPLICANT: Boldog, Ferenc
; APPLICANT: Li, Li
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Mishra, Vishnu
; APPLICANT: Patturajan, Meera
; APPLICANT: Shenoy, Suresh
; APPLICANT: Rastelli, Luca
; APPLICANT: Tchernev, Velizar
; APPLICANT: Vernet, Corine
; APPLICANT: Zethusen, Bryan
; APPLICANT: Malyankar, Uriel
; APPLICANT: Guo, Xiaojia
; APPLICANT: Miller, Charles
; APPLICANT: Gangolli, Esha
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-214
; CURRENT APPLICATION NUMBER: US/10/218,779
; CURRENT FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: 60/253,834
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: 60/250,-926
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: 60/264,180
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/313,656
; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: 60/327,456
; PRIOR FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 216
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 82
; LENGTH: 1754
; TYPE: PRT

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Qy	810	SCGLCKADPDFACGWCQPGQCTLRQHCFAQ-ESQWLELSGAKSKCTNPRITETIIPVTG	868
Db	793	SCGLCKADPRFECGWCVAERCSRHRHCAADTPASWMAHARHGSSRCTDKILKSPETG	852
Qy	869	PREGTKVTIRGENLGEFRIASHVKVAVGECSPLDVGIYIPABQIVCEMEAKPSQ-HA	927
Db	853	PROGTRLTITGLENLGRFEDVRLGVKLVCSFVESEYISABQIVCEIGDASSVRAHD	912
Qy	928	GFEIVCAVCRPEFMARSSQLYYFWTLTLDLSPKSPRGMGGTQVTTTGTNNAGSNVVV	987
Db	913	ALVEVCVRDCSPHYRALSPKRFTEVTPTFVRVSPSRGFLSGGTWIGIEGSHNAGSDVAV	972
Qy	988	MFGKQPCLFHRSRPSYIVCNTSSDVELEMKVSVQVDRAKI-HODLVFQVYVEDFTIVRIE	1046
Db	973	SVGRPCSFWRNSREIRCLTPQCSGSAPIIININRAQLTNPVKXNYTEDFTILRID	1032
Qy	1047	PEWSIVSGNTPIAVMGTHLDLIQNPQIRAKHGKHEHINI CEVLNATEMTQAPALALGPD	1106
Db	1033	PEWSINSGLTLLTVGTNLATVRSPRIAKYGGIERENGCLVYNDTTCVCRAPSANPVR	1092
Qy	1107	HQSDUTERPEFGFILDNVQSLILINKNTFYNNPVPFPAFGPSGILKPGTPIILKGGK	1166
Db	1093	SPPELGERPDBLGFYMDNVRSLVNLNSTFLYYPDPVLEPLSPGTGLLEKSPSLLIKGR	1152
Qy	1167	NLIPPVAGCNKLVNLVGEKPCCTVTIVSDVQLLCESPNLIGRHKWARVGMGEYSPOMV	1226
Db	1153	NLLPP-APGNSRLNVTYLGSTPCTLTIVSETQLLCEAPNLGQHKVTVRAGGFSPGTL	1211
Qy	1227	YIAPSPISLPAIVSIAVAGGLIIFIVANLIYAKRRESDLTKRLQMDNLESVA	1286
Db	1212	QVYSLSLTLTPAIVGIGGGGLLLVIVAVLIYAKRSDADRTLKRLQMDNLESVA	1271
Qy	1287	LECKEAFAELOTDIHELTSDLDDGAGIPFLDYRTYTMRVLPFGIEDHPVRLDVEGVRQE	1346
Db	1272	LECKEAFAELOTDIHELINDLDGAGIPFLDYRTYTMRVLPFGIEDHPVRLDVEGVRQE	1327
Qy	1347	RYEKGKLPFAQIINNKNVFLLSFIRLESQRSFSDRGNVASLIMTVLQSKLEYATDVLK	1406
Db	1328	NVEKSLTLFGQLTKKHFLLPTIRLEAQRSPSMDRGNVASLIMTVLQSKLEYATDVLK	1387
Qy	1407	QLLADLIDKNLKNHPKLLLRRTESVAEKMLTNWFTLLYKFLKECAGEPLFLCAIK	1466
Db	1388	QLLSDLIEKNLKNHPKLLLRRTESVAEKMLTNWFTLLYKFLKECAGEPLFLCAIK	1447
Qy	1467	QOMEKGPIDAITGEARYSLSEDKLIROQIDYKTLVLSVSPDNANSPEVPVKILNCDTIT	1526
Db	1448	QOMEKGPIDAITGEARYSLSEDKLIROQIDYKTLVLSVSPDNANSPEVPVKILNCDTIT	1507
Qy	1527	QVKEKILDAIFKNVPCSHRPAADMDLEWROGSGARWILQDESDITTKIENDWKRLNTLAH	1586
Db	1508	QAKEKILDAAYKGVPPYQRPKAADMDLEWROGSGARWILQDESDITTKIENDWKRLNTLAH	1567
Qy	1587	YQVPGSVVALYSKQVTAYNVNNSTVSRSTSASKYENMIRYTGSPDSLSRSTPMTTPDLE	1646
Db	1568	YQVTDGSSVALVPKQTSAYNISSTFTK-SLSRYESMLRTASSPDSLSRSTPMTTPDLE	1626
Qy	1647	SGVMMHLVKNHEHGDQEGDGRGSKVSEIYITRLLATKGTLOKQVDDLFETIFSTAHG	1706
Db	1627	SGTKLWHLVKNHDLQDREGDGRGSKVSEIYITRLLATKGTLOKQVDDLFETIFSTAHG	1686
Qy	1707	SALPLAIKVMFDFLBQADKHGIDHPVHRTWKSNCPLRFVFWNMINKPQFVFDIHKNSI	1766
Db	1687	SALPLAIKVMFDFLBQADKHGIDHPVHRTWKSNCPLRFVFWNMINKPQFVFDIHKNSI	1746
Qy	1767	TDACLSW 1774	
Db	1747	TDACLSW 1754	

RESULT 15  
US-09-964-956-45

;	ORGANISM:	Homc sapiens	
;	FEATURE:		
;	NAME/KEY:	VARIANT	
;	LOCATION:	(78)	
;	OTHER INFORMATION:	Wherein Xaa is any amino acid.	
;	FEATURE:		
;	NAME/KEY:	VARIANT	
;	LOCATION:	(123)	
;	OTHER INFORMATION:	Wherein Xaa is any amino acid.	
;	FEATURE:		
;	NAME/KEY:	VARIANT	
;	LOCATION:	(620)	
;	OTHER INFORMATION:	Wherein Xaa is any amino acid.	
;	FEATURE:		
;	NAME/KEY:	VARIANT	
;	LOCATION:	(1474)	
;	OTHER INFORMATION:	Wherein Xaa is any amino acid.	
;	US-10-218-779-82		
	Query Match	58.58; Score 5847.5; DB 12; Length 1754;	
	Best Local Similarity	63.78; Pred. No. 0;	
	Matches 1114; Conservative 237; Mismatches 378; Indels 19; Gaps 12;		
Qy	37	QRGSFVFRGEPAGFNHLVVDERTGHIYLGAVNRIYKLSDDLKLVLTHTGTGPDDEPNKCY	96
Db	16	QPPRFISGSD-WGLTHLLVHEQTEGVYVGVAVNRIYKLSGNLTLRAHVTGPVEDNEKY	74
Qy	97	PPRIQVTCNPLTTNNVNMKLLIDYKENRLIAGSLYQIGICKLLRLEDLFLKLGEPHYKK	156
Db	75	PPXVQSCPHGLGNTDNVKNLLLDYAAANRLACGSASQIGCSLSRLDLFLKLGEPHYKK	134
Qy	157	EHLVSGVNEGSVFGVIVS--YSNLDDBKLFIAATVADGKPEYFPTISRRKLTQKSEADGMF	214
Db	135	EHLVSSVQEGAGSVAGVLIAGPPGQOAKLFVGTPIDGSEYFPTLSRRLLWANEADMF	194
Qy	215	AYVHDFEFAVMIKIPSDTFTIIPDIYVYGFSSGNFVFTLQ--PEMVSPGSGTTK	272
Db	195	GFVYQDEFVSSQLKIPSDTLTKFPAPDIYVYSPRSEQFVYLTQLDQLTQTSF--DAAG	252
Qy	273	EQVYTSKLVRLCKEDTAFNSVVEYPIGERSGVBYRLQAAAYLSKAGAVLGRITLVGHPDD	332
Db	253	EHFTSKIVRLUCVDDPKFYSEYPIGCEQAGVEYRLVQAYLSRPGALAHQGLAEDE	312
Qy	333	DLFTVFSKGQRKMKLSDSALCIFIILKQINDRIKELQSCYRGEGTLDLAWLKVQDIP	392
Db	313	DVLTFTVFAQGGKNRVKPPKESALCLFTLRAIKERIKERIQSCYRGEGKLSLPMILNKBELG	372
Qy	393	CSSALLTIDNFCGLDNAPRGVSDMVRGIPVFTEDRMTSVIAYVYKHSFLAFVGTKS	452
Db	373	CINSPQLIDDFRGQDFNQPLGGVTIEGTPLFVDKDDGLTAVAAVYRGRTVVVFAGTRS	432
Qy	453	GKLKKIRVD--GPRGN-ALQYETVQVVDPPGVLRDMAFSKDHEQLYIMSEQLTRVPVES	509
Db	433	GRIRKILVDLSNPGGRPALAYESVVAQEGSPILRDVLSPNHQVLYAMTEKQVTRVPVES	492
Qy	510	CGYQSCGECILGSGDPHCGWCVLHNTCTRKERCERSKEPRFASSEMKCQVRLTVHPNIS	569
Db	493	CVQYTSCELCIGSRDPHCGWCVLHNSICRRDACCRADEPQRFADLQCVQLTVQPRNVS	552
Qy	570	VSQYNVLVLETYNVPELSAGVNCCTFEDLSMDGLVVGNOIQCYSPAAKEVPRITENG	629
Db	553	VIMSQVPLVLAQWNPDLASAGVNSCFEDFTSESVLEDRTHCESPSAREVAPITRQGD	612
Qy	630	HVVVOLQLKSKETGTMFTASTSFVFNCSVHNSCLSCVESPRCHWKYRHHVCTHDPTCS	689
Db	613	QRVVKLYKSKETGKFPASVDFVFNCSVHNSCLSCVNSGSPFCHWKYRHHVCTHNADCA	672
Qy	690	FOEGSVKLPEDCPQLLRVDKILVPEVVKPTTLAKNLPQPSGORGVEICLINTQSGEQR	749
Db	673	FLEGKVNVEDCPQLPSTQIVPVGVVVKPTTLARNLPQPSGORGVEICLPHFGSPAR	732
Qy	750	VPALRNFSSSSVOQNTSYSEGMENINLPVLTVVWNGHFNIDNPAQNKHLYKCGAMRE	809

	Query Match	33.9%	Score 3386.5	DB 12	Length 813
Best Local Similarity	79.1%	Pred. No. 1.5e-299			
Matches 641	Conservative	76	Mismatches 92	Indels 1	Gaps 1
QY	1085	ICEVLNATMTCOAPALALGPDHQSILTERPEFEGFILDNVQSLILINKTNFYYPNVF 1144			
Db	5	VCKVNVTTTLTCLAPSLTTDYRGLDVERDPDFGVFNNVQSLIIVNDTKFYYPNPF 64			
QY	1145	EAFGPSGILELKGFTPIILKGNKLIIPPVAGNVKLVNTVLVGEKPTVTVSDVOLCESP 1204			
Db	65	ELLSPTGVLDQKFGPIILKGNLCPPASGG-AKLVNTVLIGTTCAVTVSETQLICEPP 123			
QY	1205	NLIGRHKVMARVGMGMYSPGVYIADPSLSPALVSIAGVGLLIIFIVAVLIAYKRKS 1264			

Search completed: May 25, 2004, 04:27:57  
Job time : 94 secs

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: May 23, 2004, 12:26:29 ; Search time 178 Seconds  
(without alignments)  
5911.162 Million cell updates/sec

Title: US-09-964-956-13  
Perfect score: 9990  
Sequence: 1 MKAMPWNWTCLLSHLMVGM.....QKLYAKLEQVITLMSLDSNK 1896

Scoring table: BLOSUM62

Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters: -DEV=xlh  
-MODEL=frame+ p2n.model -US09964956/runat 19052004 160715 10947/app query.fasta\_1.2055  
-O=/cgn2\_1/uspto.spool/US09964956 -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0  
-DB=Issued Patents NA -QFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0  
-LOOPTXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
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-NO WMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THRAD=10 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA:\*

1:	/cgn2_6/prodata/2/ina/5A-COMB.seq:*
2:	/cgn2_6/prodata/2/ina/5B-COMB.seq:*
3:	/cgn2_6/prodata/2/ina/6A-COMB.seq:*
4:	/cgn2_6/prodata/2/ina/6B-COMB.seq:*
5:	/cgn2_6/prodata/2/ina/6C-COMB.seq:*
6:	/cgn2_6/prodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES			
Result No.	Score	Query Match Length	ID Description
1	1359.5	13.6	2477 4 US-09-907-794A-169 Sequence 169, App
2	1359.5	13.6	2477 4 US-09-905-125A-169 Sequence 169, App
3	1359.5	13.6	2477 4 US-09-902-775A-169 Sequence 169, App
4	1349	13.5	4707 3 US-09-181-706-1 Sequence 1, Appl
5	1349	13.5	4707 3 US-09-458-791-1 Sequence 1, Appl
6	1349	13.5	4707 3 US-09-459-066-1 Sequence 1, Appl
7	1349	13.5	4707 3 US-09-459-066-1 Sequence 1, Appl
8	657	6.6	3458 4 US-09-023-655-603 Sequence 603, App
9	629.5	6.3	4626 1 US-08-306-691B-22 Sequence 22, Appl
10	629.5	6.3	4626 5 PCT-US93-06251-27 Sequence 27, Appl
11	323	3.2	2433 4 US-09-300-958A-24 Sequence 24, Appl
12	263	2.6	3524 4 US-09-077-940A-3 Sequence 3, Appl

ALIGNMENTS

RESULT 1  
US-09-907-794A-169  
; Sequence 169, Application US/09907794A  
; Patent No. 6635468  
; GENERAL INFORMATION:  
; APPLICANT: Genentech, Inc.  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, A.  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth, J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Mather, Jennie P.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William, I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: 10466-14  
; CURRENT APPLICATION NUMBER: US/09/907,794A  
; CURRENT FILING DATE: 2001-07-17  
; PRIOR APPLICATION NUMBER: PCT/US00/04414

PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 169
LENGTH: 2477
TYPE: DNA
ORGANISM: Homo sapiens
US-09-907-794A-169
Alignment Scores:
Pred. No.: 8,8e-138 Length: 2477
Score: 1359.50 Matches: 271
Percent Similarity: 69.88% Conservative: 84
Best Local Similarity: 53.35% Mismatches: 124
Query Match: 13.61% Indels: 31
DB: 4 Gaps: 7
US-09-964-956-13 (1-1896) x US-09-907-794A-169 (1-2477)
QY 5 ProTIPAsnTrpThrCysLeuLeuMetValGlyMetGlySerSerThr 24
DB 857 CCCTGGAGTGGACAGCGCTCTGNG-GTCCTGCTCTCAGT-GGTCCTGGTGGCTGCT--- 911
QY 25 LeuLeuThrArgGlnProAlaProLeuSerGlnLysGlnArgSer-PheValThrPheAr 44
DB 912 -----GGCCCCCCCCGACCGCGATGCTTCAGTTTCAGCACCTTCCA 953
QY 44 gGlyGluProAlaGlu---GlyPheAsnHisLeuValValAspGluArgThrGlyHisI1 63
DB 954 CTCCTGAGAATCGTACTGGACCTTCAACACCTTGACCTGCCAAGAGGACGGGGCGCT 1013
QY 63 eTyrluGlyAlaValAsnArgIleTyrluSerSerSerAspLeuLysValLeuValTh 83
DB 1014 CTATGTGGGGGCATCAACCGGGTCTATAAGCTGACAGGCAACCTGACCTCCAGGTGGC 1073
QY 83 rHisGluThrGlyProAspGluAspAsnProLysCysTyrlProArgIleValGlnTh 103
DB 1074 TCATAGACAGAGCCAGAGAGAGACACAAAGTCTGTTACCGCCCTCATCTGTCGACGCC 1133
QY 103 rCysAsnGluProLeuThrThrThrAsnAsnValAsnLysMetLeuLeuIleAspTyrlY 123
DB 1134 CTGCAGCGAAGTGTCTCACCTCCACCAACAATGTCAACAGCTGCTCATCAATTGACTACTC 1193

123 sGluAsnArgLeuIleAlaCysGlySerLeuTyrdGlnGlyIleCysLysLeuLeuArgIe 143
1194 TGAGAACCCGCTGCTGGCTGTGGAGCCTCTACACAGGGGGTCTGCAAGCTGTGGGGT 1253
143 uGluAspLeuPheLeuGlyGluProTyrlHisLysLysGluHisTyrlLeuSerGlyVa 163
1254 GGATGACCTCTTCATCTGCTGGAGCATCCACACAAGAGGAGCACTACCTGTCTCCAGTGT 1313
163 lAsnGluSerGlySerValPheGlyValIleValSerTyrlSerAsnLeuAspLysIe 183
1314 CAACAAGAGCGGCACCATACGCGGTGATTGTGGCTCTGAGGGTGGAGTGGCAAGCT 1373
183 uPheIleAlaThrAlaValAspGlyLysProGluTyrlPheProThrIleSerSerArgly 203
1374 CTTTCATCGGCACGGCTGTGGTGAAGCAGGATTACTTCCCGACCTCTCCAGCCGAA 1433
203 sLeuThrLysAsnSerGluAlaAspGlyMetPheAlaTyrlValPheHisAspGluPheVa 223
1434 GCTGCCCGGAGACCCCTGAGTCTCAGCCATGCTCGACTATGACTACACAGCATTTTGT 1493
223 lAlaSerMetIleLysIleProSerAspThrPheThrIleIleProAspPheAspIleTy 243
1494 CTCCTCTCTCATCAAGATCCCTTCAGACACCCCTGGCCCTGGTCTCCCATCTTTCATCT 1553
243 rTyrlValTyrlGlyPheSerSerGlyAsnPheValTyrlPheLeuThrLeuGlnProGluMe 263
1554 CTACATCTACGGCTTTGCTAGTGGGGCTTTGCTACTTTCTCACTGTCCAGCCCGAG-- 1611
263 tValSerProProGly-----SerThrThrLysGluGlnValTyrlThrSerLysIe 280
1612 ----ACCTCTGAGGGTGGCCATCACTCCGCTGGAGACCTCTTCTACCTCAGCAT 1667
280 uValArgLeuCysLysGluAspThrAlaPheAsnSerTyrlValGluValProIleGlyCy 300
1668 CGTGGCGCTCTGCAAGGATGACCCCAAGTTCCACTCATACGTGTCTCCCTCCCTTCCGGCTG 1727
300 sGluArgSerGlyValGluTyrlArgLeuLeuGlnAlaAlaTyrlLeuSerLysAlaGlyAl 320
1728 CACCCGGCGGGTGGATATACCGCTCTCTGAGGCTGTTTACCTGGCCCAAGCTGGGGA 1787
320 aValLeuGlyArgThrLeuGlyValHisProAspAspLeuLeuPheThrValPheSe 340
1788 CTCACCTGGCCAGCGCTTCAATATACACAGCAGGACGATGACTCTTTGGCATCTCTC 1847
340 rLysGlyGlnLysArgLysMetLysSerLeuAspGluSerAlaLeuCysIlePheIleLe 360
1848 CAAGGGCGAGACAGTATCACCCCGCCGATGACTCTGCCCTGTGTGCTTCCCTAT 1907
360 uLysGlnIleAsnAspArgIleLysGluArgLeuGlnSerCysTyrlArgGlyGluGlyTh 380
1908 CCGGGCCATCACTTCAGATCAAGAGCGCTGCACTCTGCTACAGGGGAGGCAA 1967
380 rLeuAspLeuAlaTrpLeuLysValLysAspIleProCysSerSerSerAlaLeuLeuThrI 400
1968 CCTGGAGCTCACTGGCTCTGGGGAAGGACGTCAGTGCAGAGGCGCTGCTCCCAT 2027
400 eAspAspAsnPheCysGlyLeuAspMetAsnAlaProLeuGlyValSerAspMetValAr 420
2028 CGATGATACTTCTGTGGATGGACATCAACAGCCCTCTGGAGGCTCAACTCCAGTGA 2087
420 gGlyIleProValPheThrGluAspArgAspArgMetThrSerValIleAlaTyrlValTy 440
2088 GGGCCTGACCTCTACACACCCAGGAGGACCGCATGACTCTGTGGCTCTCTACCTTTA 2147
440 rLysAsnHisSerLeuAlaPheValGlyThrLysSerGlyLysLeuLysLysIleArgVa 460
2148 CAACGGCTACAGCTGGTGTGTTTGTGGGACTAAGAGTGCAGAGTGAAGAAAGGTAAAGT 2207
460 lAspGlyProArgGlyAsnAlaLeuGlnTyrlGlu-----ThrValGlnVa 475
2208 C-----TATGAGTTTCAGATGCTCCCAATGCCATTACCT 2240

QY 475 lvalaspproglyprovalleuargaspmetalapheSerlyS---AspHisGluGlnLe 494  
Db 2241 CCTGACAAAGAGTCCCTCTGGAGGTAGCTATTGGTGGAGATTAACTATAGGCAACT 2300  
QY 494 utVrileMetSerGluArgGln 501  
Db 2301 TTATTTCTTGGGACAAAGG 2322

RESULT 2  
US-09-905-125A-169  
; Sequence 169, Application US/09905125A  
; Patent No. 6664376  
; GENERAL INFORMATION:  
; APPLICANT: Genentech, Inc.  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Cao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, A.  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth, J.  
; APPLICANT: Kijavini, Ivar J.  
; APPLICANT: Mather, Jennie P.  
; APPLICANT: Pan, James  
; APPLICANT: Pao, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William, I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: 10466-14  
; CURRENT APPLICATION NUMBER: US/09/905,125A  
; PRIOR FILING DATE: 2001-07-12  
; PRIOR APPLICATION NUMBER: PCT/US00/04414  
; PRIOR FILING DATE: 2000-02-22  
; PRIOR APPLICATION NUMBER: US 60/143,048  
; PRIOR FILING DATE: 1999-07-07  
; PRIOR APPLICATION NUMBER: US 60/145,698  
; PRIOR FILING DATE: 1999-07-26  
; PRIOR APPLICATION NUMBER: US 60/146,222  
; PRIOR FILING DATE: 1999-07-28  
; PRIOR APPLICATION NUMBER: PCT/US99/20594  
; PRIOR FILING DATE: 1999-09-08  
; PRIOR APPLICATION NUMBER: PCT/US99/20944  
; PRIOR FILING DATE: 1999-09-13  
; PRIOR APPLICATION NUMBER: PCT/US99/21090  
; PRIOR FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: PCT/US99/21547  
; PRIOR FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: PCT/US99/23089  
; PRIOR FILING DATE: 1999-10-05  
; PRIOR APPLICATION NUMBER: PCT/US99/28214  
; PRIOR FILING DATE: 1999-11-29  
; PRIOR APPLICATION NUMBER: PCT/US99/28313  
; PRIOR FILING DATE: 1999-11-30  
; PRIOR APPLICATION NUMBER: PCT/US99/28564  
; PRIOR FILING DATE: 1999-12-02  
; PRIOR APPLICATION NUMBER: PCT/US99/28565  
; PRIOR FILING DATE: 1999-12-02  
; PRIOR APPLICATION NUMBER: PCT/US99/30095  
; PRIOR FILING DATE: 1999-12-16  
; PRIOR APPLICATION NUMBER: PCT/US99/30911  
; PRIOR FILING DATE: 1999-12-20

; PRIOR APPLICATION NUMBER: PCT/US99/30999  
; PRIOR FILING DATE: 1999-12-20  
; PRIOR APPLICATION NUMBER: PCT/US00/00219  
; PRIOR FILING DATE: 2000-01-05  
; NUMBER OF SEQ ID NOS: 423  
; SEQ ID NO 169  
; LENGTH: 2477  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-905-125A-169  
Alignment Scores:  
Pred. No.: 8.8e-138 Length: 2477  
Score: 1359.50 Matches: 271  
Percent Similarity: 69.88% Conservative: 84  
Best Local Similarity: 53.35% Mismatches: 124  
Query Match: 13.61% Indels: 31  
DB: 4 Gaps: 7  
US-09-964-956-13 (1-1896) x US-09-905-125A-169 (1-2477)  
QY 5 ProTrpAsnTrpThrCysLeuLeuSerHisLeuLeuMetValGlyMetGlySerSerThr 24  
Db 857 CCTGGAGGTGGACAGCGGCTCTGTG-GTCTCTCTCAGT-GGTCTGGGTGCTGCT--- 911  
QY 25 LeuLeuThrArgGlnProAlaProLeuSerGlnLysGlnArgSer-PheValThrPheAr 44  
Db 912 -----GGCCCCCAGCAGCGGCTGCTCAGTTCAGCAGCCTTTCCA 953  
QY 44 gGlyGluProAlaGlu---GlyPheAsnHisLeuValValAspGluArgThrGlyHisIl 63  
Db 954 CTCTGAGATCTGCTGCTGAGCTTCAACCTTCAACCTTCAACCTTCAACCTTCAACCTTCAACCTT 1013  
QY 63 eTyLeuGlyAlaValAsnArgGlyLeuLeuSerSerAspLeuLysValLeuValTh 83  
Db 1014 CTATGTGGGGCCCATCAACCGGTCTATAAGCTGACAGGCAACCTGACCATCCAGGTGGC 1073  
QY 83 rHisGluThrGlyProAspGluAspAsnProLysCysTyProProArgGlyLeuValGlnTh 103  
Db 1074 TCATAAGACAGGCGCAGAGGAGGACAAAGTCTGTTACCCGCCCTCATCTGTCAGGCC 1133  
QY 103 rCysAsnGluProLeuThrThrThrAsnAsnValAsnLysMetLeuLeuLeuLeuLeu 123  
Db 1134 CTGCAGCGAGTGTCTACCTCCACCAATGTCAACAAAGTGTCTCATCTGCTGCTGCTGCTGCT 1193  
QY 123 sGluAsnArgLeuLeuAlaCysGlySerLeuTyGlnGlyLeuLeuLeuLeuLeuLeu 143  
Db 1194 TGAGAACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1253  
QY 143 uGluAspLeuPheLysLeuGlyGluProTyHisLysLysGluHisTyLeuSerGlyVa 163  
Db 1254 GGATGACCTCTTTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1313  
QY 163 lAsnGluSerGlySerValPheGlyValIleValSerTySerAsnLeuAspAspLysLe 183  
Db 1314 CAACAAGACGGGCGCCATGTACGGGGTGATTGTGCGCTCTGAGGGTGAGGATGGCAAGCT 1373  
QY 183 uPheIleAlaThrAlaValAspGlyLysProGluTyPheProThrIleSerSerArgLy 203  
Db 1374 CTTTCATCGCAGCGCTGTGGATGGAGACAGATTAATCTCCGACCTGCTCCAGCGGAA 1433  
QY 203 sLeuThrLysAsnSerGluAlaAspGlyMetPheAlaTyValPheHisAspGluPheVa 223  
Db 1434 GCTGCCCGGAGACCTGAGTCTCAGCCATGCTGAGCTATGAGCTATGAGCTATGAGCTATGAGCT 1493  
QY 223 lAlaSerMetIleLeuLeuProSerAspThrPheThrIleLeuProAspPheAspIleTy 243  
Db 1494 CTCCTCTCTCATCAAGATCCCTTCAGACACCTGCGCCCTGGTCTCCCACTTTGACATCTT 1553  
QY 243 rTyValTyGlyPheSerSerGlyAsnPheValTyPheLeuThrLeuGlnProGluMe 263  
Db 1554 CTACATCTACGGCTTTGCTAGTGGGGGCTTTGCTACTTTCTACTTCTACTGCTCCAGCCGAG-- 1611



RESULT 3  
US-09-902-775A-189  
; Sequence 169, Application US/09902775A  
; Patent No. 6686451  
; GENERAL INFORMATION:  
; APPLICANT: Genentech, Inc.  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Botstein, David  
; APPLICANT: Desnovers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, A.  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth, J.

QY	5	ProT	Leu	Val	Met	Val	Gly	Met	Gly	Ser	Ser	Thr	24
		trp	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	
Db	857	CCCTGGAGGTGGACAGCGCTCTGTG-GTCTGCTCTCAAGT-GGTCTGGGTGGTGTCTGCT---	911										
QY	25	Leu	Leu	Thr	Arg	Gln	Pro	Ala	Pro	Leu	Ser	Gln	Arg
		Ser	Gln	Leu	Ser	Gln	Leu	Ser	Gln	Leu	Ser	Gln	Arg
Db	912	-----GGCCCCCAGAGCGGGCATGCTCCCTCAGTTCAGACACCTTCAC	953										

Alignment Scores:		
Pred. No.:	8.8e-138	2477
Score:	1359.50	271
Percent Similarity:	69.88%	Conservative: 84
Best Local Similarity:	53.35%	Mismatches: 124
Query Match:	13.61%	Indels: 31
DB:	4	Gaps: 7

QY 44 gGlyGluProAlaGlu---GlyPheAsnHisLeuValValAspGluArgThrGlyHis11 63  
Db 954 CTCTGAGATCGGTGACCTTCAACACCTTGACCGTCCACCAAGGAGCGGGCGCT 1013  
QY 63 eTyLeuGlyAlaValAsnArgileTyrylsLeuSerSerAspLeuValLeuValth 83  
Db 1014 CTATGTGGGGCCCATCAACCGGTCTATAAGCTGACAGCAACCTCACCATCCAGGTGC 1073  
QY 83 rHisGluThrGlyProAspGluAspAsnProLysCysTyProProArgileValGlnth 103  
Db 1074 TCATAAGACAGCGCCAGAGAGACACAAAGTCTCGTTACCGCCCTCATGTGCAGCC 1133  
QY 103 rCysAsnGluProLeuThrThrThrAsnAsnValAsnLysMetLeuLeuLeuAspTyryl 123  
Db 1134 CTCACGCGAGTCTCACCTCCACCAACATGTCACAAAGCTGCTCATCATGACTACTC 1193  
QY 123 sGluAsnArgLeuLeuAlaCysGlySerLeuTyGlnGlyLeCysValLeuLeuArgle 143  
Db 1194 TGAGAACCGCTCTGCTGGCTGTGGAGCCTTACACAGGGGTCTGCAAGCTGCTGGCT 1253  
QY 143 uGluAspLeuPheLeuLeuGlyGluProTyryHisLysLysGluHisTyryLeuSerGlyVa 163  
Db 1254 GGATGACCTCTTCATCTGCTGGAGCCATCCCAAGAGGAGCAGCTACTCTGTCCAGTGT 1313  
QY 163 lAsnGluSerGlySerValPheGlyValleValSerTyrySerAsnLeuAspAspyle 183  
Db 1314 CAACAAGCGGACCATGTACCGGTGATGTGGCTCTGAGGTGAGGTGCGAAGCT 1373  
QY 183 uPheileAlaThrAlaValaspGlyLysProGluTyryPheProThrIleSerSerArgly 203  
Db 1374 CTTTCATCGGACGGCTGTGATGGAGGAGGAGGATTACTTCCGAGCCCTGTCCAGCGGAA 1433  
QY 203 sLeuThrLysAsnSerGluAlaaspGlyMetPheAlaTyryValPheHisAspGluPheVa 223  
Db 1434 GCTGCCCGAGACCCCTGAGGCTTCACCCATGCTGAGTATGAGTACACAGCGATTTGT 1493  
QY 223 lAlaSerMetIleLysileProSerAspThrPheThrIleIleProAspPheAspilety 243  
Db 1494 CTCCTCTCTCATCAAGATCCCTTCAGACACCCCTGGCCCTGGTCTCCACCTTGACATCT 1553  
QY 243 rTyryValTyGlyPheSerSerGlyAsnPheValTyryPheLeuThrLeuGlnProGluMe 263  
Db 1554 CTACATCTACGGTTTGTAGTGGGGCTTGTCTACTTCTTCTACGTCCAGCCCGAG-- 1611  
QY 263 tValSerProProGly-----SerThrThrLysGluGlnValTyryThrSerLysLe 280  
Db 1612 ----ACCCCTGAGGTGTGCCATCACTCCGCTGGAGACCTTCTACACCTCAGCAT 1667  
QY 280 uValArgLeuCysLysGluAspThrAlaPheAsnSerTyryValGluValProIleGlyCy 300  
Db 1668 CGTGGCGCTCTGCAAGGATGACCCCAAGTTCCACTCATAGTCTGCTGCTGCTTCCGCTG 1727  
QY 300 sGluArgSerGlyValGluTyryArgLeuGlnAlaAlaTyryLeuSerLysAlaGlyAl 320  
Db 1728 CACCGGGCGGGTGAATACCGCTCTGCGAGGTGCTTACTGCGCAAGCTGGGA 1787  
QY 320 aValLeuGlyArgThrLeuGlyValHisProAspAspLeuLeuPheThrValPheSe 340  
Db 1788 CTCACCTGGCCAGGCTTCAATACACAGCAGGAGCATGTACTCTTTGCCATCTTCTC 1847  
QY 340 rLysGlyGlnLysArgLysMetLysSerLeuAspGluSerAlaLeuCysallePhelele 360  
Db 1848 CAAGGCGAAGAGAGATCAACACCGCCGAGTACTGCGCTGTGCTTCCCTAT 1907  
QY 360 uLysGlnIleAsnAspArgileLysGluArgLeuGlnSerCysTyryArgGlyGluGlyTh 380  
Db 1908 CCGGGCCATCACTTGAGATCAAGGAGCGCTGCTGCTGCTTACAGCGCGAGGCGAA 1967  
QY 380 rLeuAspLeuAlaTrpLeuLysValLysAspIleProCysSerSerAlaLeuLeuThrll 400  
Db 1968 CCTGGAGCTCAACTGGGTGTGGGAAAGGAGCTCCAGTGCAGGAAGCGCTGCCCAT 2027  
QY 400 eAspAspAsnPhcCysGlyLeuAspMetAsnAlaProLeuGlyValSerAspMetValAr 420

Db 2028 CGATGATAACTTCTGTGGACTGGACATCAACACCCCTGGAGGCTCAACTCCAGTGGA 2087  
QY 420 sGlylleProValPheThrGluAspArgAspArgMetThrSerValIleAlaTyryValTy 440  
Db 2088 GGGCTTACCTGACCTGTACACCAACAGGAGCGGATGACCTCTGTGGCTCTTACGTTA 2147  
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Db 2148 CAACGGCTACAGCTGTTTGTGGGACTAAGAGTGGCAAGCTGAAAGAGGTAAAGAGT 2207  
QY 460 lAspGlyProArgLysAsnAlaLeuGlnTyryGlu-----ThrValGlnVa 475  
Db 2208 C-----TATGAGTTTCAGATGCTTCCCAATGCCATTCACCT 2240  
QY 475 lValAspProGlyProValLeuArgAspMetAlaPheSerLys---AspHisGluGlnLe 494  
Db 2241 CCTCAGCAAGAGTCCCTCTTGGAGGTAGCTATGTGGAGATTAACTATAGGCAACT 2300  
QY 494 uTyrylleMetSerGluArgGln 501  
Db 2301 TTATTTCTTGGGGAACAAGG 2322  
  
RESULT 4  
US-09-181-706-1  
; Sequence 1, Application US/09181706  
; Patent No. 6130068  
; GENERAL INFORMATION:  
; APPLICANT: Melanie K. Spriggs, Michael R. Comeau,  
; APPLICANT: Robert F. DuBose, Richard S. Johnson  
; TITLE OF INVENTION: VIRAL ENCODED SEMAPHORIN PROTEIN  
; TITLE OF INVENTION: RECEPTOR DNA AND POLYPEPTIDES  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Janis C. Henry  
; STREET: 51 University St.  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: US  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/181,706  
; FILING DATE: October 28, 1998  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/958,598 (converted to a  
; APPLICATION NUMBER: Provisional, see below)  
; FILING DATE: October 28, 1997  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: --to be assigned-- (USN 08/958,598  
; APPLICATION NUMBER: conversion to Provisional application)  
; FILING DATE: October 26, 1998  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Henry, Janis C.  
; REGISTRATION NUMBER: 34,347  
; REFERENCE/DOCKET NUMBER: 2631-A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206)470-4189  
; TELEFAX: (206)233-0644  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4707 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA

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; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..4707
US-09-181-706-1

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Alignment Scores:

Pred. No.:	4,268-136	Length:	4707
Score:	1349.00	Matches:	480
Percent Similarity:	39.78%	Conservative:	291
Best Local Similarity:	24.77%	Mismatches:	551
Query Match:	13.50%	Indels:	576
DB:	3	Gaps:	74

US-09-964-956-13 (1-1896) x US-09-181-706-1 (1-4707)

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Qy	             	
92	AsnProLysCysTyrProProArgIleValGlnThrCysAsnGluProLeuThrThrThr	111
Db	             	
256	-----AACTGCACAGAGCCGGTCTCGCTGGCG	282
Qy	             	
112	-----AsnAsnValAsnLysMetLeuLeuLysAspTyrLys	123
Db	             	
283	CCCCCGCGCGGCCCGCGGAGCAGCTTCAGCAAG--CTGCTGCTGCCCTACC	339
Qy	             	
124	GluAsnArg-----LeulleAlaCysGlySerLeuTyrGlnGlyIle	137
Db	             	
340	GAGGGCGCGCGCCTCGGGGGCTGCTGCTCATCCGGCTGGAGCTTCGACGGCGCGC	399
Qy	             	
138	CysLysLeuLeuArgLeuGluAspLeuPheLysLeuGlyGluProTyrHisLysLysGlu	157
Db	             	
400	TGCGAGGTGCGGCCCTGGGCAACTG-----AGCCGCAAC	435
Qy	             	
158	HisTyrLeuSerGlyVal-----AsnGluSerGlySerValPheGlyVal	172
Ddb	             	
436	TCCCTGCCAACAGCGCACCGAGGTGTGCTGTCACCCCGCAGGCGCTCGACGGCGCGTG	495
Qy	             	
173	IleValSerTyrSerAsnLeuAspAspLysLeuPheIleAla-----	186
Ddb	             	
436	GTTATACCG---GCGGGCGGAACAACCGCTGGTACTCTGGCGTGGCGGCACCTACGTG	552
Qy	             	
187	-----ThrAla	188
Db	             	
553	CTGCTGAGCGGAGACGGCGGCGCTGCAACCCCGCGGCATCCGACACGACACGGCC	612
Qy	             	
189	ValAspGlyLysProGluTyrPheProThrIleSerSerArgLysLeuThrLysAsnSer	208
Ddb	             	
613	ATCGCGCTCAAAGGACCGAGGGCGCAGCGCTGCGCCACGACGAGCTGGCGCGCTCAAG	672
Qy	             	
209	GluAlaAspGlyMetPheAlaTyrValPheHisAspGluPheVal---AlaserMetile	227
Ddb	             	
673	CTGTGCGAGGCGGGCAGCTGCATCTCGTAGCGCCTTCTCTGGAACGGCAGCATC	732
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248	PheSerSerGlyAsnPheValTyrPheLeuThrLeuGlnProGluMetValSerProPro	267
Ddb	             	
757	TATACGAGCGC-----GCTGCCACCGCGTGGCCCGACGATGGCGCGCATCGCG	804
Qy	             	
268	GlySerThrThrLysGluGlnValTyrThrSerLysLeuValArgLeuCysLysGluAasp	287
Ddb	             	
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Qy	             	
288	ThrAlaPheAsnSerTyrValGluValProIleGlyCysGluArgSerGlyValGlu---	306
Db	             	
817	GTGCTGTTCCAGGCG-----CAGGCATCCTCTGACTGCGGCCACCGGCCACCCCGACGCG	870

Db	1579	TTC-----TCTCCAAGACACTCAAGTGCATGTGTGAAGATGTGGACTCTAGC	1626
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Db	1627	-----AGGAGCTCTGC-----	1638
Qy	690	PheGlnGluGlyArgValLysLeuProGluAspCysProGlnLeuLeuArgValAspLys	709
Db	1638	-----	1638
Qy	710	IleLeuValProValGluValIleLysProIleThrLeuLysAlaLysAsnLeuProGln	729
Db	1639	-----CAGATAAAAGTCAG-----	1653
Qy	730	ProGlnSerGlyGlnArgGlyTyrGluCysIleLeuAsnIleGlnGlySerGluGlnArg	749
Db	1654	CCCAACCGG-----ACCTGCACCTGTAGCATC-----	1680
Qy	750	ValProAlaLeuArgPheAsnSerSerValGlnCysGlnAsnThrSerTyrSerTyr	769
Db	1681	-----CCAACGACGACCACTCAAGATGTTTCAGTTGTCAACGTGATGTTCTCTCTTC	1734
Qy	770	GluGlyMetGluIleAsnAsnLeuProValGluLeuThrValTyrAsn-----Gly	787
Db	1735	GGTTCT-----TGAATTTATCAGAC	1755
Qy	788	HisPheAsnIleAspAsnProAlaGlnAsnLysValHisLeuTyrLysCysGlyAlaMet	807
Db	1756	AGATTCAACTTTTACCAAC-----TGCTCATCATTA	1785
Qy	808	ArgGluSerCysGlyLeuCysLeuLysAlaAspProAspPheAlaCysGlyTyrCysGln	827
Db	1786	AAAGAA-----TGCCAGCATGGTAGAACT-----GGCTGGCGGTGGTGTAAA	1830
Qy	828	GlyProGlnCysThrLeuArgGlnHisCysProAlaGlnGluSerGlnTrpLeuGlu	847
Db	1831	AGTGCAAGAGGTGT-----	1845
Qy	848	LeuSerGlyAlaLysSerLysCysThrAsnProArgIleThrGluIleIleProValThr	867
Db	1846	-----ATCCACCCCTTCACA	1860
Qy	868	GlyProArgGluGlyThrLysValThrIleArgGlyGluAsnLeuGlyLeuGluPhe	887
Db	1861	GCT-----	1863
Qy	888	ArgAspIleAlaSerHisValLysValAlaGlyValGluCysSerProLeuValAspGly	907
Db	1864	-----TCT	1875
Qy	908	TyrIleProAlaGluGlnIleValCysGluMet-----GlyGluAla	921
Db	1876	GATTATGAGAGAAACCGAAGACAGTGTCCAGTGTGCGAGAGACATCAGGAGGAGGA	1935
Qy	922	LysProSerGlnHisAlaGlyPheValGluIleCysValAlaValCysArgProGluPhe	941
Db	1936	AGACCAAGGAGAACAGGG-----AACAGA	1962
Qy	942	MetAlaArgSerSerGlnLeuTyrTyrPheMetThrLeuThrLeuSerAspLeuLysPro	961
Db	1963	ACCAACCGGCTTTACAGTCTTCTAC-----ATTAGTCCATTGAGCCA	2007
Qy	962	SerArgGlyProMetSerGlyGlyThrGlnValThrIleThrGlyThrAsnLeuAsnAla	981
Db	2008	CAGAAAGTATCGACATTAGGGAAGAACACGTGTAGTAAACGGGACAAACTTTACCCGG	2067
Qy	982	GlySerAsnVal---ValValMetPheGlyLysGlnProCys-----	994
Db	2068	GCATCGACATCACAAATGATCTGAAAGAACACAGTACTGTGATAAGGATGTATACAG	2127
Qy	995	IlePheHisArgSerProSerTyrIleValCysAsnThrThrSerSerAspGluVal	1014
Db		-----	

Db	2128	GTTAGCCATGTGCTAAATGACACCACCATGAATAATCTCTTTCATCAAGCCGGAAA---	2184
Qy	1015	LeuGluMetLys---ValSerValGlnValAspArgAlaLysIleHisGlnAspLeuVal	1033
Db	2185	---GAAATGAAGGATGTGTGTATCCAGTTTGTATGCTGGGAACTGCTCTTCTGTGGATCC	2241
Qy	1034	PheGlnTyrValGluAspProThrIleValArgIleGluProGluTyrSerIleValSer	1053
Db	2242	TTATCTCATATGCTCTCCCATTTGTTCCCTTATATTTCTCTGCTACCATCTGGATCAGT	2301
Qy	1054	GlyAsnThrProIleAlaValTyrPglyThrHisLeuAspLeuIleGlnAsnProGlnIle	1073
Db	2302	GTTGTGTCAAATATTAACCATGATGGCAGAAATTTTGTATGTAATGACAAC-----TTA	2355
Qy	1074	ArgAlaLysHisGlyGlyLysGluHisIleAsnIleCysGluValLeuAsnAlaThrGlu	1093
Db	2356	ATCATTTTCATGAATTAAGAAACATAAATGCTCTGTAATATTTGTGTGCGACTTAC	2415
Qy	1094	MetThrCysGlnAlaProAlaLeuAlaLeuGlyProAspHisGlnSerAspLeuThrGlu	1113
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Qy	1134	Thr-----AsnPheThrTyrTyrProAsnProValPheGluAlaPheGly	1148
Db	2491	ACTTACTTGATGTGGAAACCTCGAGATCGGAGGACCCCGAGATTACGGGTATCGG	2550
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Qy	1189	ProCysThrValThrVal-----SerAspValGlnLeuLeuCysGluSerProAsn	1205
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Qy	1223	ProGlyMetValTyrIleAlaProAspSer---ProLeuSerLeuProAlaIleValSer	1241
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Db	2851	CTCCCTGTC-----TTGCTAGTATGTCATTTTTCGCGCGTGGGGTGACAGG	2901
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Qy	1282	GluSerArgValAlaLeuGluCysLysGluAlaPheAlaGluLeuGlnThrAspIleHis	1301
Db	2953	GAAAGGAGCTCGGAAAGAGATACGTGACCGCTTTGCTGAGCTGAGATGATATAATTG	3012
Qy	1302	GluLeuThrSerAspLeuAspGlyAlaGly---IleProPheLeuAspTyrArgThrTyr	1320
Db	3013	GATGTG-----GTTGATAGTTTTGGAACCTGTTTCTCTTCTGACTACAAACATTTT	3063
Qy	1321	ThrMetArgValLeuPhePro-----GlyIleGluAspHisProValLeuArgAspLeu	1338
Db	3064	GCTCTGAGAACTTTCTTCTCCCTGAGTCAGGTGGCTTCAACCCACATCTTCACTGAATATG	3123

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Qy 1689 GlnLysPheValaspLeuPheGluThrIlePheSerThralahisArgGlySerAla 1708
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Qy 1829 MetAsnalaTyrrLeuAlaGluInSerArgMechHisMetAsnGluPheAsnThrMetSer 1848
Db 4498 ATGGAAGAATTTTTAACTCAGGATCTTAAAGAAACATGAAAATGAATTAATGAAGAAGTG 4557
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Db 4558 GCCTTGACAGAAATTTACAATACATCGTAAATATTTTGTGATGAGATCTCTAAATAACTA 4617
Qy 1869 AspHisasp-----AspGlnCysGlyLysGlnLysLeualaTyrrLysLeu 1883
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RESULT 5
US-09-458-791-1
; Sequence 1, Application US/09458791
; Patent No. 6174689
; GENERAL INFORMATION:
; APPLICANT: Spriggs, Melanie
; TITLE OF INVENTION: VIRAL ENCODED SEMAPHORIN PROTEIN
; RECEPTOR DNA AND POLYPEPTIDES
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Janis C. Henry
; STREET: 51 University St.
; CITY: Seattle
; STATE: WA
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS-DOS/Windows 95
; SOFTWARE: Word for Windows 95, 7.0a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/458,791
; FILING DATE: 10-Dec-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/958,598
; FILING DATE: 28-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Henry, Janis C
; REGISTRATION NUMBER: 34,347
; REFERENCE/DOCKET NUMBER: 2631
; TELECOMMUNICATION INFORMATION:

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## RESULTS

US-09-458-791-1  
Sequence 1, Application US/09458791  
Patent No. 6174689  
GENERAL INFORMATION:  
APPLICANT: Spriggs, Melanie  
TITLE OF INVENTION: VIRAL ENCODED SEMAPHORIN PROTEIN  
RECEPTOR DNA AND POLYPEPTIDES  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Janis C. Henry  
STREET: 51 University St.  
CITY: Seattle  
STATE: WA  
COUNTRY: US  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: MS-DOS/Windows 95  
SOFTWARE: Word for Windows 95, 7.0a  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/458,791  
FILING DATE: 10-Dec-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/958,598  
FILING DATE: 28-OCT-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Henry, Janis C  
REGISTRATION NUMBER: 34,347  
REFERENCE/DOCKET NUMBER: 2631  
TELECOMMUNICATION INFORMATION:

Qy	1339	GluValProGlyTyrArgGlnGluArgValGluIysGlyLeuLysLeuPheAla-----	1355
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Db	3172	GCCTTAATCTGTAAATAAGCTTCTGTGTACTGTATCCACACCCCTTGAAGACGAGAAG	3231
Qy	1377	SerPheSerMetArgAspArgGlyAsnValAlaSerIleuLeuMetThrValLeuGlnSer	1396
Db	3232	AACTTTCTGTGAAGGACAGTGTCTGTTTGGCTCTCTCTTAACCAATTCACCTGCAAAACC	3291
Qy	1397	LysLeuGluTyrAlaThrAspValLeuGlnLeuLeuAlaAspLeuIleAspLysAsn	1416
Db	3292	AAGCTGTCTACCTGACCAGCATCTAGAGGTCTGACCGAGGACTTGATGGAACAGTGT	3351
Qy	1417	LeuGluSerLysAsnHisProLysLeuLeuLeuArgArgThrGluSerValAlaGluLys	1436
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Qy	1437	MetLeuThrAsnTrpPheThrPheLeuLeuTyrLysPheLeuLysGluCysAlaGlyGlu	1456
Db	3406	CTCTCACAAATGGATGCGGTCTGCTTCTGGATTCTCCGGGAGACTGTCGCGAG	3465
Qy	1457	ProLeuPheSerLeuPheCysAlaIleLysGlnGlnMetGluLysGlyProIleAspAla	1476
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Qy	1477	IleThrGlyGluAlaArgTyrSerLeuSerGluAspLysLeuIleArgGlnGlnIleAsp	1496
Db	3526	ATCACTTGCAAGCCCTGTACACACTTAATGAAGACTGGCTGTGTGGCAGGTTCGGAA	3585
Qy	1497	TyrLysThrLeuValLeuSerCysVal-----SerProAspAsnAlaAsnSerPro	1513
Db	3586	TTCACTACTGTGGCATTAAACGTGCTTTGAAAAATCCCGAAACGAGATGCAGAT	3645
Qy	1514	-----GluValProValLysIleLeuAsnCysAspThrIleThrGlnValLysGlu	1530
Db	3646	GTCTGTCCGAATATTTTCAGTCAATGTCTCGACTGTGACACCATTTGGCCAAAGCAA	3705
Qy	1531	LysIleLeuAspAlaIlePheLysAsnValProCysSerHisArgProLysAlaAlaAsp	1550
Db	3706	AAGATTTCGAAGCATCTTAAGCAAAATGGCTCTCTTATGGACTTCAGCTTAATGA	3765
Qy	1551	MetAspLeuGluTrpArgGlnGlySerGlyAlaArgMetIleLeuGlnAspGluAspIle	1570
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Db	3826	TCCGTGATCTTTGAATGTAATCACCAAGCTTAACCAATTTGCCCTATGAGATATCA	3885
Qy	1591	AspGlySerValAlaLeuValSerLysGlnValThrAlaTyrAsnAlaValAsnAsn	1610
Db	3886	AATGGATCCACTATAAAAGTC-----	3906
Qy	1611	SerThrValSerArgThrSerAlaSerLysTyrGluAsnMetIleArgTyrThrGlySer	1630
Db	3907	-----TTTGAAGATGACCAATTTTACTTCAGAT	3936
Qy	1631	ProAspSerLeuArgSerArgThrProMetIleThrProAspLeuGluSerGlyValLys	1650
Db	3937	GTGGAGTACTCGGATGACCACTGGCATTTGATTTTACAGATTCCGAAGCA-----	3987
Qy	1651	MetTrpHisLeuValLysAsnHisGluHisGlyAspGlnLysGluGlyAspArgGlySer	1670
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Qy	1671	Lys-----MetValSerGluIleTyrIleuThrArgLeuLeuAlaThrLysGlyThrLeu	1688
Db	4024	CACAAGTTCAAAAGTAAAGAAATGTATCTGCAAAAGTGTCTGCGACCAAGGTGGCAAT	4083

TELEPHONE: (206)470-4189  
TELEFAX: (206)233-0644  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4707 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..4707  
SEQUENCE DESCRIPTION: SEQ ID  
US-09-458-791-1

Alignment Scores:

Pred. No.:	4.26e-136	Length:	4707
Score:	1349.00	Matches:	480
Percent Similarity:	39.78%	Conservative:	291
Best Local Similarity:	24.77%	Mismatches:	531
Query Match:	13.50%	Indels:	576
DB:	3	Gaps:	74

US-09-964-956-13 (1-1896) x US-09-458-791-1 (1-4707)

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Qy	92	AsnProLysCysTyrProProArgIleValGlnThrCysAsnGluProLeuThrThrThr	111
Dd	256	-----AACTGCACAGACGGGTCTCGTCGGCG 282	
Qy	112	-----AsnAsnValAsnLysMetLeuLeuleaspTyrIlys	123
Dd	283	CCCCCGCGCGCCCGCCCGGAGCAGCTTCAGCAAG---CTGCTGTCTGCCCTACCGC	339
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Qy	158	HisTyrLeuSerGlyVal-----AsnGluSerGlySerValPheGlyVal	172
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Qy	187	-----Thrala	188
Dd	553	CTGCTGTAGCGGAGACGGCGGTGTCAAACCCCGCGCATCCGACACGACACGGCC	612
Qy	189	ValAspGlyLysproGluTyrPheProThrIleSerSerArgLysLeuThrIlysAsnSer	208
Dd	613	ATCGCCTCAAGAACAACGAGGGGGCGGCGCTGTGCCACGACGAGGTGGGGCGCTCAAG	672
Qy	209	GluAlaaspGlyMetPheAlatyrValPheHisaspGluPheVal---AlaserMetille	227
Dd	673	CTGTGCGAGGGCGCGGACGCTGCACCTTCGTGACGCGCTTTCTCTGGAACGGCAGCATC	732
Qy	228	LysIleProSerAspThrPheThrIleIleProaspPheAspiletyrTyrValTyrGly	247
Dd	733	TACTTCCCC-----TACTTACCCCTAACAC	756
Qy	248	PheSerSerGlyAsnPheValTyrPheLeuThrLeuGlnProGluMetValSerProPro	267



2953 GAAAGCGAGCTCCGGAAGAGATACGTGACGCGCTTTGCTGAGCTGCGAGATGATAAATTG 3012
1302 GluLeuThrSerAspLeuAspGlyAlaGly---lleProPheLeuAspTyrArgThrTyr 1320
3013 GATGTG-----GTTGATAGTTTGGAACTGTTCCCTTCCTTGACTACAAACATTTT 3063
1321 ThrMetArgValLeuPhePro-----GlyIleGluAspHisProValLeuArgAspLeu 1338
3064 GCTCTGAGAACTTTCTTCCCTGAGTCAGGTGCGTCTCACCCACACTCTTCACTGAGAGATATG 3123
1339 GluValProGlyTyrArgGluValGlyValGlyValGlyLeuLeuLeuPheAla----- 1356
3124 -----CATACAGAGAGCGCCACACAGCAAGATGAAGTCTCACAGCTTTGGAT 3171
1357 GlnLeuIleAsnAsnLysValPheLeuLeuSerPheIleArgThrLeuGluSerGlnArg 1376
3172 GCCCTAATCTGTAATAAGCTTTCTTCTTACTGTCTACACACCCCTTGAAGACAGAAAG 3231
1377 SerPheSerMetArgAspArgGlyAsnValAlaSerLeuIleMetThrValLeuGlnSer 1396
3232 AACTTTTCTGTGAAGGACAGGTGCTGTTGCTTCCCTTCCCTTAACCATGCTCAACCAACC 3291
1397 LysLeuGluTyrAlaThrAspValLeuLysGlnLeuLeuAlaAspLeuIleAspLysAsn 1416
3292 AAGCTGGTCTACCTGACCAGCATCTAGAGGTGCTGACCAGGACTTGTATGGAACAGTGT 3351
1417 LeuGluSerLysAsnHisProLysLeuLeuLeuArgThrGluSerValAlaGluLys 1436
3352 -----AGTAACATGACGCCGAACACTCATGCTGACAGCGAGTCCGCTGCGTGAAGAA 3405
1437 MetLeuThrAsnTyrPheLeuLeuTyrLysPheLeuLysGluCysAlaGlyGlu 1456
3406 CTCCTCACAAAGTGGTCCGCTGCTGCTTCTGGAATTTCTCCGGAGACTGTCGGAGAG 3465
1457 ProLeuPheSerLeuPheCysAlaIleLysGlnMetGluLysGlyProIleAspAla 1476
3466 CCCTTCTATTGCTGGTGACGACTCTGAAACCCAGAAATTAACAAGGGTCCGCTGGATGA 3525
1477 IleThrGlyGluAlaArgTyrSerLeuSerGluAspLysLeuIleArgGlnIleAsp 1496
3526 ATCATTCTCAAGCCCTGTACACACTTAATGAGACTGCTGCTGTCGACAGTTCGGAA 3585
1497 TyrLysThrLeuValLeuSerCysVal-----SerProAspAsnAlaAsnSerPro 1513
3586 TTCAGTACTGTGGCATTAACGCTGCTTTGAAATAATCCCGGAAACGAGAGTGCAGAT 3645
1514 -----GluValProValLysIleLeuAsnCysAspThrIleThrGlnValLysGlu 1530
3646 GTCTGTGGAATATTTCAGTCAATGTTCTGACTGTGACACCATTTGGCCAGCCAGAA 3705
1531 LysIleLeuAspAlaIlePheLysAsnValProCysSerHisArgProLysAlaAlaAsp 1550
3706 AAGATTTTCCAAGCATTTTAAGCAAAAATGCTCTCTCTATGGAAGTTCAGCTTAATGAA 3765
1551 MetAspLeuGluTyrArgGlnGlySerGlyAlaArgMetIleLeuGlnAspGluAspIle 1570
3766 ATGTGCTTGAAGCTTCAATGGGCACACAGCAAGAAAGACTTCTGGAATCGACAGTTC 3825
1571 ThrThrLysIleGluAsnAspTrpLysArgLeuAsnThrLeuAlaHisTyrGlnValPro 1590
3826 TCCGTGATCTTGAAGATGAATCACCAGCTAAACACCATTTGGCCACTATGAGATATCA 3885
1591 AspGlySerValValAlaLeuValSerLysGlnValThrAlaTyrAsnAlaValAsnAsn 1610
3886 AATGGATCCATATAAAGTC----- 3906
1611 SerThrValSerArgThrSerAlaSerLysTyrGluAsnMetIleArgTyrThrGlySer 1630
3907 -----TTTGAAGATGACAAATTTACTTCAGAT 3936
1631 ProAspSerLeuArgSerArgThrProMetIleThrProAspLeuGluSerGlyValLys 1650

3937 GTGAGTACTCGATGACACCTGCCATTTGATTTTACCAGATTCGAAGCA----- 3987
1651 MetTrpHisLeuValLysAsnHisGluHisGlyAspGlnLysGluGlyAspArgGlySer 1670
3988 ---TTCGAAGATGTGCAAGGAAGAGACAT-----CGAGGGAAG 4023
1671 Lys-----MetValSerGluIleTyrLeuThrArgLeuLeuAlaThrLysGlyThrLeu 1688
4024 CACAAGTTCAAAGTAAAGAAATGATCTGACAAGAGCTCTGTGACCAAGGTGGCAATT 4083
1689 GlnLysPheValAspAspLeuPheGluThrIlePheSerThrAlaHisArgGlySerAla 1708
4084 CATTTCTGTCTTGAAAACTTTTGAAGCAATTTGGAGTTTACCCAAC-----AGCAGA 4137
1709 LeuProLeuAlaIleLysTyrMetPheAspPheLeuAspGluGlnAlaAspLysHisGly 1728
4138 GTCTCAATTTGCTATATAAATACTTTGTGACTTTTGGACGCCAGCTGAAAAACAAAAA 4197
1729 IleHisAspProHisValArgHisThrTrpLysSerAsnCysLeuProLeuArgPheTrp 1748
4198 ATCACAGATCTCTGACGCTCGTACATATTTGGAACAAACACAGCTTCTCTCGCTTCTCG 4257
1749 ValAsnMetIleLysAsnProGlnPheValPheAspIleHisLysAsnSerIleThrAsp 1768
4258 GTAAACATCTCTGAAGAACCTCAGTTTGTCTTTGACATTTAAGAGAGACACCATATAGAC 4317
1769 AlaCysLeuSerValValAlaGlnThrPheMetAspSerCysSerThrSerGluHisArg 1788
4318 GCGCTGTTGTGAGTATGCGCAGGCAATTCATGGATGCAATTTCTCTCACAGAGCAGCA 4377
1789 LeuGlyLysAspSerProSerAsnLysLeuLeuTyrAlaLysAspIleProSerTyrLys 1808
4378 CTAGGAAGAGAGACCAACTAATAGCTTCTATGCAAGGATATCCCAACCTACAAA 4437
1809 AsnTrpValGluArgTyrTyrSerAspIleGlyLysMetProAlaIleSerAspGlnAsp 1828
4438 GAAGAAGTAAATCTTTATCAAGCAATCAGGATTTGCTCCATTCATCTCCCTCAGAA 4497
1829 MetAsnAlaTyrLeuAlaGluGlnSerArgMetHisMetAsnGluPheAsnThrMetSer 1848
4498 ATGGAAGAAATTTTAACTCAGGAATCTAAGAAACATGAAATTAATTAATGAAGAAGTG 4557
1849 AlaLeuSerGluIlePheSerTyrValGlyLysTyrSerGluGluIleLeuGlyProLeu 1868
4558 GCCTTGACAGAAATTTACAAATACATCGTAAATAATTTTGTATGAGATTTCTAATAACTA 4617
1869 AspHisAsp-----AspGlnCysGlyLysGlnLysLeuAlaTyrLysLeu 1883
4618 GAAAGAGAACGAGGCTGGAAGAGCTCAGAAACAACTCTTGCAATGTAAGATC 4671

RESULT 6

US-09-459-066-1
Sequence 1, Application US/09459066
Patent No. 6187909
GENERAL INFORMATION:
APPLICANT: Spriggs, Melanie
TITLE OF INVENTION: VIRAL ENCODED SEMAPHORIN PROTEIN
TITLE OF INVENTION: RECEPTOR DNA AND POLYPEPTIDES
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESS: Janis C. Henry
STREET: 51 University St.
CITY: Seattle
STATE: WA
COUNTRY: US
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS/Windows 95
SOFTWARE: Word for Windows 95, 7.0a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/459,066



```

1 FILING DATE:
2 CLASSIFICATION:
3 PRIOR APPLICATION DATA:
4 APPLICATION NUMBER: 08/958,598
5 FILING DATE:
6 ATTORNEY/AGENT INFORMATION:
7 NAME: Henry, Janis C
8 REGISTRATION NUMBER: 34,347
9 REFERENCE/DOCKET NUMBER: 2631
10 TELECOMMUNICATION INFORMATION:
11 TELEPHONE: (206)470-4189
12 TELEFAX: (206)233-0644
13 INFORMATION FOR SEQ ID NO: 1:
14 SEQUENCE CHARACTERISTICS:
15 LENGTH: 4707 base pairs
16 TYPE: nucleic acid
17 STRANDEDNESS: double
18 TOPOLOGY: linear
19 MOLECULE TYPE: cDNA
20 HYPOTHETICAL: NO
21 ANTI-SENSE: NO
22 FEATURE:
23 NAME/KEY: CDS
24 LOCATION: 1..4707
25 US-09-459-066-1
26
27 Alignment Scores:
28 Pred. No.: 4,26e-136 Length: 4707
29 Score: 1349.00 Matches: 480
30 Percent Similarity: 39.78% Mismatches: 291
31 Best Local Similarity: 24.77% Indels: 591
32 Query Match: 13.50% Gaps: 76
33 DB: 3
34
35 US-09-964-956-13 (1-1896) x US-09-459-066-1 (1-4707)
36
37 QY 72 TyrLysLeuSerSerAspLeuLyLeValLeuValThrHisGluThrGlyProAspGluAsp 91
38 Db 208 TACAGCTGGAGCAGACGCCCTCGCGCTGTACCGGACCAACGGGCG----- 255
39 QY 92 AsnProLysCysTyrProProArgIleValGlnThrCysAsnGluProLeuThrThrThr 111
40 Db 256 -----AACTGCACAGAGCGGCTCTCGCTGGCG 282
41 QY 112 -----AsnAsnValAsnIysMetLeuLeuLeuAspTyrLys 123
42 Db 293 CCCCCCGCGCGCCCCCGCGCGGAGCAGCTTACGCAAG---CTGCTGCTGCCCTACCGC 339
43 QY 124 GluAsnA-r-----LeuIleAlaCysGlySerLeuTyrGlnGlyIle 137
44 Db 340 GAGGGGGCGCGCGCCTCGGGGGCTGTCTGCACCGCTGGACCTTCACCGGGGGCGCC 399
45 QY 138 CysLysLeuLeuArgLeuGluAspLeuPheLysLeuGlyCluProTyrHisLysLysGlu 157
46 Db 400 TCGAGGGTGGCGGCCCTGGGCAACCTG-----AGCCGCAAC 435
47 QY 158 HistYrLeuSerGlyVal-----AsnGluSerGlySerValPheGlyVal 172
48 Db 436 TCCCTGCACACGGGACCGGAGGTGTGTGTGTCGCCACCCCGCAGGSGCTCGACGGCGCGGTG 495
49 QY 173 lleValSerTyrSerAsnLeuAspLysLeuPheIleAla----- 186
50 Db 496 GTGTACCGC---GCGGGCCGGAACAACCGCTGGTACCTGGCGGTGCGCCGCCACTACGTG 552
51 QY 187 -----ThrAla 188
52 Db 553 CTGCCTGAGCGGAGACGGCGCGCTGCAACCCCGCGGCATCCGACACGACGACGGCG 612
53 QY 189 ValAspGlyLysProGluTyrPheProThrIleSerSerArgLysLeuThrLysAsnSer 208
54 Db 613 ATTCGGCTCAAGACACGAGGGGGCGAGCCTGGCCACGAGAGTGGGGGGCGCTCAAG 672

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Db 1462 -----GTACATTCAGAGAACTTAGAA--- 1482  
QY 571 SerGlnTyrAsnValLeuValLeuGluThrTyrAsnValProGluLeuSerAlaGly 590  
Db 1483 -----AACTGGCTGGATATTTCTCTGGA 1506  
QY 591 ValAsnCysThrPheGluAspLeuSerGluMetAspGlyLeuValValGlyAsnGlnIle 610  
Db 1506 ----- 1506  
QY 611 GlnCysTyrSerProAlaAlaLysGluValProArgIleIleThrGluAsnGlyAspHis 630  
Db 1507 -----GCAAAAGAGTGCCTAAAT--- 1527  
QY 631 HisValValGlnLeuLeuLysSerIysGluThrGlyMetThrPheAlaSerThrSer 650  
Db 1528 -----CAGATAATTCGAAGCAGTAAGAAAAGACTACAGTGACTATGGTGGGAAGC 1578  
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Db 1579 TTC-----TCTCCAGACACTCAAGTGCATGGTGAAGATGGAGATCTGAGC 1626  
QY 670 TyrArgCysHisTyrCysLysTyrArgHisValCysThrHisAspProLysThrCysSer 689  
Db 1627 -----AGGAGCTCTGC----- 1638  
QY 690 PheGlnGluGlyArgValLysLeuProGluAspCysProGlnLeuLeuArgValAspLys 709  
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QY 710 IleLeuValProValGluValIleLysProIleThrLeuLysAlaLysAsnLeuProGln 729  
Db 1639 -----CAGATAAAGTCAG 1653  
QY 730 ProGlnSerGlyGlnArgGlyTyrGluCysIleLeuAsnIleGlnGlySerGluGlnArg 749  
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QY 750 ValProAlaLeuArgPheAsnSerSerSerValGlnCysGlnAsnThrSerTyrSerTyr 769  
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Db 1735 GGTGCT-----TGGAATTTATCAGAC 1755  
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QY 828 GlyProGlyGlnCysThrLeuArgGlnHisCysProAlaGlnGluSerGlnTyrLeuGlu 847  
Db 1831 AGTCAAGAGGTGT----- 1845  
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Db 1846 -----ATCCACCCCTTCACA 1860  
QY 868 GlyProArgGluGlyGlyThrLysValThrIleArgGlyGluAsnLeuGlyLeuGluPhe 887  
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Db 1864 -----TCGACCTC-----TCT 1875  
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QY 922 LysProSerGlnHisAlaGlyPheValGluIleCysValAlaValCysArgProGluPhe 941  
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Db 1963 ACCAACCCAGGCTTTACAGTCTTCTAC-----ATTAAGTCCATTGAGCCA 2007  
QY 962 SerArgGlyProMetSerGlyGlyThrGlnValThrIleThrGlyThrAsnLeuAsnAla 981  
Db 2008 CAGAAAGATTCACACATTTAGGAAAGCAACGATAGTAGTAACCGGAGCAAACTTTACCCGG 2067  
QY 982 GlySerAsnVal---ValValMetPheGlyLysGlnProCys----- 994  
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Db 2128 GTTAGCCATGTCTAAATGACACCAACATGAAATCTCTCTCCATCAGCCGGA--- 2184  
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Db 2185 ---GAAATGAAGATGTGTATCCAGTTGTGATGTGGGAACGTCTCTCTGTGGATCC 2241  
QY 1034 PheGlnTyrValGluAspProThrIleValArgIleGluProGluTyrTrpSerIleValSer 1053  
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QY 1054 GlyAsnThrProIleAlaValTyrGlyThrHisLeuAspLeuIleGlnAsnProGlnIle 1073  
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Db 2416 TGGCGGTTTTAGCCCCAGTTTA----- 2439  
QY 1114 A-gProGluGluPheGlyPheIleLeuAspAsnValGlnSerLeuLeuIleLeuAsnLys 1133  
Db 2440 -----AAGAGTTTCAAAAGTGGCGACAGATGTCTGTGAAGTCAAGAGTCAAGAC 2490  
QY 1134 Thr-----AsnPheThrTyrTyrProAsnProValPheGluAlaPheGly 1148  
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QY 1189 ProCysThrValThrVal-----SerAspValGlnLeuLeuCysGluSerProAsn 1205  
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QY 1223 ProGlyMetValTyrIleAlaProAspSer-----ProLeuSerLeuProAlaIleValSer 1241  
Db 2800 -----CTCTACCTCGAGGAGGAGTCAAGTCTCTTCCACATGATTTCTTCTGATTGTG 2850

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	Db	2851	: : : : : ::: ::: ::: :::	:
	Qy	1262	ArgLysSerArgGluSerAspLeuThrLeuLyAargLeuGlnMetGlnMetAspAsnLeu	1281
	Db	2902	CACAATCGAGAG-----CTGAGTCGCAACAGAGTCAA--CAACTAGAATTGGCTG	2952
	Qy	1282	GluSerArgValAlaLeuGluCysLysGlualapheaAlagluLeuGlnThrAspIleHis	1301
	Db	2953	GAAGCCGAGCTCCGAAAGAGATACGTGACGGCTTGCTGAGCTGCAGATGGATAAATTG	3012
	Qy	1302	GluLeuThrSerAspLeuAspGlyAlaGly-IlleProPheIleuAspTyrArgThrTyr	1320
	Db	3013	GARGTG-----GITGATAGTTTGGAACTGTTCCCTCTCTTGACTACAAAACATTT	3063
	Qy	1321	ThrMetArgValLeuPhePro-----GlyileGluAspHisProValLeuArgAspLeu	1338
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	Qy	1339	GluValProGlyTyrArgGlnGluArgValGluLysGlyLeuLysLeuPheAla-	1356
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	Qy	1377	SerPheSerMetArgAspArgGlyAsnValAlaSerLeulleMetThrValLeuGlnSer	1396
	Db	3232	AACTTTTCTGTGAAGCACAGTGCTCTGTTTGCCTCTCTCTTAACCAATTGCATCGCAAACC	3291
	Qy	1397	LysLeuGluTyrAlaThrAspValLeuLysGlnLeuLeualaaspLeuilleAspLysAsn	1416
	Db	3292	ARGCTGGTCTACCTGACCAGCAVCCTAGAGGTGCTGACAGGAGCTTGATGGAAACAGTGT	3351
	Qy	1417	LeuGluSerLysAsnHisProLysLeuLeuLeuArgThrGluSerValAlaGluLys	1436
	Db	3352	-----AGTAACATGCAGCGCAAACTCATGCTGAGACGCCAGCGAGTCGTCGCAAAAA	3405
	Qy	1437	MetLeuThrAsnTrpPheThrPheLeuLeuTy-LysPheLeuLysGluCysAlaGlyGlu	1456
	Db	3406	CTCTCCAACCTGAGTGCCTCGCTGCTTCTCGAATTTCTCCGGAGACTGTCGGAGAG	3465
	Qy	1457	ProLeuPheSerLeuPheCysAlaileLysGlnGlnMetGluLysGlyProIleAspAla	1476
	Db	3466	CCCTTCTATTGCTGGTGACAGCTCTCGAACCAAGAAATTAACAGGGTCCCCTGGATGTA	3525
	Qy	1477	IleThrGlyGluAlaArgTyrSerLeuSerGluaspylserLeulleargGlnGlnIleApp	1496
	Db	3526	ATCATTGCAAGCCCCGTACACACTTAATCAAGACTGGCTGTGTGTGGCAGGTTCGGAA	3585
	Qy	1497	TyrlsythrLeuValLeuSerCysVal-----SerProAspAsnAlaAsnSerPro	1513
	Db	3586	TTCAGTACTGTGGCATTTAAACGTCGICTTTGAAAAAATCCGGAAAAACGAGTGCAGAT	3645
	Qy	1514	-----GluValProvalLyslleLeuasnCysAspThrtleThrGlnValLysGlu	1530
	Db	3646	GTCGTGCGAATATTTTCAGTCAATGTCTCGACTGTGACACCATTTGCCAAGCCAAAGAA	3705
	Qy	1531	LysilleLeuaSpAlallePheLysAsnValproCysSerHisArgProLysAlaIaAsp	1550
	Db	3706	ARGATTTTCCAGCATTTCTTAAGCAAAAATGGCTCTCTTATGGACTTCAGCTTAATGAA	3765
	Qy	1551	MetaSpLeuGluTrpArgGlnglySerGlyAlaArgMetIleLeuGlnAspGluAspIle	1570
	Db	3766	ATTGGTCTTGAGCTTCAAATGGGCACACGACAGAAAGAACTTCTGACATCGACAGTTC	3825
	Qy	1571	ThrThrylsileGluAsnAspTrpLysArgLeuanThrLeulaahisTyrGlnValPro	1590
	Db	3826	TCCGTGATTTTGAAGATGGAATCACCAAGCTAAACACCATTCGCCCATATGATATCA	3885
	Qy	1591	AspGlySerValValAlaLeuValSerLysGlnValThrAlatYrEnlaValAsnAsn	1610

## RESULT 7

US-09-459-065-1  
; Sequence 1, Application US/09459065

Patent No. 6562949  
GENERAL INFORMATION:  
APPLICANT: Striggs, Melanie  
TITLE OF INVENTION: VIRAL ENCODED SEMAPHORIN PROTEIN  
TITLE OF INVENTION: RECEPTOR DNA AND POLYPEPTIDES  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESS: Janis C. Henry  
STREET: 51 University St.  
CITY: Seattle  
STATE: WA

QY 187 -----Thra1a 188  
553 CTGCTGAGCGGAGACGGCGCTGCAACCCCGCGCATCCGACACGACGCGCC 612  
189 ValAspGlySerProGluTyrPheProThrThrLeuSerArgLysLeuThrLysAsnSer 208  
613 ATCGCGCTCAAGACACGAGCGGGCGCGCTGCGCCACGACGAGCTGGGGCGCTCAAG 672  
209 GluAlaAspGlyMetPheAlaTyrValPheHisAspGluPheVal---AlaSerMetIle 227  
673 CTGTGCGAGCGCGCGCGCTGACCTCTGCGACGCGCTTTCTCTGGAACCGGACATC 732  
228 LysIleProSerAspThrPheThrIleProAspPheAspIleTyrTyrValTyrGly 247  
733 TACTTCCCG-----TACTACCCCTACAAC 756  
248 PheSerSerGlyAsnPheValTyrPheLeuThrLeuGlnProGluMetValSerProPro 267  
757 TATACGAGCGCG-----GCTGCCACCGCGCTGCGCCAGCATGCGCGCGCTCGCG 804  
268 GlySerThrThrLysGluGlnValTyrThrSerLysLeuValArgLeuCysLysGluAsp 287  
805 CAGAGCACC-----GAG 816  
288 ThrAlaPheAsnSerTyrValGluValProIleGlyCysGluArgSerGlyValGlu---- 306  
817 GTGCTGTTCCAGCGC-----CAGGCATCCCTCGACTGCGCGCCACGCGCCACCCCGACGCG 870  
307 TyrArgLeuLeuGlnAlaAlaTyrLeuSerLysAlaGlyAlaValLeuGlyArgThrLeu 326  
871 CGCGCGCTGCTCTCTCTCCAGCTGAGTGAGGCG----- 906  
327 GlyValHisProAspAspLeuLeuPheThrValPheSer-----LysGlyGlnLys 344  
907 -----CTGCGACGTGCGGGCGGAGTGTTCAGCGCGCGCGCTGAGAGGCG 951  
345 ArgLysMetLysSerLeuAspGluSerAlaLeuCysIlePheIleLeuLysGlnIleAsn 364  
952 CAGAGCGCGCTGCG 1011  
365 AspArgIleLysGluArgLeuGlnSerCysTyrArgGlyGluGlyThrLeuAspLeuAla 384  
1012 GCGCGCGCGCAAGAGG-----GTCAGC 1032  
385 Trp---LeuLysValLysAspIleProCysSerSerAlaLeuLeuThrIleAspAspAsn 403  
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1072 -----GATCAACCT-----GAAAGAGTCCAACCAATCGCA 1101  
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1102 TCATCTACCTTGATCCATTCCGACCTCGCATCCGTTTATGGCACCGCTGTTAATGAACAGG 1161  
444 SerLeuAlaPheValGlyThrLysSerGlyLysLeuLysLysIleArgValAspGlyPro 463  
1162 ACGTGTTTATCTGGGACTGCGAGTGGCGAGTACTTAAAGTTATCTT----- 1212  
464 ArgGlyAsnAlaLeuGlnTyrGluThrValGlnValVal----- 476  
1213 ---GCTGAGAAATTTGACTTCAAAATTTGTCAGAGGTTATCTATGAAATTAAGAAGAGACA 1269  
477 -----AspProGlyProValLeuArgAspMetAlaPheSerLysAsp 490  
1270 CCTGTTTCTACAACTCGTTCTCTGATCTCTG-----AAG 1305  
491 HisGluGlnLeuTyrIleMetSerGluArgGlnLeuThrArgValProValGluSerCys 510  
1306 AATATCTACATTTTATCTAACAGCTGGGAAAGAGGTGAGGAGAATTCGTGTTGCAAACTGC 1365  
511 GlyGlnTyrGlnSerCysGlyGluCysLeuLysSerGlyAspProHisCysGlyTrpCys 530

COUNTRY: US  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: MS-DOS/Windows 95  
SOFTWARE: Word for Windows 95, 7.0a  
CURRENT APPLICATION DATA:  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/958,598  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Henry, Janis C  
REGISTRATION NUMBER: 34,347  
REFERENCE/DOCKET NUMBER: 2631  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206)470-4189  
TELEFAX: (206)233-0644  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4707 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..4707  
US-09-459-065-1  
Alignment Scores:  
Pred. No.: 4707 Length: 4707  
Score: 1349.00 Matches: 480  
Percent Similarity: 39.78% Conservative: 291  
Best Local Similarity: 24.77% Mismatches: 591  
Query Match: 13.50% Indels: 576  
DB: 4 Gaps: 74  
US-09-964-956-13 (1-1996) x US-09-459-065-1 (1-4707)  
QY 72 TyrLysLeuSerSerAspLeuLysValLeuValThrHisGluThrGlyProAspGluAsp 91  
Db 208 TAGACCTGGAGCAGACGCTCTCGCGCTGTACCGGACCAAGCGGCG----- 255  
QY 92 AsnProLysCysTyrProProArgIleValGlnThrCysAsnGluProLeuThrThr 111  
Db 256 -----AACTGCACAGACCGGCTCTCGCTGGCG 282  
QY 112 -----AsnAsnValAsnLysMetLeuLeuIleAspTyrHis 123  
Db 283 CCCCCCG 339  
QY 124 GluAsnArg-----LeuIleAlaCysGlySerLeuTyrGlnGlyIle 137  
Db 340 GAGGGGGCGCGCGCGCTCGGGGGGTGTGTCTCACCGGCTGACCTTCGACCGGGCGCGC 399  
QY 138 CysLysLeuLeuArgLeuGluAspLeuPheLysLeuGlyGluProTyrHisLysLysGlu 157  
Db 400 TCGAGGTGCGGCGCGCTGGGCAACTG-----AGCGGCAAC 435  
QY 158 HisTyrLeuSerGlyVal-----AsnGluSerGlySerValPheGlyVal 172  
Db 436 TCCCTGCGGACACGCGCGAGGT 495  
QY 173 IleValSerTyrSerAsnLeuAspAspLysLeuPheIleAla----- 186  
Db 496 GTGTACCGC---CGGGCGCGGAACACACCGCTGTACCTGGCGGTGGCGCGCACCTACGTG 552

[illegible]

QY 1208 -----GlyArgHisLysValMetAlaArgValGlyGlyMetGluTyrSer 1222  
Db 2746 AGCACCATTCACCACTCTTCTAAGAAAGTTCGGGTCAAGCTGGGAACCTGGAG----- 2799  
QY 1223 ProGlyMetValTyrIleAlaProAspSer---ProLeuSerLeuProAlaIleValSer 1241  
Db 2800 -----CTCTACGTCGACGAGGAGTCAGTCTCCTCCACATCGTATTCTTGATGTG 2850  
QY 1242 IleAlaValAlaGlyGlyLeuLeuIlePheIleValAlaValLeuLeuAlaTyrLys 1261  
Db 2851 CTCCTGTGTC-----TTGCTAGTGAATGTTCTATTTTGGCGCGGTGGGGGTGACCGG 2901  
QY 1262 ArgLysSerArgGluSerAspLeuThrLeuLysArgLeuGlnMetGlnMetAspAsnLeu 1281  
Db 2902 CACAAATCGAAGGAG-----CTGAGTCGCAACACAGAGTCAA---CAACTAGAAATTCGTG 2952  
QY 1282 GluSerArgValAlaLeuGluCysLysGluAlaPheAlaGluLeuGlnThrAspIleHis 1301  
Db 2953 GAAAGCGAGCTCCGGAAGAGATAGTCACGGCTTGTCTGAGCTGCAGATGGAATAATG 3012  
QY 1302 GluLeuThrSerAspLeuAspGlyAlaGly---IleProPheLeuAspTyrArgThrTyr 1320  
Db 3013 GATGTG-----GTTGATAGTTCGAACTGTTCCCTTCCTTACTACAAACATTTT 3063  
QY 1321 ThrMetArgValLeuPhePro-----GlyIleGluAspHisProValLeuArgAspLeu 1338  
Db 3064 GCTCTGAGAACCTTCTTCCCTGAGTCAGGTGGCTTCACCCACATCTTCCACTGAAGATATG 3123  
QY 1339 GluValProGlyTyrArgGlnGluArgValGluLysGlyLeuLysLeuPheAla----- 1356  
Db 3124 -----CATAAACAGACAGACCCACAGCAGAGATGAAGTCTCACAGCTTGGAT 3171  
QY 1357 GlnLeuIleAsnAsnLysValPheLeuLeuSerPheIleArgThrLeuGluSerGlnArg 1376  
Db 3172 GCCCTAATCTGTAATAAAGCTTCTTGTACTGTATCCACACCTTGTGAAGCAGAG 3231  
QY 1377 SerPheSerMetArgAspArgGlyAsnValAlaSerLeuIleMetThrValLeuGlnSer 1396  
Db 3232 AACTTTCTGTGAAGCAGAGTGTCTGTTGCTCTCTTCCCTAACCATTCGACTGCAACC 3291  
QY 1397 LysLeuGluTyrAlaThrAspValLeuLysGlnLeuLeuAlaAspLeuIleAspLysAsn 1416  
Db 3292 AAGCTGGTCTACTACACAGCATCTCTAGAGGTGTGACGAGGACTTGTGTAACAGTGT 3351  
QY 1417 LeuGluSerLysAsnHisProLysLeuLeuArgTArgThrGluSerValAlaGluLys 1436  
Db 3352 -----AGTAACATGCGAGCCGAACTCATGCTGAGACGCGAGTCCGTCGTAANA 3405  
QY 1437 MetLeuThrAsnTrpPheThrPheLeuLeuTyrLysPheLeuLysGluCysAlaGlyGlu 1456  
Db 3406 CTCCTCACAACTGGATGTCGCTGCTCTGCTGCTTCTCCGGGAGACTGTCGAGAG 3465  
QY 1457 ProLeuPheSerLeuPheCysAlaIleLysGlnGlnMetGluLysGlyProIleAspAla 1476  
Db 3466 CCCCTTCTATTGCTGTGACGACTCTGAACACGAAATTAACAGGGTCCCGTGGATGTA 3525  
QY 1477 IleThrGlyGluAlaArgTyrSerLeuSerGluAspLysLeuIleArgGlnGlnIleAsp 1496  
Db 3526 ATCACTTGCAGAGCCCTGTACACACTTATGAGACTGGCTGCTGTGGCAGGTTCCGGAA 3585  
QY 1497 TyrLysThrLeuValLeuSerCysVal-----SerProAspAsnAlaAsnSerPro 1513  
Db 3586 TTCAGTACTGTGGCATTAACCTCGTCTTTGAAAAAATCCCGGAAAAACGAGAGTCCAGAT 3645  
QY 1514 -----GluValProValLysIleLeuAsnCysAspThrIleThrGlnValLysGlu 1530  
Db 3646 GTCTGTGGGAATATTCAGTCAATGTTCGACTGTGACACCATTCGTCGACCCAAAGAA 3705  
QY 1531 LysIleLeuAspAlaIlePheLysAsnValProCysSerHisArgProLysAlaAlaAsp 1550  
Db 3706 AAGATTTTCAAGCATTTCTAAGCAAAAATGGCTCTCTCTATGAGACTTCAGCTTAATGAA 3765

QY 1551 MetAspLeuGluTrpArgGlnGlySerGlyAlaArgMetIleLeuGlnAspGluAspIle 1570  
Db 3766 ATTGGCTTTGAGCTTCAATGGGCACACGACAGAAAGAACTTCTTGACATCGACAGTTCC 3825  
QY 1571 ThrThrLysIleGluAsnAspTrpLysArgLeuAsnThrLeuAlaHisIleGlnValPro 1590  
Db 3826 TCCGTGATTTCTGAAGATGGAATACCAAGCTAAACACCATTTGGCCACTATGAGATACA 3885  
QY 1591 AspGlySerValValAlaLeuValSerLysGlnValThrAlaTyrAsnAlaValAsnAsn 1610  
Db 3886 AATGGATCCACTATAAAGTC----- 3906  
QY 1611 SerThrValSerArgThrSerAlaSerLysTyrGluAsnMetIleArgTyrThrGlySer 1630  
Db 3907 -----TTTAAAGAGATAGCAAAATTTTACTTTCAGAT 3936  
QY 1631 ProAspSerLeuArgSerArgThrProMetIleThrProAspLeuGluSerGlyValLys 1650  
Db 3937 GTGAGTACTCGATGACCACTGCCATTTGATTTTACAGATTCGGAAGCA----- 3987  
QY 1651 MetTrpHisLeuValLysAsnHisGluHisGlyAspGlnLysGluGlyAspArgGlySer 1670  
Db 3988 ---TTCAAAGATGTGCAAGGAAAGAGACAT-----CGAGGGAAG 4023  
QY 1671 Lys-----MetValSerGluIleTyrLeuThrArgLeuLeuAlaThrLysGlyThrLeu 1688  
Db 4024 CACAAGTTCAAGTAAAGAAATGATATCTGACAAAGCTGCTGCGACCAAGGTGGCAATT 4083  
QY 1689 GlnLysPheValAspAspLeuPheGluThrIlePheSerThrAlaHisArgGlySerAla 1708  
Db 4084 CATCTGTGCTTCAAAAACCTTTTACAGCATTTGGAGTTTACCCCAAC-----AGCAGA 4137  
QY 1709 LeuProLeuAlaIleLysTyrMetPheAspPheLeuAspGluGlnAlaAspLysHisGly 1728  
Db 4138 GCTCCATTGCTATAAATACATTTTGTGACTTTTGGAGCCCGAGCTGAAAACAAAAA 4197  
QY 1729 IleHisAspProHisValArgHisThrTrpLysSerAsnCysLeuProLeuArgPheTrp 1748  
Db 4198 ATCAGAGATCCTGACGTCGTACATATTTGAAACAAACACAGCCTTCTCTCTCTCTGG 4257  
QY 1749 ValAsnMetIleLysAsnProGlnPheValPheAspIleHisLysAsnSerIleThrAsp 1768  
Db 4258 GTAACATCTCGAAGAACCTCAGTTTGTCTTTGACATTAAGAAAGACACCATATAGAC 4317  
QY 1769 AlaCysLeuSerValValAlaGlnThrPheMetAspSerCysSerThrSerGluHisArg 1788  
Db 4318 GGCTGTTTGTGTCAGTGATGCCAGGCATTCATGATGATCTTCTCTCACAGAGCAGCAA 4377  
QY 1789 LeuGlyLysAspSerProSerAsnLysLeuLeuTyrAlaLysAspIleProSerTyrLys 1808  
Db 4378 CTAGGGAAGGAAGACCAACACTAATAAGCTTCTATGCCCCAAGGATATCCCAACTACAA 4437  
QY 1809 AsnTrpValGluArgTyrTyrSerAspIleGlyLeuMetProAlaIleSerAspGlnAsp 1828  
Db 4438 GAAGAAGTAAATCTTATTACAAAGCAATCAGGGAATTCCTCATTTGTCATCTCTAGAA 4497  
QY 1829 MetAsnAlaTyrIleAlaGluGlnSerArgMetHisMetAsnGluPheAsnThrMetSer 1848  
Db 4498 ATGGAAGATTTTAACTCAGGAATCTAAGAAACATGAAATGAATTAATGAAGAAGTG 4557  
QY 1849 AlaLeuSerGluIlePheSerTyrValGlyLysTyrSerGluIleLeuGlyProLeu 1868  
Db 4558 GCCTTGACAGAAATTTACAATATCATCGTAAATATTTTATGATGAGATCTTAATAACTA 4617  
QY 1869 AspHisAsp-----AspGlnCysGlyLysGlnLysLeuAlaTyrLysLeu 1883  
Db 4618 GAAAGAGAAGCGGCTGGAAGAAGCTCAGAAACAACTCTTGCATGTGAAAGTC 4671

RESULT 8  
US-03-023-655-603  
; Sequence 603, Application US/09023655  
; Patent No. 6607879  
; GENERAL INFORMATION:

APPLICANT: Cocks, Benjamin G.  
APPLICANT: Susan G. Stuart  
APPLICANT: Jeffrey J. Seilhamer  
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE  
TITLE OF INVENTION: EXPRESSION  
NUMBER OF SEQUENCES: 1508  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
STREET: 3174 PORTER DRIVE  
CITY: PALO ALTO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/023,655  
FILING DATE: HEREWITH  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Zeller, Karen J.  
REGISTRATION NUMBER: 37,071  
REFERENCE/DOCKET NUMBER: PA-0001 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 855-0555  
TELEFAX: (650) 845-4166  
INFORMATION FOR SEQ ID NO: 603:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3458 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: THYMNON04  
CLONE: 3191056  
US-09-023-655-603

Alignment Scores:  
Pred. No.: 1.59e-60 Length: 3458  
Score: 657.00 Matches: 146  
Percent Similarity: 61.17% Conservative: 43  
Best Local Similarity: 47.25% Mismatches: 79  
Query Match: 6.58% Indels: 42  
DB: 4 Gaps: 7

US-09-964-956-13 (1-1896) x US-09-023-655-603 (1-3458)

Qy 1615 ArgThrSerAlaSerLysTyrGluAsnMetIleArgTyrThrGly-----SerProAsp 1632  
Db 1420 AGACGTGCGCTTCTGATTAT-----TTTACTGGGGTCCATTGTCAGAT 1464  
Qy 1632 -----1632  
Db 1465 TTTCTTTGATTGTAATAATATTTTACTTTTACTTTTCTTAATTAATAATGATCCA 1524  
Qy 1633 -----SerLeuArgSerArgThrProMetIleThrProAspLeu 1645  
Db 1525 TATAAAATAAGAAATAAAGTCTTTTAAAGGAAGGTTTCTGGCCGAGTGAAGACTTG 1584  
Qy 1646 GluSerGlyValLysMetTyrHisLeuVal---LysAsnHisGluHisGlyAspGlnLys 1664  
Db 1585 GACACA---GAGAAGTATTTCATTGTTGCTGCTACGACAGCT-GGCGGANCACAG 1640  
Qy 1665 GluGlyAspArgGlySer-----LysMetValSerGluIleTyrLeuThrArgLeu 1681  
Db 1641 AAGTCTCAGCGGACAGCCATCGCAAGAGGTGCTCCCGGAATCTACCTGACCCGCTG 1700

1682 LeuAlaThrLysGlyThrLeuGlnLysPheValAspLeuPheGluThrIlePheSer 1701  
1701 CTCCTCCACCAAGGCGACGTTTCTGAGAGTTTCTGATGACCTGTTCAAGGCGCATCTCAGT 1760  
1702 ThrAlaHisArgGlySerAlaLeuProLeuAlaIleLysTyrMetPheAspPheLeuAsp 1721  
1761 ATC-----CGTGAAGACCAAGCCCTGCTGCTCAANNACTTTTTCGACTTCTCGAN 1814  
1722 GluGlnAlaAspLysHisGlyIleHisAspProHisValArgHisThrTrpLysSerAsn 1741  
1815 GANCAGGCTGAGAAAGAGGGAATCTCGACCCCGACACCTTACATCATCTGGAAGACCAAC 1874  
1742 CysLeuProLeuArgPheTyrValAsnMetIleLysAsnProGlnPheValPheAspIle 1761  
1875 AGCCTTCTCTCCGTTCTGGTGAAACATCTCTGAAGAACCCCTCAGTTTGTCTTGACATC 1934  
1762 HisLysAsnSerIleThrAspAlaCysLeuSerValValAlaGlnThrPheMetAspSer 1781  
1935 GACAAGACAGACACCATCGACGCTGCTTTCAGTCTATCGCGCAGGCTTTCATCGACGCC 1994  
1782 CysSerThrSerGluHisArgLeuGlyLysAspSerProSerAsnLysLeuLeuTyrAla 1801  
1995 TGCTCAATCTCTGACCTGACCTGGCAAGGATTCGCAACCAACACAGCTCTCTACGCC 2054  
1802 LysAspIleProSerTyrLysAsnTyrValGluArgTyrTyrSerAspIleGlyLysMet 1821  
2055 AAGGAGATTCTCTGAGTACCGGAGATGCTGCAGCGCTACTACACAGCAGATCCAGCATG 2114  
1822 ProAlaIleSerAspGlnAspMetAsnAlaTyrLeuAlaGluGlnSerArgMetHisMet 1841  
2115 AGCGGCTCAGCAGCAGAGATGATGCCATCTGCGCAGGAGTGCAGGAATATACAG 2174  
1842 AsnGluPheAsnThrMetSerAlaLeuSerGluIlePheSerTyrValGlyLysTyrSer 1861  
2175 AATGAGTTCAACACCAATGTGCCATGTGCCATGCGACAGATTTATAAGTACGCCAGAGGTATCGG 2234  
1862 GluGluIleLeuGlyProLeuAspHisAspAspGlnCysGlyLysGlnLysLeuAlaTyr 1881  
2235 CCGCAGATCATGGCGCGCTGGAGGCCAACCCACGCCGCGGAGGACACAACTGCAGCAC 2294  
1882 LysLeuGluGlnValIleThrLeuMet 1890  
2295 AAGTTTGACAGGTGCTGCTTTGATG 2321

RESULT 9  
US-08-306-691B-22  
Sequence 22, Application US/08306691B  
Patent No. 5734039  
GENERAL INFORMATION:  
APPLICANT: Calabretta, Bruno  
APPLICANT: Skorski, Tomasz  
TITLE OF INVENTION: ANTISENSE  
TITLE OF INVENTION: OLIGONUCLEOTIDES TARGETING COOPERATING ONCOGENES  
NUMBER OF SEQUENCES: 55  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Seidel, Gonda, Lavoigna & Monaco, P.C.  
STREET: Two Penn Center, Suite 1800  
CITY: Philadelphia  
STATE: Pennsylvania  
COUNTRY: U.S.A.  
ZIP: 19102  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 720 KB  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/306,691B  
FILING DATE: September 15, 1994  
CLASSIFICATION: S14  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:

FILING DATE: 2.86e-57 Length: 4626  
ATTORNEY/AGENT INFORMATION: NAME: Monaco, Daniel A. Matches: 282  
REGISTRATION NUMBER: 30,480 Conservative: 204  
REFERENCE/DOCKET NUMBER: 8321-8 Best Local Similarity: 20.58%  
TELECOMMUNICATION INFORMATION: TELEPHONE: (215) 568-8383 Mismatches: 409  
TELEFAX: (215) 568-5549 Indels: 475  
TELEX: No. 5734039e Gaps: 59  
INFORMATION FOR SEQ ID NO: 22: SEQUENCE CHARACTERISTICS: US-08-306-691B-22  
LENGTH: 4626 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear

Alignment Scores:  
Pred. No.: 2.86e-57 Length: 4626  
Score: 629.50 Matches: 282  
Percent Similarity: 35.47% Conservative: 204  
Best Local Similarity: 20.58% Mismatches: 409  
Query Match: 6.30% Indels: 475  
DB: 1 Gaps: 59

US-09-964-956-13 (1-1896) x US-08-306-691B-22 (1-4626)

Qy 62 HisLeuThrLeuGlyAlaValAsnArgIleTyrLysLeuSer---SerAspLeuLysVal 80  
Db 375 CACATTTTCCTTGTGTCACCTAACATACATTTATGTTTAAATGAGGAGACCTTCAGAAG 434  
Qy 81 LeuValThrHisGluThrGlyProAspGluAspAsnProLysCysTyrProProArgIle 100  
Db 435 GTTCTGAGTACAAAGATGGCGCTGTCTGGAACACCCACGATGTTTCCCA----- 485  
Qy 101 ValGlnThrCysAsnGluProLeuThrThrThr-----AsnAsnValAsn 115  
Db 486 TGTGAGGACTGCACGACCAAGCAATTTATCAGAGGTGTTTGGAAAGATACATCAAC 545  
Qy 116 LysMetLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 134  
Db 546 ATGGCTCTAGTTGTCGACACCTACTATGATGATCACTATGATGATGATGATGATGATGAT 605  
Qy 135 GlnGlyIleCysLysLeuLeuArgLeuGluAspLeuPheLysLeuGlyGluProTyrHis 154  
Db 606 AGAGGACCTGCCAG-----CGACATGCTCTTT-----CCCCAAT 641  
Qy 155 LysLysGluHisTyrLeuSerGlyValAsn-----GluSer 166  
Db 642 CATACTGCTGACATACATACGAGGTTCAGTATATTCCTCCACAGATAGAGAGCCC 701  
Qy 167 GlySerValPheGlyValIleValSer-----TyrSerAsnLeuAsp 180  
Db 702 AGCCAGTGTCTGACTGTGTGTGAGCGCCCTGGGAGCCAAAGTCTTTTCATCTGTAAAG 761  
Qy 181 AspLys-----LeuPheIleAlaThrAlaValAspGlyLysProGluTyrPhePro 197  
Db 762 GACCGGTTTCATCACTCTTTGTAGGCAATACCAATAATTCT-----TCTTATTTCCCA 815  
Qy 198 -----ThrIleSerSerArgLysLeuThrLysAsnSerGluAlaAspGly 212  
Db 816 GATCATCATTCATTCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 869  
Qy 213 MetPheAlaTyrValPheHisAspGluPheValAlaSerMetIleLysIleProSerAsp 232  
Db 870 ---TTTATGTTTGTGAGGACCACTCTACAT----- 899  
Qy 233 ThrPheThrIleLeuProAspPhe-----AspIleTyrTyrValTyrGlyPhe 248  
Db 900 -----GATGTTTTCCTGAGTTCAGAGATTTTACCCCATTAAGTATGTCATGCTTTT 953  
Qy 249 SerSerGlyAsnPheValTyrPheLeuThrLeuGlnProGluMetValSerProGly 268

Db 954 GAAAGCAACAATTTTATTCTTCTTACGCTTCAAGGGAA----- 995  
Qy 269 SerThrThrLysGluGlnValTyrThrSerLysLeuValArgLeuCysGlyGluAspThr 288  
Db 996 ---ACTCTAGATGCTCAGACTTTTACACAGAATAATCAGGTTCTGTTCATAAACTCT 1052  
Qy 289 AlaPheAsnSerTyrValGluValProIleGlyCys-----Glu 301  
Db 1053 GGATTGTCATTCTACATGGAATGCTCTGGAGTGTATTCTCACAGAAAAGAAAAG 1112  
Qy 302 ArgSerGlyValGlu-----TyrArgLeuLeuGlnAlaIleTyrLeuSerLysAlaGly 319  
Db 1113 AGATCCACAAAGAGAGGAAGTGTTTAATATATCTTACAGGCTGCGTATGTGTCAGCAAGCTGGG 1172  
Qy 320 AlaValLeuGlyArgThrLeuGlyValHisProAspAspAspLeuLeuPheThrValPhe 339  
Db 1173 GCCCAGCTTGTAGACAAATAGGACCCAGCTGATGATGATGATGATGATGATGATGATGATGAT 1232  
Qy 340 SerLysGlyGlnLysArgLysMetLysSerLeuAspGluSerAlaLeuCysIlePheIle 359  
Db 1233 GCACAAAGCAGCCAGACTTCTGCCGAACCAATGATGATGATGATGATGATGATGATGATGATGAT 1292  
Qy 360 LeuLysGlnIleAsnAspArgIleLysGluArgLeuGlnSerCysTyrArgGlyGluGly 379  
Db 1293 ATCAAAATATGTCACGACTTCTTCAACAG----- 1322  
Qy 380 ThrLeuAspLeuAlaTrpLeuLysValLysAspIleProCysSerSerAlaLeuLeuThr 399  
Db 1322 ----- 1322  
Qy 400 IleAspAspAsnPheCysGlyLeuAspMetAsnAlaProLeuGlyValSerAspMetVal 419  
Db 1322 ----- 1322  
Qy 420 ArgGlyIleProValPheThrGluAspArgAspArgMetThrSerValIleAlaTyrVal 439  
Db 1323 -----ATCGTC 1328  
Qy 440 TyrLysAsnHisSerLeuAlaPheValGlyThrLysSerGlyLysLeuLysLysIleArg 459  
Db 1329 AACAAAAACAATGTG----- 1343  
Qy 460 ValAspGlyProArgGlyAsnAlaLeuGlnTyrGluThrValGlnValValAspProGly 479  
Db 1344 -----AGATGCTCTCCAGAT----- 1358  
Qy 480 ProValLeuArgAspMetAlaPheSerLysAspHisGluGlnLeuTyrIleMetSerGlu 499  
Db 1359 -----TTTACGACCCCAATCATGAG----- 1379  
Qy 500 ArgGlnLeuThrArgValProValGluSerCysGlyGlnTyrGlnSerCysGlyGluCys 519  
Db 1379 ----- 1379  
Qy 520 LeuGlySerGlyAspProHisCysGlyTrpCysValLeuHisAsnThrCysThrArgLys 539  
Db 1380 -----CACTGC-----TTTAATAGGACACTTCTGAGAAT 1409  
Qy 540 GluArg---CysGluArgSerLysGluProArgArg-----PheAlaSerGluMetLys 556  
Db 1410 TCATCAGGCTGTGAACCGCGCGTGTGATGATATCAACAGAGTTTACACAGCTTTGACAG 1469  
Qy 557 GlnCysValArgLeuThrValHisProAsnAsnIleSerValSerGlnTyrAsnValLeu 576  
Db 1470 CGCGTT-----GACTTATTCTGGTCAATTCAGCGAAGTC 1505  
Qy 577 LeuVal-----LeuGluThrTyrAsnValProGluLeuSerAlaGlyValAsnCysThr 594  
Db 1506 CTTCTTAACATCTATATCCACCTTTCATTAAGAGAGACCTC-----ACC 1547  
Qy 595 PheGluAspLeuSerGluMetAspGlyLeuValValGlyAsnGlnIleGlnCysTyrSer 614  
Db 1548 ATAGCTAATCTTTGGGACATCAGAGGTCGCTTCATGCGAGGTGCTGCTTCGATCAGCA 1607



QY 615 ProAlaAlaLysGluValProArgIleIleThrGluAsnGlyAspHisHisValValGln 634  
Db 1608 CCATCAACCCCTCATGTGAATTTCTCTG-----GACTCCCATCCAGT--- 1652  
QY 635 LeuGlnLeuLysSerLysGluThrGlyMetThrPheAlaSerThrSerPheValPheTyr 654  
Db 1652 ----- 1652  
QY 655 AsnCysSerValHisAsnSerCysLeuSerCysValGluSerProTyrArgCysHisTrp 674  
Db 1653 -----TCGCCA----- 1658  
QY 675 CysLysTyrArgHisValCysThrHisAspProLysThrCysSerPheGlnGluArg 694  
Db 1658 ----- 1658  
QY 695 ValLysLeuProGluAspCysProGlnLeuLeuArgValAspLysIleLeuValProVal 714  
Db 1658 ----- 1658  
QY 715 GluValIleLysProIleThrLeuLysAlaLysAsnLeuProGlnProGlnSerGlyGln 734  
Db 1659 GAAGTGATGTGGAGCATACATTA-----AACCAA 1688  
QY 735 ArgGlyTyrGluCysIleLeuAsnIleGlnGlySerGluGlnArgValProAlaLeuArg 754  
Db 1689 AATGGCTACACTGGTTATCACT----- 1712  
QY 755 PheAsnSerSerValGlnCysGlnAsnThrSerTyrSerTyrGluGlyMetGluIle 774  
Db 1713 -----GGGAAGAAGATC 1724  
QY 775 AsnAsnLeuProValGluLeuThrValValTrpAsnGly-----HisPheAsn 790  
Db 1725 ACGAATGCCATTC-----AATGGCTGGGCTGCAGCATTC----- 1763  
QY 791 IleAspAsnProAlaGlnAsnLysValHisLeuTyrLysCysGlyAlaMetArgGluSer 810  
Db 1764 -----CAGTCC 1769  
QY 811 CysGlyLeuCysLeuLysAlaAspProAspPheAlaCysGlyTrpCysGlnGlyProGly 830  
Db 1770 TGCAGTCAATGCCTCTCTGCCACCCTTTGTTCAGTGTGGTGGTCCAC-----GAC 1823  
QY 831 GlnCysThrLeuArgGlnHisCysProAlaGlnGluSerGlnTrpLeuGluLeuSerGly 850  
Db 1824 AATGTGTGGATCGGAGGNATCC-----CTGAGCGGG 1856  
QY 851 AlaLysSerLys-----CysThrAsnProArgIleThrGluIleIleProValThrGly 868  
Db 1857 ACATGGACTCAACAGATCTGTCTG-----CCTGCAATCTACAAGGTTTCCCAATAAGTGCA 1913  
QY 869 ProArgGluGlyThrLysValThrIleArgGlyGluAsnLeuGlyLeuGluPheArg 888  
Db 1914 CCCTTGAAGAGGACAGGCTGACATATGTGGCTGGACTTGG-----TTTCGG 1967  
QY 889 -----AspIleAlaSerHisValLysValAlaGlyValGluCysSerPro 903  
Db 1968 AGGAATAATAAATTTGATTTAAAGAAAACTAGAGTTCTCTCGGAATGAGAGCTGCACC 2027  
QY 904 LeuValAspGlyTyrIleProAlaGluGlnIleValCysGluMetGlyGluAlaLysPro 923  
Db 2028 TTGACTTTAAGTGAGGACGATGATACATACATGAATGCACAGTTGGT-----CCT 2078  
QY 924 SerGlnHisAlaGlyPheValGluIleCysValAlaValCysArgProGluPheMetAla 943  
Db 2079 GCCATGAATAAGCATTTTC-----AATATGTCCATAATTATTCAATGGCCACGGGACAACA 2135  
QY 944 ArgSerSerGlnLeuTyrTyrPheMetThrLeuThrLeuSerAspLeuLysProSerArg 963  
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QY 964 GlyProMetSerGlyGlyThrGlnValThrIleThrGlyThrAsnLeuAsnAlaGlySer 983  
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QY 984 AsnValValValMetPheGlyLysGlnProCysLeuPheHisArgArgSerProSerTyr 1003  
Db 2253 TCTAGACACATTTCAATTTGGTGGAAAAACATGACTTTAAAAAGTGTGTCAACACAGTATT 2312  
QY 1004 IleValCysAsnThrThrSerSerAspGluValLeuGluMetLysValSerValGlnVal 1023  
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QY 1024 AspArgAlaLysIleHisGlnAspLeuValPheGlnTyrValGluAspProThrIleVal 1043  
Db 2373 GACTTAGCCCAAC---CGAGAGACAAGCATCTTCAGTTACCGTGAAGATCCCATGTTCTAT 2429  
QY 1044 ArgIleGluProGluTrpSerIleVal----- 1052  
Db 2430 GAATTCATCCACCAAAATCTTTTATTAGTACTTGGTGAAGAACCTCTCAACATTGTC 2489  
QY 1053 -----SerGlyAsnThrProIleAlaValTrpGlyThrHisLeu 1065  
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QY 1066 AspLeuIleGlnAsnProGln-----IleArgAlaLysHisGlyGlyLysGluHisIle 1083  
Db 2550 AATTCAGTGTGTCGCCAGATGGTCATAAATGTGCATGAAGCAGAGGAAGACTTTACA 2609  
QY 1084 AsnIleCysGluValLeuAsnAlaThrGlu---MetThrCysGlnAlaProAlaLeuAla 1102  
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QY 1103 LeuGlyProAspHisGlnSerAspLeuThrGluArgProGluGluPheGlyPheIleLeu 1122  
Db 2667 -----CAACAGCTGAATCTGCAACTCCCTCGAAACCAAGCCCTTT---TTCTGTTTA 2717  
QY 1123 AspAsnValGlnSerLeuLeuIleLeuAsnLysThrAsnPheThrTyrTyrProAsnPro 1142  
Db 2718 GATGGGATCCTTCCAAATACTTT-----GATCTCATTTATGTACATAATCCT 2765  
QY 1143 ValPheGluAlaPheGlyProSerGlyIleLeuGluLeuLysProGlyThrProIleIle 1162  
Db 2766 GTGTTTAAAGCCTTTTGAAGAGCCAGTGTATCTCAATGGGCAATGAAATGACTGCGAA 2825  
QY 1163 LeuLysGlyLysAsnLeuIleProProValAlaGlyGlyAsnValLysLeuAsnTyrThr 1182  
Db 2826 ATTAAGGGAATGATATTGACCTCTGAAGCAGTTAAAGTCAAGTG----- 2870  
QY 1183 ValLeuValGlyGluLysProCys---ThrValThrValSerAspValGlnLeuLysCys 1201  
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QY 1202 GluSerProAsn---LeuIleGlyArgHisLysValMetAlaArgValGlyGlyMetGlu 1220  
Db 2931 ACGGTCCCAATGACTGCTGMAATTGAACAGCGAGCTA-----AATATAGAG 2978  
QY 1221 TyrSerPro-----GlyMetValTyrIleAlaProAspSerPro 1233  
Db 2979 TGGAAAGCAAGCAATTTCTCAACCGCTCTTGGAAAGTAATAGTTCAACAGATCAGAAAT 3038  
QY 1234 LeuSer-----LeuProAlaIleValSerIleAlaValAlaGlyGlyLeuLeuIleIle 1251  
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QY 1252 PheIleValAlaValLeuIleAlaTyrLysArgLysSerArgGluSerAspLeuThrLeu 1271  
Db 3099 TTTTCTCTGTGGCTGAAAAAGAGAAAGCAAAATTAAGATCTGGGCACTGAATTAGTTCCG 3158  
QY 1272 LysArgLeuGlnMetGlnMetAspAsnLeuGluSerArgValAlaLeuGluCysLysGlu 1291  
Db 3159 TACGATGCAAGAGTACACACTCTCATTTGGATAGGCTTGTAGTGGCCCGAAGTGTAGC 3218  
QY 1292 AlaPheAlaGluLeuGlnThrAspIleHisGluLeuThrSerAspLeuAspGlyAlaGly 1311

Db 3219 CCAACTACAGAAATGGTTTCAAAAT----- 3242  
Qy 1312 IleProPheLeuAspTyrArgThrTyrThrMetArgValLeuPheProGlyIleGluAsp 1331  
Db 3243 --GAATCTGTAGACTACCGAGTACTTTTCCAGAAAGATCAGTTTCTTAATTCATCTCAG 3299  
Qy 1332 HisProValLeuArgAspLeuGluValPro 1341  
Db 3300 AACGGTTTCATGCCGACAAAGTGCAGATATCCT 3329  
RESULT 10  
PCT-US93-06251-27  
; Sequence 27 Application PC/TUS9306251  
; GENERAL INFORMATION:  
; APPLICANT: Wickstrom, Eric and Rife, Jason P.  
; TITLE OF INVENTION: Trivalent Synthesis of Oligonucleotides Containing  
; TITLE OF INVENTION: Stereospecific Alkylphosphonates and Arylphosphonates  
; NUMBER OF SEQUENCES: 93  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER  
; STREET: 400 Garden City Plaza  
; CITY: Garden City  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 11530  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US93/06251  
; FILING DATE: 19930630  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Digiglio, Frank S.  
; REGISTRATION NUMBER: 31,346  
; REFERENCE/DOCKET NUMBER: 8586  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 516-742-4343  
; TELEFAX: 516-742-4366  
; TELEX: 230 901 SANS UR  
; INFORMATION FOR SEQ ID NO: 27:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4626 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLSCULE TYPE: DNA (genomic)  
PCT-US93-06251-27  
Alignment Scores:  
Pred. No.: 2,86e-57 Length: 4626  
Score: 629.50 Matches: 282  
Percent Similarity: 35.47% Conservative: 204  
Best Local Similarity: 20.58% Mismatches: 409  
Query Match: 6.30% Indels: 475  
DB: 5 Gaps: 59  
US-09-964-956-13 (1-1896) x PCT-US93-06251-27 (1-4626)  
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Db 375 CACATTTTCTGTGTCCTACTACTACTATTTATGTTTAAATCAGGAAACCTTCAGAG 434  
Qy 81 LeuValThrHisGluThrGlyProAspGluAspAsnProLysCysTyrProArgIle 100  
Db 435 GTTGCTGAGTACAAAGATGGGCTGTGCTGGAACACCCAGATTTGTTTCCCA----- 485  
Qy 101 ValGluThrCysAsnGluProLeuThrThr-----AsnAsnValAsn 115  
Db 486 TGTGAGACTGTCAGCAGCAAGCAATTTATCAGGAGGTGTTTGGAAAGATACATCAAC 545

Qy 116 LysMetLeuLeuIleAsp---TyrLysGluAsnArgLeuIleAlaCysGlySerLeuTyr 134  
Db 546 ATGGCTCTAGTTGTCGACACCTACTATGATGATCACTCACTAGCTGTGGCAGCGTCAAC 605  
Qy 135 GlnGlyIleCysLysLeuLeuArgLeuLeuAspLeuPheLysLeuGlyGluProTyrHis 154  
Db 606 AGAGGAGCTGCCAG---CGACATGTCTTT-----CCCAACAAT 641  
Qy 155 LysLysGluHisTyrLeuSerGlyValAsn-----GluSer 166  
Db 642 CATACTGCTGACATACAGTCGAGGTTTCTGTCATATTTCTCCACACATAGAGAGGCC 701  
Qy 167 GlySerValPheGlyValIleValSer-----TyrSerAsnLeuAsp 180  
Db 702 AGCCAGTGTCTGACTGTGTGTGAGCGCCCTGGGAGCCAAAGTCTTTCATCTCTAAAG 761  
Qy 181 AspLys-----LeuPheIleAlaThrAlaValAspGlyLysProGluTyrPhePro 197  
Db 762 GACCGGTTTCATCAACTTCTTTGTAGGCAATACCATAATTCT-----TCITATTCCCA 815  
Qy 198 -----ThrIleSerSerArgLysLeuThrLysAsnSerGluAlaAspGly 212  
Db 816 GATCATCCATTGCAATTCGATATCAGTGAGAGCGCTAAAGGAACCAAGAAA-----GATGCT 869  
Qy 213 MetPheAlaTyrValPheHisAspGluPheValAlaSerMetIleLysIleProSerAsp 232  
Db 870 ---TTTATGTTTGTGAGGACCGAGTCTTACAT----- 899  
Qy 233 ThrPheThrIleIleProAspPhe-----AspIleTyrTyrValTyrGlyPhe 248  
Db 900 -----GATGTTTACCTGAGTTCAGAGATTCTTACCCCATTAAGTATGTCATGCTCTT 953  
Qy 249 SerSerGlyAsnPheValTyrPheLeuThrLeuGlnProGluMetValSerProGly 268  
Db 954 GAAAGCAACAATTTTATTACTTCTTGACGGTCCAAAGGGAA----- 995  
Qy 269 SerThrThrLysGluGlnValTyrThrSerLysLeuValArgLeuCysLysGluAspThr 288  
Db 996 ---ACTCTAGATGCTCAGACTTTTCACAGAATAATCAGGTTCTGTTCATAAACTCT 1052  
Qy 289 AlaPheAsnSerTyrValGluValProIleGlyCys-----Glu 301  
Db 1053 GGATTGCATCTTACATGGAATTCCTGAGTGTATTCTCAGAGAAAGAGAAAAAG 1112  
Qy 302 ArgSerGlyValGlu-----TyrArgLeuLeuGlnAlaAlaTyrLeuSerLysAlaGly 319  
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Qy 320 AlaValLeuGlyArgThrLeuGlyValHisProAspAspLeuPheThrValPhe 339  
Db 1173 GCCCAGCTTGTAGACAAATAGGAGCCGCTGAATGATGACATTTCTTTGGGGGTGTT 1232  
Qy 340 SerLysGlyGlnLysArgLysMetLysSerLeuAspGluSerAlaLeuCysIlePheIle 359  
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Qy 360 LeuLysGlnIleAsnAspArgIleLysGluArgLeuGlnSerCysTyrArgGlyGluGly 379  
Db 1293 ATCAATATGTCACGAGCTTCTTCAACAAG----- 1322  
Qy 380 ThrLeuAspLeuAlaThrLeuLysValLysAspIleProCysSerSerAlaLeuLeuThr 399  
Db 1322 ----- 1322  
Qy 400 IleAspAspAsnPheCysGlyLeuAspMetAsnAlaProLeuGlyValSerAspMetVal 419  
Db 1322 ----- 1322  
Qy 420 ArgGlyIleProValPheThrGluAspArgAspArgMetThrSerValIleAlaTyrVal 439  
Db 1323 -----ATGCTC 1328

QY 440 TyrLysAsnHisSerLeuAlaPheValGlyThrLysSerGlyLysLeuLysLysIleArg 459  
Db 1329 AACAAAAACAATGTG----- 1343  
QY 460 ValAspGlyProArgGlyAsnAlaLeuGlnTyrGluThrValGlnValValAspProGly 479  
Db 1344 -----AGATGCTCCAGCAT----- 1358  
QY 480 ProValLeuArgAspMetAlaPheSerLysAspHisGluGlnLeuTyrIleMetSerGlu 499  
Db 1359 -----TTTACGAGCCCAATCATGAG----- 1379  
QY 500 ArgGlnLeuThrArgValProValGluSerCysGlyGlnTyrGlnSerCysGlyGluCys 519  
Db 1379 ----- 1379  
QY 520 LeuGlySerGlyAspProHisCysGlyTyrCysValLeuHisAsnThrCysThrArgLys 539  
Db 1380 -----CACTGC----- 1409  
QY 540 GluArg-----CysGluArgSerLysGluProArgArg-----PheAlaSerGluMetLys 556  
Db 1410 TCATCAGGCTGTGAAGCGCGCCGTGATGAATATCGAAGAGAGTTTACCACAGCTTTCAG 1469  
QY 557 GlnCysValArgLeuThrValHisProAsnAsnIleSerValSerGlnTyrAsnValLeu 576  
Db 1470 CGCGTT-----GACTTATTCATGGTCAATTCAGCGAAGTC 1505  
QY 577 LeuVal-----LeuGluThrTyrAsnValProGluLeuSerAlaGlyValAsnCysThr 594  
Db 1506 CTCTTAACATCTATATCCACTTCATTAAAGGAGACCTC-----ACC 1547  
QY 595 PheGluAspLeuSerGluMetAspGlyLeuValValGlyAsnGlnIleGlnCysTyrSer 614  
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QY 615 ProAlaAlaLysGluValProArgIleIleThrGluAsnGlyAspHisValValGln 634  
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QY 635 LeuGlnLeuLysSerLysGluThrGlyMetThrPheAlaSerThrSerPheValPheTyr 654  
Db 1652 ----- 1652  
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Db 1653 -----TCTCCA----- 1658  
QY 675 CysLysTyrArgHisValCysThrHisAspProLysThrCysSerPheGlnGluGlyArg 694  
Db 1658 ----- 1658  
QY 695 ValLysLeuProGluAspCysProGlnLeuLeuArgValAspLysIleLeuValProVal 714  
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QY 715 GluValIleLysProIleThrLeuLysAlaLysAsnLeuProGlnProGlnSerGlyGln 734  
Db 1659 GAAGTGATTTGGAGCATACATTA-----AACCAA 1688  
QY 735 ArgGlyTyrGluCysIleLeuAsnIleGlnGlySerGluGlnArgValProAlaLeuArg 754  
Db 1689 AATGGCTACACACTGGTTATCACT----- 1712  
QY 755 PheAsnSerSerValGlnCysGlnAsnThrSerTyrSerTyrGluGlyMetGluIle 774  
Db 1713 -----GGGAAGAAGATC 1724  
QY 775 AsnAsnLeuProValGluLeuThrValValTrpAsnGly-----HisPheAsn 790  
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1764 -----CAGTCC 1769  
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QY 851 AlaLysSerLys-----CysThrAsnProArgIleThrGluIleIleProValThrGly 868  
Db 1857 ACATGGACTCAACAGATCTGTCTG---CCTGCAATCTACAGGTTTTCACAAATAGTGCA 1913  
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QY 889 -----AspIleAlaSerHisValLysValAlaGlyValGluCysSerPro 903  
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QY 904 LeuValAspGlyTyrIleProAlaGluGlnIleValCysGluMetGlyGluAlaLysPro 923  
Db 2028 TTGACTTTAGTGAGAGACAGATGATACATTAATGTCACAGTTGCT-----CCT 2078  
QY 924 SerGlnHisAlaGlyPheValGluIleCysValAlaValCysArgProGluPheMetAla 943  
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QY 1004 IleValCysAsnThrThrSerAspGluValLeuGluMetLysValSerValGlnVal 1023  
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QY 1103 LeuGlyProAspHisGlnSerAspLeuThrGluArgProGluGluPheGlyPheIleLeu 1122  
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Alignment Scores:  
 Pred. No.: 3,22e-24 Length: 2433  
 Score: 323.00 Matches: 184  
 Percent Similarity: 36.19% Conservative: 128  
 Best Local Similarity: 21.35% Mismatches: 309  
 Query Match: 3.23% Indels: 241  
 DB: 4 Gaps: 42

US-09-964-956-13 (1-1896) x US-09-300-959A-24 (1-2433)

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QY 56 ValAspGluArgThrGlyHisIleTyrLeuGlyValAlaAsnArgIleTyrLysLeuSer 75
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QY 76 SerAspLeuLysValLeuValThrHisGlu-----ThrGlyProAspGlu 90
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Db 121 AGCAACCTCAGCTCTTTGCCAGCGGGGAGTACCAAGAGCTACTGGAGTGCAGATGCT 180
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QY 91 AspAsnProLysCysTyrProProArgIleValGlnThrCysAsn-----Glu 106
   :::::|||||  |||||  |||||  |||||
Db 181 GACAGGAG-----CAGCAGTGCAGCTTCAAGGCGCAAGGAC 216
   :::::|||||  |||||  |||||  |||||
QY 107 ProLeuThrThrThrAsnAsnValAsnLysMetLeuLeuLeuLeuLeuLeuLeuLeu 126
   |||||  |||||  |||||  |||||  |||||  |||||
Db 217 CCAGAAGCGTACTGTCAAACTACATCAAGATCCTCTGT---CCATCAACAGCAGCCAC 273
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QY 127 LeuIleAlaCysGly---SerLeuTyrGlnGlyIleCysLysLeuLeuArgLeuGluAsp 145
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Db 274 CTGCTCACTGTGGCAGCGCGCTTCAAGCCCTGTGTGCTTACATTACATAGCGAGC 333
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QY 146 LeuPheLysLeuGlyGluProTyrHisLysLysGluHisTyrLeuSerGlyValaAsnGlu 165
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QY 181 -----AspLysLeuPheIleAlaThrAla-----ValAspGlyLysProGluTyr 195
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Db 391 TGTCCCTTTGACCCCAACTTCAAGTCCACGGCTGTGTGTGTGATGGT-----GAGCTG 444
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Db 445 TACACTGGAACAGTCAGTAGCTTCCAGGGAAAAGCACCAGCCATTTCGGAGCCAGAGT 504
   :::::|||||  |||||  |||||  |||||
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   :::::|||||  :::::|||||  :::::|||||  :::::
QY 225 SerMetIleLysIleProSerAspThrPheThrIleIleProAspPheAspIleTyr 244
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Db 565 TCGGCTACGTCCCGCAGAGCGCTGGCAGCGCCCATAGGTGATGATGAATCTACTTTC 624
   :::::|||||  :::::|||||  :::::|||||  :::::
QY 245 ValTyrGlyPheSerSerGlyAsnPheValTyrPheLeuThrLeuGlnProGluMetVal 264
   :::::|||||  |||||  |||||  |||||
Db 625 TTCTTCAGCGAGCGGCGGCGAGGTTTGAGTTCCTT-----660
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QY 265 SerProProGlySerThrThrLysGluGlnValTyrThrSerLysLysValArgLeuCys 284
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Db 661 -----GAGAACACATCGTGTCCCGAGTTGCCGAGTCTGT 696
   :::::|||||  |||||  |||||  |||||
QY 285 LysGluAspThrAla-----PheAsnSerTyrValGluVal 296
   :::::|||||  |||||  |||||  |||||
Db 697 AAGGGCGATAGGGTGGAGCGGGTGTTCAGCAACCGCTGGACCTCTCTTCTCAAGGCT 756
   :::::|||||  |||||  |||||  |||||
QY 297 ProIleGlyCysGluArg-----SerGlyValGluTyrArgLeuLeuGlnAlaTyr 314
   :::::|||||  |||||  |||||  |||||
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QY 315 LeuSerLysAlaGlyAlaValLeuGlyArgThrLeuGlyValHisProAspAsp----- 332  
Db 817 -----ACCCCTGAACCCCAACCTCAGAGTGGCGC 846  
QY 333 ---AspLeuLeuPheThrValPheSerLysGlyGlnLysArgLysMetLysSerLeuAsp 351  
Db 847 AAGACCCCTTCATCGGGTCTTTACCTCCAGTGGCAGAG-----GGGACCACAGAA 900  
QY 352 GluSerAlaLeuCysIlePheIleLeuLysGlnIleAsnAspArgLysGluArgLeu 371  
Db 901 GGCTGTGCATCTGGTCTTCCACATG-----AATGAT---GTCCAGAAGCCCTTT 948  
QY 372 GlnSerCysTyrArgGlyGluGlyThrLeuAspLeuAlaTTP---LeuLysValLysAsp 390  
Db 949 GACGGCCTGTACAAGAAAGTAAACAGAGAGACACAGCAGTGTATACCGAGACCACACAG 1008  
QY 391 IleProCysSerSerAlaLeuLeuThrIleAspAspAsnPheCysGlyLeuAspMetAsn 410  
Db 1009 GTGCCACACCCCGCGGAGCGTGCATTACCAACAGTGCCTGGGAGCGGAGGATCAAC 1068  
QY 411 AlaProLeuGlyValSerAsp----- 417  
Db 1069 TGGTCCCTGCAGCTCCAGACCGAGTGTGTAACCTTCTCAAGGATCACTTCTTGATGGAT 1128  
QY 418 ---MetValArgGlyIleProValPheThrGluAspArgAspArgMetThrSerValIle 436  
Db 1129 GGGCAGGTCCGAGTCCGCTGCTGCTGCTGAGCCAGAGCCGCTACAGCGTGTGCT 1188  
QY 437 AlaTyr-----ValTyrLysAsnHisSerLeuAlaPheValGlyThrLysSer 452  
Db 1189 GTGCACCGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1248  
QY 453 GlyLysLeuLysIleArgValAspGlyProArgGlyAsnAlaLeuGlnTyrGluThr 472  
Db 1249 GGGCGGCTGCACAAAGCAGTGCCTGAGCTCCAGCTCCAGAGTCCACATCATT-----GAGGAG 1302  
QY 473 ValGlnValValAspProGlyProValLeuArgAspMetAlaPheSerLysAspHisGlu 492  
Db 1303 CTGCAGATCTTCCTCAGAGCAGCTGTGAGAGACCTCTCTTGGACAGCCATGGGGA 1362  
QY 493 GlnLeuTyrIleMetSerGluArgGlnLeuThrArgValProValGluSerCysGlyGln 512  
Db 1363 CTGTTGTATGCTCCCTCCATTCGGGTGTGTGTAAGTCCCGGTAGCCAACTGCAGCGCTG 1422  
QY 513 TyrGlnSerCysGlyGluCysLeuGlySerGlyAspProHisCysGlyTrp----- 529  
Db 1423 TACCCCACTGTGGAGTGCCTCTGCTGCTGAGACCCCTACTGCGCCTGGACTGCTCT 1482  
QY 530 ---CysValLeuHisAsnThr----- 535  
Db 1483 GCCTGCAGGCTGCTAGCTCTACAGCTGATCTGCGCTCCAGGCGCATGGACCCAGGAC 1542  
QY 536 ---CysThrArgLysGluArgCysGluArgSerLysGluProArgArgPheAla 552  
Db 1543 ATTGAGGGTCCAGTGTCAAGGAACCTGCAAGAATTCTCATACAAAGCCCGGTTCTT 1602  
QY 553 SerGluMetLysGlnCysValArgLeuThrValHisProAsnAsnIleSerValSerGln 572  
Db 1603 GTGCCAGGTAAAGCATGTAACAGTCCAGATCCAAACCAACACAGTGAACACCTGGCC 1662  
QY 573 TyrAsnValLeuValLeuGluThr-----TyrAsnValProGluLeuSer 588  
Db 1663 TGCCCACTCTCTCAAACTGGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1722  
QY 589 AlaGlyValAsnCysThrPheGluAspLeuSerGluMetAspGlyLeuValValGlyAsn 608  
Db 1723 GCCTCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1776  
QY 609 Gln-----IleGlnCys----- 612  
Db 1777 CAGCAGGGTTTGGGGGTGTTCCAGTGTGCTGATAGAGAGGATTCCAGCAGCTTGTG 1836

QY 613 ---TyrSerProAlaAlaLysGlu----- 619  
Db 1837 GCAGCTACTGCCAGAGGTGATGGAGGGGGTAATGGACCAAAAGAACCCAGCGTGAT 1896  
QY 620 ---ValProArgIleIle-ThrGluAsnGlyAspHisValValGlnLeuGlnLeu 638  
Db 1897 GTPACCCCACTGATTAATCAACA-----CATCAGAGTGAAGTCCACCGGCTGT 1944  
QY 638 sSerLysGluThrGlyMetThrPheAlaSerThrSerPheValPheTyrAsnCysSerVa 658  
Db 1945 GGCAGGAGCAGCTGGGTGGGCAAGTCTTACTGGAATGAATTCCTGCTGATGTGCTACT 2004  
QY 658 lHisAsnSerCysLeuSerCysValGluSerProTyrArgCysHisTyrCysLysTyrAr 678  
Db 2005 C-----TGTTGTGTTGCTA-----TGSTGC----- 2026  
QY 678 gHisValCysThrHisAspProLysThrCysSerPheGlnGlu----- 692  
Db 2027 ---TTTTGT-----TTCGTGTTCTTCTACCGACATCGGATGGCATG 2067  
QY 693 ---GlyArgValLysLeuProGluAspCysProGlnLeu----- 704  
Db 2068 AAACCTCTTCTTAAAGCAGGCGAGTGTGCGCAGTGTGCACCCCAAGACTCGCCCTATAGTG 2127  
QY 705 ---LeuArgValAspLysIleLeuValProValGluValIleLysProIleThrLe 722  
Db 2128 CTACCACTGAGACCGCGCTGATGTTGCGCCCTCTAGCACCACCTGACCCAC 2187  
QY 722 uLysAlaLysAsnLeu-----ProGln---ProGlnSerGly-----G1 734  
Db 2188 CGAGGCTACCAAGGCTCTGTCGGATAGTCTCCAGGCGCCAGAGTCTTCACTGAATCAGAG 2247  
QY 734 nArgGlyTyr-----GluCysIleLeuAsnIleGlnGlySe 746  
Db 2248 AAGAGGCGCACTGAGCATCCAGGACAGCTTTGTAGAGTGTCTCCCGTGTGTCGCCGCC 2307  
QY 746 rGlu 747  
Db 2308 CGAG 2311  
RESULT 12  
US-09-077-940A-3  
; Sequence 3, Application US/09077940A  
; Patent No. 6576441  
; GENERAL INFORMATION:  
; APPLICANT: KIMURA, Toru et al.  
; TITLE OF INVENTION: NOVEL SEMAPHORIN Z AND GENE ENCODING THE SAME  
; FILE REFERENCE: 0020-4426P  
; CURRENT APPLICATION NUMBER: US/09/077,940A  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3  
; LENGTH: 3524  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: 5'UTR  
; LOCATION: (1)..(38)  
; OTHER INFORMATION:  
; NAME/KEY: 3'UTR  
; LOCATION: (2706)..(3524)  
; OTHER INFORMATION:  
; NAME/KEY: CDS  
; LOCATION: (39)..(2702)  
; OTHER INFORMATION:  
; US-09-077-940A-3  
Alignment Scores:  
Pred. No.: 2 456-17 Length: 3524  
Score: 263.00 Matches: 144  
Percent Similarity: 36.91% Conservative: 90  
Best Local Similarity: 22.71% Mismatches: 208

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Query Match: 2.63% Indels: 192
DB: 4 Gaps: 34
US-09-964-956-13 (1-1896) x US-09-077-940A-3 (1-3524)

QY 11 LeuLeuSerHisLeuLeuMetValGlyMetGlySerSerThrLeuLeuThrArgGlnPro 30
DB 75 CTGCTCTTCTGCTGCTACTACTGGGG---GGCGCCACGCGCTCTTCTCCTGAGACCCG 131
QY 31 AlaProLeuSerGlnLysGlnArgSerPheValThrPhe----- 43
DB 132 CCGCCCTTAGCTGCGCCCGCCAGGACTACCTGAACCATATCCCGTGTGTGGGCAGC 191
QY 44 -----ArgGlyGluProAlaGluGlyPheAsnHisLeuValValAsp----- 57
DB 192 GGGCCCGGAGCGCTGACCCCGCAGAGAGTGTGACGACCTCAACATCCAGCGAGTCCTG 251
QY 58 -----GluArgThrGlyHisIleTyrLeuGlyAlaValAsnArgIleTyrLysLeu--- 74
DB 252 CGGGTCAACAGGAGC-----CTGTTCAATGGGGACAGGACAACTCTACCGGTAGAG 305
QY 75 -----SerSerAspLeuLysVal-----LeuValThrHisGluThrGly 87
DB 306 CTGAGAGCCCGCCACGCTCCAGGAGTCCGCTACAGAGGAGCTGACCTGGAGATCTAAC 365
QY 88 ProAspGluAspAsnProLysCysTyrProProArgIleValGlnThrCysAsnGluPro 107
DB 366 CCCAGGCACATAACGCTGCTCGGATGAAGGCAACAGAGGCGGAGTGTCA----- 419
QY 108 LeuThrThrThrAsnAsnValAsnLysMetLeuLeuIleAspTyrLysGluAsnArgLeu 127
DB 420 -----AACTTCGTAAGGTGCTGCTCTCTTCGGGAC-----GAGTCCACGCTC 461
QY 128 IleAlaCysGlySer---LeuTyrGlnGlyIleCysLysLeuLeuArgLeuGluAspLeu 146
DB 462 TTTGTGTGCGGTTCACACGCTTCAACCGGTGTGCGCAACTACAGCATAGACACCCCTG 521
QY 147 PheLysLeuGlyGlu-----ProTyrHisLysLysGluHis 158
DB 522 CAGCCCGTCGGAGACAACATCAGCGGTATGCGCGCTGCGGACAGCCCAAG---CAC 578
QY 159 TyrLeuSerGlyValAsnGluSerGlySerValPheGlyValIleValSer----- 175
DB 579 GCCAATGTTGCCCTTCTCTGACGGGATGCTCTTCAACGCTACTGTACCGACTTCCTA 638
QY 176 -----TyrSerAsnLeuAspLysLeuPheIleAlaThrAlaVal 189
DB 639 GCCATTGATGCTCATCTACCGCAGCGCTCGGGACAGG----- 677
QY 190 AspGlyLysProGluTyrPheProThrIleSerSerArgLysLeuThrLysAsnSerGlu 209
DB 678 -----CCACCGCTGGCACCCTGAAA----- 698
QY 210 AlaAspGlyMetPheAlaTyrValPheHisAspGluPheValAlaSerMetIleLysIle 229
DB 699 -----CATGAC-----TCCAAAGTGTTCAAAGAG 722
QY 230 ProSerAspThrPheThrIleIleProAspPheAspIleTyrTyrValTyrGlyPheSer 249
DB 723 CCT-----TACTTTGTCCATCGCGTGGAG 746
QY 250 SerGlyAsnPheValTyrPheLeuThrLeuGlnProGluMetValSerProGlySer 269
DB 747 TGGGGCAGCCATGCTACTCTTCTTCGGGAGATTGCGATG-----GAGTTT 794
QY 270 ThrThrLysGluGlnValTyrThrSerLysLeuValArgLeuCysLysGluAspThrAla 289
DB 795 AACCTACCTGGAGAGGTGTGTGTCGCGCTGCGCGGAGTGTGCAAGACGAGCTGGGA 854
QY 290 -----PheAsnSerTyrValGluValProIleGlyCys 300
DB 855 GGCTCCCCCGCTGCTGGAGAGCAGTGGAGCTCTCTCTGTAAGCGCGGCTCACTGTC 914

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QY 301 GluArgSerGly-----ValGluTyrArgLeuLeuGlnAlaTyrLeuSerLys 317
DB 915 TCTGTACCGGAGACTCCCATTTTCTACTTCAAGTGTCTGAGGCTGTC----- 962
QY 318 AlaGlyAlaValLeuGlyArgThrLeuGlyValHisProAspAspLeuLeuPheThr 337
DB 963 ACGGGCGTGTCT-----AGCTCGGGGCGCGGCC-----GTGGTCTGGCC 1004
QY 338 ValPheSerLysGlyGlnLysArgLysMetLysSerLysLeuAspGluSerAlaLeuCysIle 357
DB 1005 GTTTTTTCTC-----ACGCCAGCAACAGCATCCCTGCTGGCTGTCTGGGCC 1052
QY 358 PheIleLeuLysGlnIleAsnAspArgIleLysGluArgLeuGlnSerCysTyrArgGly 377
DB 1053 TTGACCTGACACAGGTGGCAGCTGTGTTGAAGGCCGC-----TTCGAGAG 1100
QY 378 GluGlyThrLeuAspLeuAlaTyrLeuLysValLysAsp-----IlePro----- 392
DB 1101 CAGAAGTCCCGGATCCATCTGACGCGGTGCGGAGGATCAGGTGCTCTGACCCCGG 1160
QY 393 -----CysSerSerAlaLeuLeuThrIleAspAspAsnPheCysGlyLeuAspMetAsn 410
DB 1161 CCCGGGTGCTCGCGAGCC-----CCCGGATGCACTACAT 1196
QY 411 Ala-----ProLeuGlyValSerAspMetValArgGlyIleProValPheThr 426
DB 1197 GCCTCCAGCGCTTCGCGGATGACATCTCAACTTTGTCAAGACCCACCTCTGTATGAC 1256
QY 427 GluAsp-----ArgAspArg 431
DB 1257 GAGCGGTGCTCGTGGCCATCGCCCTGGATCGCGACCTGATGAGGACCCAG 1316
QY 432 MetThrSerValIleAlaTyrVal-----TyrLysAsnHisSerLeuAlaPhe 447
DB 1317 CTGACTCAGTGTGCTGTGACGCGCGCCCTGGGCAACCGACGCGTTGTCTTC 1376
QY 448 ValGlyThrLysSerGlyLysLeuLysLysIleArgVal-----Asp 461
DB 1377 CTGGGTTCTGAGCGGGACGCTCTCAAGTTCCTGCTCGGCCCAATGCCAGACCTCA 1436
QY 462 GlyProArgGlyAsnAlaLeuGlnTyrGluThrValGlnValAlaAspPro----- 478
DB 1437 GGGAGCTCTGGCTCAGTGTCTTCTGAGGAGTTTGAGACTTACCGCGCGGACAGGTGT 1496
QY 479 -----GlyProValLeuArgAspMetAlaPheSerLysAsp 490
DB 1497 GGACGGCGCGGCTGGCGAGACAGGCGGCTGCTGAGCTTGGAGCTGGACGAGCT 1556
QY 491 HisGluGlnLeuTyrIleMetSerGluArgGlnLeuThrArgValProValGluSerCys 510
DB 1557 TCGGGGGCGCTCTGCTGCTGCTTCCCGCTGCGGTGCTCGAGTCCCTGTGGCTCGCTGC 1616
QY 511 GlyGlnTyrGlnSerCys---GlyGluCysLeuGlySerGlyAspProHisCysGlyTyr 529
DB 1617 CAGCAGTACTCGGGGTGTATGAAGAACTGTATCGGAGCTCAGGACCCCTACTCTCGCGTGG 1676
QY 530 -----CysValLeuHisAsnThrCysThrArg 538
DB 1677 GCCCGCGAGCGCTCTGCTGATCTTCTCAGCCCGGCGACAG 1718

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RESULT 13
US-09-077-940A-1
; Sequence 1, Application US/09077940A
; Patent No. 6576441
; GENERAL INFORMATION:
; APPLICANT: KIMURA, Toru et al.
; TITLE OF INVENTION: NOVEL SENAPHORIN Z AND GENE ENCODING THE SAME
; FILE REFERENCE: 0020-4426P
; CURRENT APPLICATION NUMBER: US/09/077,940A
; CURRENT FILING DATE: 1998-06-05
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1

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; LENGTH: 3692
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: (1)..(18)
; OTHER INFORMATION:
; NAME/KEY: CDS
; LOCATION: (19)..(2682)
; OTHER INFORMATION:
; NAME/KEY: 3'UTR
; LOCATION: (2683)..(3653)
; OTHER INFORMATION:
; NAME/KEY: polyA site
; LOCATION: (3654)..(3692)
; OTHER INFORMATION:
US-09-077-940A-1

Alignment Scores:
Pred. No.: 2,86e-15 Length: 3692
Score: 244.50 Matches: 141
Percent Similarity: 35.69% Conservative: 86
Best Local Similarity: 22.17% Mismatches: 206
Query Match: 2.45% Indels: 203
DB: 4 Gaps: 34

US-09-964-956-13 (1-1896) x US-09-077-940A-1 (1-3692)

Qy 8 TtpThr-----CysLeuSerHisLeuMetValGly 19
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Db 22 TGAACCCCGAGCGCCCTCCAGCCCGGCCCTGCTGTTCCTCTGCTGTGCTTCG 81

Qy 20 MetGlySerSerThrLeuLeuThrArgGlnProAlaProLeuSerGlnLysGlnA+GSer 39
   |||||
Db 82 AGGTCACCCATGGCCTTTCCCATGAACCACTCCATCAGTGTGGCTCCAGGAC 141

Qy 40 PheValThrPhe-----ArgGlyGluProAlaGlu 49
   |||||
Db 142 TACCTGAGCACTACCCCGTGTCTGGGAGCGGGCTGTGCTGTGACCCCTGCAGAG 201

Qy 50 GlyPheAsnHisLeuValValAsp-----GluArgThrGlyHisIleTyr 64
   |||||
Db 202 GGTGCTGAGGACCTCAACATCAGAGAGTGTACGTGTTACAGGACA-----CTGTTTC 255

Qy 65 LeuGlyAlaValAsnArgIleTyrLysLeu-----SerSerAspLeu 78
   |||||
Db 256 ATCGGGGACAGAGACAACCTGTACCAGTAGAAGTGGAGCCATCCATCCACGGAGCTG 315

Qy 79 LysVal-----LeuValThrHisGlnThrGlyProAspGluAspProLysCysTyr 96
   |||||
Db 316 CGGTATCAGCGGAGCTTACTCGCGCTCCAAACCCAGTGAC----- 357

Qy 97 ProProArgIleValGlnThrCys-----AsnGluProLeuThrThrAsn 112
   |||||
Db 358 -----ATCATGTGTGTCGGATGAAGGGCAAGCAGAGGGTGAGTGTCCGGAAC 405

Qy 113 AsnValAsnLysMetLeuLeuIleAspTyrLysGluAsnArgLeuIleAlaCysGlySer 132
   |||||
Db 406 TTGTCAAGGTGCTCTGCTTCGTGAC-----GAATCCAGCTCTTCGTGTGGGCTCC 459

Qy 133 ---LeuTyrGlnGlyIleCysLysLeuLeuArgLeuGluAspLeuPheLysLeuGlyGlu 151
   |||||
Db 460 AATGCATTCAATCCCATCTGTGCCAATTACAGTATGGACACACTGCAGCTTCTTGGAGAC 519

Qy 152 -----ProTyrHisLysLysGluHisIleThrLeuSerGlyVal 163
   |||||
Db 520 AACATCAGTGGTATGGCCCGCTGCCCTACGACCCCAAG---CATGCCAATGTCCGCTC 576

Qy 164 AsnGluSerGlySerValPheGlyValIleValSer----- 175
   |||||
Db 577 TTCTCAGATGGGATGCTCTTTCACAGCCACAGTAATCTACTCTTCAGCCATCGACGTGTT 636

Qy 176 ---TyrSerAsnLeuAspLysLeuPheIleAlaThrAlaValAspGlyLysProGlu 194

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101 ValGlnThrCysAsnGluProLeuThrThrThrAsnAsnValAsnLysMetLeuLeuLe 120
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776 AAAGATGAATGCCCAACTTATC-----AAAGTATTGGTT 811
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
121 AspTyrLysGluAsnArgLeuLeuAlaCysGly--SerLeuTyrGlnGlyLeCysLys 139
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
812 CCAAGAAACCATGATGATGGTTTTGTGTGTGGTACCAATGCATGCAATCCCATGTGTAGA 871

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copy 123

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872  TACTACAGGTTGAGTACCTTAGAATATGATGGGAGAGAA----- 910

160  LeuSerGlyVal-----AsnGluSerGlySerValPheGly 171
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911  ATTAGTGGCTGGCAAGATGCCATTTGATGCCAGACAAACCAATGTTGCCCTCTTTGCT 970
      |||:|||||

172  ValIleValSerTyrSerAsnLeuAspAspLysLeuPheIleAlaThrAlaValAspGly 191
      |||:|||||
971  -----GATGGGAGAGCTGATTCTGCCACAGTGGCTGAC--- 1003
      |||:|||||

192  LysProGluTyrPheProThrIleSerSerArgLysLeuThrLysAsnSerGluAlaAsp 211
      |||:|||||
1004 -----TTCTTGGCCAGCGATGCCGTTATTTATCGAAGCATGGTGTGAT 1045

212  GlyMetPheAlaTyrValPheHisAspGluPheValAlaSerMetIleIleValProSer 231
      |||:|||||
1046  GGATCTGCCCTTCCGCAATA-----AAATATGATTCCAAATGGATAAAGAGGCCA--- 1096

232  AspThrPheThrIleIleProAspPheAspIleTyrValTyrGlyPheSerSerGly 251
      |||:|||||
1097 -----CACTTTCTTCATGCCATAGAATATGGA 1123

252  AsnPheValTyrPheLeuThrLeuGlnProGluMetValSerProGlySerThrThr 271
      |||:|||||
1124  AACATATGCTATTTCTTCTTTCGAGAA-----ATCGCTGTGGAACATAATAATTTA 1174
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272  LysGluGlnValTyrThrSerLysLeuValArgLeuCysLysGluAspThrAla----- 289
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SECRET

290 -----PhaAsnSerTyrValGluValProIleGlyCysGluArg 302  
 1232 CAGCGGGTCTGGAGAAACACTGGACTCATTTCTAAGGCTCGGCTGAAGTTCGTGTC 1291  
 303 SerGly-----ValGluTyrArgLeuGlnAlaAlaTyrLeu 315

FOIA b 7

[illegible]



QY 421 ylleProValPheThrGluAsp-----ArgAspArgMetThrSerVal----- 435
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QY 436 -lleAlaTyrrValTyrrLysAsnHisSerLeuAlaPheValGlyThrLysSerGlyLysLe 455
Db 1717 TTCAGCGGACCTTACAGACTACAGACTCATCTTTGTTGGCTCGAAGCTGGCATGGT 1776
QY 455 uLysLysIle----- 458
Db 1777 ACTTAAAGTTCTGGCAAGACCAAGTCTTTCTTTTGAACGACAGCGTATTACTGGAAGA 1836
QY 459 -----ArgValAspGlyProArgGlyAsnAlaLeuGlnTyrrGluThrValGlnValVa 476
Db 1837 GATTGAAGCTTACACCAAGTCAAGTGCAGTCTGAGATGAGGAGACAAAGAGTCAAT 1896
QY 476 lAspProGlyProValLeuArgAspMetAlaPheSerLysAspHisGluGlnLeuTyrrI 496
Db 1897 C-----TCATTACAGITGGATAAAGATCAACACGCTTTTATGT 1935
QY 496 eMetSerGluArgGlnLeuThrArgValProValGluSerCysGlyGlnTyrrGlnSerCy 516
Db 1936 GGGTCTCTAGCTGATATTCGCAATCCCTCAGTCCGCTGAGCGGTATGGATCATG 1995
QY 516 sGlyGlu---CysLeuGlySerGlyAspProHisCysGlyTyrCysValLeuHisAsnTh 535
Db 1996 TAAAAAGTCTTGATTGATCTCTGACCCGATTGCTGGTGG---TTAAGCCAGGATC 2052
QY 535 rCysThrArg 538
Db 2053 CTGTGGTAGA 2062
RESULT 15
US-09-653-274-5
; Sequence 5, Application US/09653274
; Patent No. 6635742
; GENERAL INFORMATION:
; APPLICANT: Boyle, Bryan J
; APPLICANT: Yeung, George Y
; APPLICANT: Arterburn, Matthew C
; APPLICANT: Mize, Nancy K
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Dmanac, Radoje T
; TITLE OF INVENTION: Methods and Materials Relating to Semaphorin-Like
; FILE REFERENCE: HYS-23
; CURRENT APPLICATION NUMBER: US/09/653,274
; PRIOR APPLICATION DATE: 2000-08-31
; PRIOR FILING DATE: 2000-01-10
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 5
; LENGTH: 3261
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-653-274-5
Alignment Scores:
Pred. No.: 1,45e-13 Length: 3261
Score: 228.00 Matches: 128
Percent Similarity: 37.30% Conservative: 101
Best Local Similarity: 20.85% Mismatches: 224
Query Match: 2.28% Indels: 162
DB: 4 Gaps: 29
US-09-964-956-13 (1-1896) x US-09-653-274-5 (1-3261)
QY 10 CysLeuSerHisLeuLeuMetValGlyMetGlySerSerThrLeuLeuThrArgGln 29
Db 19 TGTGCTACATATCTGCTGATGTTTCCAGCTTGGGCGAGTCTTCTCTGAGAT 78

QY 30 ProAlaProLeuSer-----GlnLysGlnArgSerPheValThrPheArgGly 45
Db 79 GATGAACCCCTTATATCTGCTGACTATCACTATTCAAGGCAATATCCGGTTTTTAGAGGA 138
QY 46 GluProAlaGluGlyPheAsnHisLeuValValAsp-----GluArgThr 60
Db 139 CGCCCTTCAGGCAATGATCGCAGCAGAGCTTTCAGCTGATGTTGAAATTCGA 198
QY 61 GlyHisIleTyrrLeuGlyAlaValAsnArgIleTyrrLysLeuSerSerAspLeuLysVal 80
Db 199 GACACACTTATATGCTGCGAGGATCAAGTTTATACAGTA-----AACTTAAATGAA 252
QY 81 LeuValThrHisGluThrGlyProAsp-----Gluasp 91
Db 253 ATGCCCAAAACAGAAAGTAATACCCACACAGAAACTGACATGGCGATCAAGACACAGAT 312
QY 92 AsnProLysCys---TyrrProArgIleValGlnThrCysAsnGluProLeuThrThr 110
Db 313 CGAGAAACTGCTGATGAAAGGCAAGCATAAAGATGAATGCCCAACTTTATC----- 366
QY 111 ThrAsnAsnValAsnLysMetLeuLeuLeuAspTyrrLysGluAsnArgLeuIleAlaCys 130
Db 367 -----AAAGTATTGTTTCCAGAAACGATGAGATGGTGTGTTTGT 408
QY 131 Gly---SerLeuTyrrGlnGlyIleCysLysLeuLeuArgLeuGluAspLeuPheLysLeu 149
Db 409 GGTACCAATGCAATCCATGCTGATAGTACTACAGGTTGAGTACCTTTAGAATATGAT 468
QY 150 GlyGluProTyrrHisLysLysGluHisTyrrLeuSerGlyVal----- 163
Db 469 GGGGAGAA-----ATTGTCGCTGGCAAGCTGTGTAT---TCCCGCGTGGCC 507
QY 164 -----AsnGluSerGlySerValPheGlyValIleValSerTyrrSerAsnLeuAspAsp 181
Db 508 GCCAGACAAACCAATGTTGCCCTTTTGT-----GATGGG 543
QY 182 LysLeuPheIleAlaThrAlaValAspGlyLysProGluTyrrPheProThrIleSerSer 201
Db 544 AAGCTGATTCTGCCACAGTGGCTGAC-----TTCTGGCCAGC 582
QY 202 ArgLysLeuThrLysAsnSerGluAlaAspGlyMetPheAlaTyrrValPheHisAspGlu 221
Db 583 GATCGCTATTATTCGAGCATGGGTGATGGATCTGCCCTTCCACAAATA-----AAA 636
QY 222 PheValAlaSerMetIleLysIleProSerAspThrPheThrIleIleProAspPheAsp 241
Db 637 TATGATTCCAAATGGATAAAAGAGCCA----- 663
QY 242 IleTyrrValTyrrGlyPheSerSerGlyAsnPheValTyrrPheLeuThrLeuGlnPro 261
Db 664 ---CACTTTCTTATGCGATAGATATGGAACATATGTTCTTCTTCTTCGAGAA--- 717
QY 262 GluMetValSerProGlySerThrThrLysGluGlnValTyrrThrSerLysLeuVal 281
Db 718 -----ATCGCTGTGGAACATAATAATTAGCAAGGCTGTGTAT---TCCCGCGTGGCC 768
QY 282 ArgLeuCysLysGluAspThrAla-----PheAsnSer 292
Db 769 CGCATATGTAATAAACGACATGGGTGGTTCGAGCGGTCTCGAGAAACACTGGACTTCA 828
QY 293 TyrValGluValProIleGlyCysGluArgSerGly-----Val 305
Db 829 TTTCTAAAGGCTCGGCTGAACCTGTTCTGCTCGAGATCGGTTTTTCTTACTTTGATGTT 888
QY 306 GluTyrrArgLeuLeuGlnAlaAlaTyrrLeuSerLysAlaGlyAlaValLeuGlyArgThr 325
Db 889 CTGCAGTCTATTACAGACATAATAACAATCAATGGCATCCCACTGGTGGTGGG----- 942
QY 326 LeuGlyValHisProAspAspLeuPheThrValPheSerLysGlyGlnLysArg 345
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GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

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Scoring table:

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Searched: 2953838 seqs, 2272363821 residues

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Listing first 45 summaries

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Database : Published Applications NA:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Query Match	Score	Length	DB ID	Description
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## RESULT 1

US-09-964-956-12  
; Sequence 12, Application US/09964956  
; Publication No. US20040043926A1

## GENERAL INFORMATION:

; APPLICANT: Gerlach, Valerie L  
; APPLICANT: MacDougall, John R  
; APPLICANT: Smithson, Glennda  
; APPLICANT: Millet, Isabelle  
; APPLICANT: Stone, David  
; APPLICANT: Gunther, Erik  
; APPLICANT: Ellerman, Karen  
; APPLICANT: Grosse, William M  
; APPLICANT: Alsobrook II, John P  
; APPLICANT: Lepley, Denise M  
; APPLICANT: Burgess, Catherine E  
; APPLICANT: Padigar, Muralidhara  
; APPLICANT: Kekuda, Ramesh  
; APPLICANT: Spytek, Kimberly A  
; APPLICANT: Leach, Martin D  
; APPLICANT: Shimkets, Richard A  
; TITLE OF INVENTION: No. US20040043926A1 Proteins and Nucleic Acids Encoding Same  
; FILE REFERENCE: 21402-124

## ALIGNMENTS

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4	6357	63.6	6147	13	US-10-312-352-70	Sequence 70, Appl
5	6267.5	62.7	5895	13	US-10-087-684-31	Sequence 31, Appl
6	6267.5	62.7	5895	13	US-10-218-779-31	Sequence 31, Appl
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9	2539	25.4	6329	13	US-10-276-774-838	Sequence 838, App
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, CURRENT APPLICATION NUMBER: US/09/964,956
, CURRENT FILING DATE: 2001-09-26
, PRIOR APPLICATION NUMBER: 60/235,631
, PRIOR FILING DATE: 2000-09-27
, PRIOR APPLICATION NUMBER: 60/235,633
, PRIOR FILING DATE: 2000-09-27
, PRIOR APPLICATION NUMBER: 60/235,808
, PRIOR FILING DATE: 2000-09-27
, PRIOR APPLICATION NUMBER: 60/235,064
, PRIOR FILING DATE: 2000-09-27
, PRIOR APPLICATION NUMBER: 60/236,065
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, PRIOR APPLICATION NUMBER: 60/236,135
, PRIOR FILING DATE: 2000-09-28
, PRIOR APPLICATION NUMBER: 60/237,434
, PRIOR FILING DATE: 2000-10-03
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, PRIOR FILING DATE: 2000-10-05
, PRIOR APPLICATION NUMBER: 60/238,399
, PRIOR FILING DATE: 2000-10-06
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, PRIOR FILING DATE: 2000-10-06
, PRIOR APPLICATION NUMBER: 60/276,667
, PRIOR FILING DATE: 2001-03-16
, PRIOR APPLICATION NUMBER: 60/294,823
, PRIOR FILING DATE: 2001-05-31
, PRIOR APPLICATION NUMBER: 60/304,868
, PRIOR FILING DATE: 2001-07-12
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, SOFTWARE: PatentIn Ver. 2.1
, SEQ ID NO 12
, LENGTH: 5691
, TYPE: DNA
, ORGANISM: Homo sapiens
US-09-964-956-12

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1381 ArgAspArgGlyAsnValAlaSerLeuIleMetThrValLeuGlnSerLysLeuGluTyr 1400  
4141 CCGGACCGTGGCAACGTGGCTCTCATCATGACCGCTGCTGAGCAAGCTGGAGTAC 4200  
1401 AlaThrAspValLeuLysGlnLeuAlaAspLeuIleAspLysAsnLeuGluSerLys 1420  
4201 GCCACTGATGTGCTGAAGCAGCTGCTGGCCGACCTCATTTGACAAGAACCTGGAGAGCAAG 4260  
1421 AsnHisProLysLeuLeuLeuArgThrGluSerValAlaGluLysMetLeuThrAsn 1440  
4261 AACCAACCTTAAGTGTGCTGCTGAGGAGCTGAGTCAAGTGGCTGAGAAAGTGTGACCAAT 4320  
1441 TrpPheThrPheLeuLeuTyrLysPheLeuLysGluCysAlaGlyGluProLeuPheSer 1460  
4321 TGGTTTACTTCT 4380  
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4381 CTGTTCTGCTCCATCAAGCAGCAGATGGAGAAAGGCGCCCATTTGACGCCATCAGCGCGAG 4440  
1481 AlaArgTyrSerLeuSerGluAspLysLeuIleArgGlnGlnIleAspTyrLysThrLeu 1500  
4441 GCCCGCTACTCTTGAGCGAGGACAGCTCATCCGCGACAGATTGACTACAAACCCCTG 4500  
1501 ValLeuSerCysValSerProAspAsnAlaAsnSerProGluValProValLysIleLeu 1520  
4501 GTCTCTGAGCTGTCTCAGCCAGACAATGCCAACAGCCCGGAGTCCCGAAGAAATCCTC 4560  
1521 AsnCysAspThrIleThrGlnValLysGluLysIleLeuAspAlaIlePheLysAsnVal 1540  
4561 AACTGTGACACCATCTCTAGGTCAAGGAGAGATTCTGGATGCCATCTTCAAGAAATGTG 4620  
1541 ProCysSerHisArgProLysAlaAlaAspMetAspLeuGluTrpArgGlnGlySerGly 1560  
4621 CCTTGTCTCCACCGGCCCAAGCTGCAGATATGGATCTGGAGTGGCGACAAGAAAGTGGG 4680  
1561 AlaArgMetIleLeuGlnAspGluAspIleThrThrLysIleGluAsnAspTrpLysArg 1580  
4681 GCAAGGATGATCTTGACGGATGAAGACATCCACCAGATGAGAAATGATTGGAGGCGA 4740  
1581 LeuAsnThrLeuAlaHisTyrGlnValProAspGlySerValAlaLeuValSerLys 1600

4741 CTGAACACACTGGCCCACTACCAAGTGCAGATGGTTCGGTGGCATTTAGTGTCCAAG 4800  
1601 GlnValThrAlaTyrAsnAlaValAsnAsnSerThrValSerArgThrSerAlaSerLys 1620  
4801 CAGGTGACAGCCTATAACCGCAGTGAACAACCTCACCGTCTCCAGGACCTCAGCAAGTAAA 4860  
1621 TyrGluAsnMetIleArgTyrThrGlySerProAspSerLeuArgSerArgThrProMet 1640  
4861 TATGAATAACATGATCCGGTACACGGGACGCCCCGACAGACCTCCGCTCAGGACACCTATG 4920  
1641 IleThrProAspLeuGluSerGlyValLysMetTrpHisLeuValLysAsnHisGluHis 1660  
4921 ATCACTCTCAGCTGGAGAGTGGAGTCAAGATGTGCACCTAGTAGAAGAACACGAGCAC 4980  
1661 GlyAspGlnLysGluLysAspArgGlySerLysMetValSerGluIleTyrLeuThrArg 1680  
4981 GGAGACCAGAAAGGAGGGGACCGGGGAGCAAGATGGTGTCTGAATCTACCTGAGCCCGA 5040  
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5041 CTCCTGCGCACTAAGGCGACACTGCAGAAATTTGTGGATGACCTCTTTGAGACCATCTTC 5100  
1701 SerThrAlaHisArgGlySerAlaLeuProLeuAlaIleLysTyrMetPheAspPheLeu 1720  
5101 AGCAGGCAACACCGTGGCTCTGCCCTGCCCTGCCATCAAGTACATGTTTGACTTCTCTG 5160  
1721 AspGluAlaAspLysHisGlyIleHisAspProHisValArgHisThrIlePheSer 1740  
5161 GATGAGCAGGCTGATAAACATGCAATCATGACCCGCACTCGCGCCATACCTGGAAGAGC 5220  
1741 AsnCysLeuProLeuArgPheTrpValAsnMetIleLysAsnProGlnPheValPheAsp 1760  
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1761 IleHisLysAsnSerIleThrAspAlaCysLeuSerValAlaGlnThrPheMetAsp 1780  
5281 ATCCATAAGAACAGCATCACAGACGCTGCTCTCTGTGGTGGCTCAGACCTTCATGGAC 5340  
1781 SerCysSerThrSerGluHisArgLeuGlyLysAspSerProSerAsnLysLeuLeuTyr 1800  
5341 TCTTGTCTCCAGCTCAGAGACCGGCTGGGCAAGAGACTCGCCCTCCAAACAAGCTGCTGAT 5400  
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5401 GCCAAGGACATCCCCAGCTACAGAAATTGGTGGAGAGGTATTACTCAGACATAGGGAAG 5460  
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5461 ATGCCAGCCATCAGCGACCAAGACATGAACGCATACCTGGCTGAGCAGTCCCGGATGCAC 5520  
1841 MetAsnGluPheAsnThrMetSerAlaLeuSerGluIlePheSerTyrValGlyLysTyr 1860  
5521 ATGAATGATTTCAACACCATGAGTGCATCTCAGAGATCTTCTCTATGTGGCAATATC 5580  
1861 SerGluGluLeuLeuGlyProLeuAspHisAspAspGlnCysGlyLysGlnLysLeuAla 1880  
5581 AGCAGGAGATCTCTTGGACCTCTGGACCATCGATGAGCAGTGGGAGAGCAAGAACTGGCC 5640  
1881 TyrLysLeuGluGlnValIleThrLeuMetSerLeuAspSer--AsnLys 1896  
5641 TACAACTAGAACAAAGTCATAACCTCTATGAGCTTAGACAGCTGAATATAA 5691

## RESULT 2

US-10-451-010-19  
; Sequence 19, Application US/10451010  
; Publication No. US20040082761A1  
; GENERAL INFORMATION:  
; APPLICANT: INCYTE GENOMICS, INC.  
; APPLICANT: DUGGAN, Brendan M.  
; APPLICANT: XU, Yuming  
; APPLICANT: LEE, Ernestine A.  
; APPLICANT: LEE, Sally

APPLICANT: LU, Dyoung Aina M.  
APPLICANT: WARREN, Bridget A.  
APPLICANT: YUE, Henry  
APPLICANT: GIETZEN, Kimberly J.  
APPLICANT: HONCHELL, Cynthia D.  
APPLICANT: BURFORD, Neil  
APPLICANT: BAUGHN, Mariah R.  
APPLICANT: TANG, Y. Tom  
APPLICANT: JACKSON, Jennifer L.  
APPLICANT: GANDHI, Ameena R.  
APPLICANT: KALLICK, Deborah A.  
APPLICANT: BANDMAN, Olga  
APPLICANT: GRAUL, Richard C.  
APPLICANT: CHAWLA, Narinder K.  
APPLICANT: LU, Yan  
APPLICANT: RAMKUNAR, Javalaxmi  
APPLICANT: YAO, Monique G.  
APPLICANT: LAL, Preeti G.  
TITLE OF INVENTION: CELL ADHESION PROTEINS  
FILE REFERENCE: PF-0867 USN  
CURRENT APPLICATION NUMBER: US/10/451.010  
CURRENT FILING DATE: 2003-06-17  
PRIOR APPLICATION NUMBER: PCT/US01/49206  
PRIOR FILING DATE: 2001-12-18  
PRIOR APPLICATION NUMBER: US 60/256,542  
PRIOR FILING DATE: 2000-12-18  
PRIOR APPLICATION NUMBER: US 60/259,604  
PRIOR FILING DATE: 2000-12-22  
PRIOR APPLICATION NUMBER: US 60/260,101  
PRIOR FILING DATE: 2001-01-05  
NUMBER OF SEQ ID NOS: 20  
SOFTWARE: PERL Program  
SEQ ID NO 19  
LENGTH: 6367  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc feature  
OTHER INFORMATION: Incyte ID No: 7156379CB1  
FEATURE:  
NAME/KEY: unsure  
LOCATION: 166  
OTHER INFORMATION: a, t, c, g, or other  
US-10-451-010-19  
Alignment Scores:  
Pred. No.: 0 Length: 6367  
Score: 9979.00 Matches: 1894  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 99.89% Indels: 0  
DB: 17 Gaps: 0  
US-09-964-956-13 (1-1896) x US-10-451-010-19 (1-6367)  
Qy 1 MetLysAlaMetProTtpAsnTrpThrCysLeuLeuSerHisLeuLeuMetValGlyMet 20  
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Qy 21 GlySerSerThrLeuLeuThrArgGlnProAlaProLeuSerGlnLysGlnArgSerPhe 40  
Db 626 GGCTCCTCCACTTGGCTCACCCGCGACGCCCTGTCTCCAGAACGACGCGGTCAATT 685  
Qy 41 ValThrPheArgGlyGluProAlaGluGlyPheAsnHisLeuValValAspGluArgThr 60  
Db 686 GTCACATTCGAGAGAGACCCCGCGAGGTTTCAATCACCTGGTGGTGGATGAGAGACA 745  
Qy 61 GlyHisIleTyrLeuGlyAlaValAsnArgIleTyrLysLeuSerSerAspLeuLysVal 80  
Db 746 GGACACATTTACTTGGGGGGCGGTCAATCGGATTTTACAGCTCTCCAGCGACCTGAAGTC 805  
Qy 81 LeuValThrHisGluThrGlyProAspGluAspAsnProLysCysTyrProProArgIle 100

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Qy 101 ValGlnThrCysAsnGluProLeuThrThrThrAsnAsnValAsnLysMetLeuLeuIle 120  
Db 866 GTCCAGACCTTGAATGAGCCCTTACACACCAACCAATGTCACCAAGATGCTCTCTATA 925  
Qy 121 AspTyrLysGluAsnArgLeuIleAlaCysGlySerLeuTyrGlnGlyIleCysLysLeu 140  
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Qy 141 LeuArgLeuGluAspLeuPheLysLeuGlyGluProTyrHisLysLysGluHisTyrLeu 160  
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Qy 161 SerGlyValAsnGluSerGlySerValPheGlyValIleValSerTyrSerAsnLeuAsp 180  
Db 1046 TCAGGTGTCAACGAGAGCGGCTCAGTCTTTGGAGTGATCGTCTCTCAGCAACCTGGAT 1105  
Qy 181 AspLysLeuPheIleAlaThrAlaValAspGlyLysProGluTyrPheProThrIleSer 200  
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Db 1166 AGCCGGAACCTGACCAAGAACTCTGAGGCGGATGGCATGTTCCGCTAGCTCTTCCATGAT 1225  
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Db 1286 GATATCTACTATGCTATGGTTTTAGCAGTGGCAACTTTTGTCTACTTTTGTACCCCTCAA 1345  
Qy 261 ProGluMetValSerProGlySerThrThrLysGluGlnValTyrThrSerLysLeu 280  
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Db 1466 GAGCGCAGTGGGTGGAGTACCGCTGTGCGAGGTGCTCTACCTGTCCAAAGCGGGGCG 1525  
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Db 1526 GTGCTTGGCAGGACCTTGGAGTCCATCCAGATGATGACCTGCTCTTACCGCTCTTCTCC 1585  
Qy 341 LysGlyGlnLysArgLysMetLysSerLeuAspGluSerAlaLeuCysIlePheIleLeu 360  
Db 1586 AAGGCCAGAGCGGAAATGAAATCCCTGGATGAGTGGCCCTGTGCATCTTTCATCTTG 1645  
Qy 361 LysGlnIleAsnAspArgIleLysGluArgLeuGlnSerCysTyrArgGlyGluGlyThr 380  
Db 1646 AAGCAGATAAATGACCGCATTAAGGAGCGGTGCAGTCTTGTATCCGGGCGAGGCGCAG 1705  
Qy 381 LeuAspLeuAlaTrpLeuLysValLysAspIleProCysSerSerAlaLeuLeuThrIle 400  
Db 1706 CTGAGCCTGGCTGGCTCAAGGTGAAGGACATCCCTGCAGGAGTGGCGCTCTTAACCAT 1765  
Qy 401 AspAspAsnPheCysGlyLeuAspMetAsnAlaProLeuGlyValSerAspMetValArg 420  
Db 1766 GAGCATAACTTCTGTGGCTGGACATGAATGCTCCCTGGGAGTGTCCACATGTGTGCT 1825  
Qy 421 GlyIleProValPheThrGluAspArgAspArgMetThrSerValIleAlaTyrValTyr 440  
Db 1826 GGAATTTCCGCTTTCAGGAGGACAGGACCCCATGACGCTGTATCCCATATGTCTAC 1885  
Qy 441 LysAsnHisSerLeuAlaPheValGlyThrLysSerGlyLysLeuLysLysIleArgVal 460  
Db 1886 AAGAACCCTCTCTGGCTTTTGTGGGCACCAAAAGTGGCAAGCTGAAGAAGATCCGGGTG 1945

Qy	461	AspGlyProArgGlyAsnAlaLeuGlnTyrGluThrValGlnValValAspProGlyPro	480
Db	1946	GATGGACCCAGGGCAACGCCCTCCAGTATGAGACGGTGCGAGTGGTGGACCCCGGCCCA	2005
Qy	481	ValLeuArgAspMetAlaPheSerLysAspHisGluGlnLeuTyrIleMetSerGluArg	500
Db	2006	GTCCTCCGGGATATGGCTCTTCCAGAGCACAGAGCACTCTACATCATGTGTCAGAGAGG	2065
Qy	501	GlnLeuThrArgValProValGluSerCysGlyGlnTyrGlnSerCysGlyGluCysLeu	520
Db	2066	CAGCTCACAGAGTCCCTGTGGAGTCTGTGGTCAGTATCAGAGCTGCGCGAGTGCCTT	2125
Qy	521	GlySerGlyAspProHisCysGlyTyrCysValLeuHisGlnThrCysThrArgLysGlu	540
Db	2126	GGCTCAGCGACCCCACTGTGGCTGGTGTGTCTGCACAACTTGTGCACCCCGAAGGAG	2185
Qy	541	ArgCysGluArgSerLysGluProArgArgPheAlaSerGluMetLysGlnCysValArg	560
Db	2186	CGGTGTAGCGGTCCAAGGACCCCGCAGGTTTGCTCCGAGATGAAGCAGTGTGTCCGG	2245
Qy	561	LeuThrValHisProAsnAsnIleSerValSerGlnTyrAsnValLeuLeuValLeuGlu	580
Db	2246	CTGACGGTCCATCCCAACATATCTCCGTCTCTCAGTACAACTGCTGCTGGTCTCGGAG	2305
Qy	581	ThrTyrAsnValProGluLeuSerAlaGlyValAsnCysThrPheGluAspLeuSerGlu	600
Db	2306	ACGTACAATGTCCCGAGCTGTCACTGGGGTCAACTGCACCTTTGAGGACCTGTTCAGAG	2365
Qy	601	MetAspGlyLeuValValGlyAsnGlnIleGlnCysTyrSerProAlaAlaLysGluVal	620
Db	2366	ATGATGGCTGGTGGTGGGCAATCAGATCCAGTGTACTCCCTCGAGCCACAGGAGGTG	2425
Qy	621	ProArgIleIleThrGluAsnGlyAspHisHisValValGlnLeuGlnLeuLysSerLys	640
Db	2426	CCCCGGATCATCAGAGATGGGGACCAACCATGTGCTACAGCTTCAGCTCAAAATCAAAG	2485
Qy	641	GluThrGlyMetThrPheAlaSerThrSerPheValPheTyrAsnCysSerValHisAsn	660
Db	2486	GAGACCGGCATGACCTTCGCCAGACACAGACTTGTCTTCTACAAATTCGACGGTCCACAT	2545
Qy	661	SerCysLeuSerCysValGluSerProTyrArgCysHisIleTyrCysIleTyrArgHisVal	680
Db	2546	TCGTGCCTGTCTCGTGGAGATCCATACCGCTGCCACTGGTGTAAATACCGGCATGTC	2605
Qy	681	CysThrHisAspProLysThrCysSerPheGlnGluArgValLysLeuProGluAsp	700
Db	2606	TGCACCCATGACCCCAAGACTGTCTCTTCCAGGAAGCCGAGTGAAGCTGCCCGAGGAC	2665
Qy	701	CysProGlnLeuLeuArgValAspLysIleLeuValProValGluValIleLysProIle	720
Db	2666	TGCCCCAGCTGCTCGAGTGGACAAGATCTGTGTGCCGTGGAGGTGATCAAGCTATC	2725
Qy	721	ThrLeuLysAlaLysAsnLeuProGlnSerGlyGlnArgGlyTyrGluCysIle	740
Db	2726	ACGCTGAAGGCCAAGAACTCCCCAGCCCCAGTCTGGGGAGCTGGCTACGAATGCATC	2785
Qy	741	LeuAsnIleGlnGlySerGluGlnArgValProAlaLeuArgPheAsnSerSerVal	760
Db	2786	CTCAACATTCAGGCGAGCAGCAGCGAGTGCCTCCCTGCGCTTCAACAGCTCCAGCGTA	2845
Qy	761	GlnCysGlnAsnThrSerTyrSerTyrGluGlyMetGluIleAsnAsnLeuProValGlu	780
Db	2846	CAGTGCCAGAACACTCTTATTCCTATGAAGGGATGGAGATCAACAACCTGCCGTGGAG	2905
Qy	781	LeuThrValValTyrAsnGlyHisPheAsnIleAspAsnProAlaGlnAsnLysValHis	800
Db	2906	TTGACAGTCGTGGATGGGCACCTTCAACATTGCACACCCAGCTCAGATAAAGTTTCA	2965
Qy	801	LeuTyrLysCysGlyAlaMetArgGluSerCysGlyLeuCysLeuLysAlaAspProAsp	820
Db	2966	CTCTACAAGTGGAGCATCGTGAAGCTCGGGCTGCTCCCTCAAGGGTGACCCAGAC	3025

Qy	821	PheAlaCysGlyTrpCysGlnGlyProGlyGlnCysThrLeuArgGlnHisCysProAla	840
Db	3026	TTCCGATGTGCTGGTGCAGGGCCAGGSCAGTGCACCTTCGCCAGCACTGCCCTGCC	3085
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Db	3086	CAGGAGCCAGTGGCTGGAGCTGTCTGGTGCCTAAAGCAAGTGCACAAACCCCGC	3145
Qy	861	ThrGluIleIleProValThrGlyProArgGluGlyGlyThrIysValThrIleArgGly	880
Db	3146	ACAGAGATAATCCCGTGCAGGCCCCCGGAGGGGACCACCAAGGTCATATCCGAGGG	3205
Qy	881	GluAsnLeuGlyLeuGluPheArgAspIleAlaSerHisValIysValIaGlyValGlu	900
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Qy	901	CysSerProLeuValAspGlyTyrrIleProAlaGluGlnIleValCysGluMetGlyGlu	920
Db	3266	TGCAGCCCTTTAGTGGATGGTTACATCCCTGCAGAACAGATCGTGTGTGAGATGGGGAG	3325
Qy	921	AlaIysProSerGlnHisAlaGlyPheValGluIleCysValaIaValCysArgProGlu	940
Db	3326	GCCAAAGCCAGCAGCATGCGAGCTTCGTGGAGATCTGGCTGGCTGTGTCTGGCCTGAA	3385
Qy	941	PheMetAlaArgSerSerGlnLeuTyrrTyrrPheMetThrLeuThrLeuSerAspLeuLys	960
Db	3386	TTCATGCCCCGCTCCTCACAGCTCTATTACTTCATGCACACTGACTCTCTCAGATCTGAAG	3445
Qy	961	ProSerArgGlyProMetSerGlyGlyThrGlnValThrIleThrGlyThrAsnLeuAsn	980
Db	3446	CCCAGCCGGGGGCCCATGTCCGAGGGACCCAAAGTACCATCAGCAGCACCAACCTGTAAT	3505
Qy	981	AlaGlySerAsnValValMetPheGlyLysGlnProCysLeuPheHisArgArgSer	1000
Db	3506	GCCGGAGCAACGTGGTGGTGATGTTGGAAAGACGCCCTGTCTCTCCACAGGCGATCT	3565
Qy	1001	ProSerTyrrIleValCysAsnThrThrSerSerAspGluValLeuGluMetLysValSer	1020
Db	3566	CCATCTCCACATTTGCTCAACACACATCCTCAGATGAGGTGCTAGAGATGAAAGGTCTCG	3625
Qy	1021	ValGlnValAspArgAlaLysIleHisGlnAspLeuValPheGlnTyrrValGluAspPro	1040
Db	3626	GTGCAGGTGCACAGGGCCAGATCCACCAGACCTGGTCTTTTCAGTATGTGGAGACCCC	3685
Qy	1041	ThrIleValArgIleGluProGluTrpSerIleValSerGlyAsnThrProIleAlaVal	1060
Db	3686	ACCATCTGGGATTGAGCCAGAGTGGAGCATTTGTCAGTGGAAACAACACCATCGCCGTA	3745
Qy	1061	TrpGlyThrHisAspLeuIleGlnAsnProGlnIleArgAlaLysHisGlyGlyLys	1080
Db	3746	TGGGGGACCCACCTGGACCTCATACAAACCCCGACATCCGTGCCAAGCATGGAGGAAG	3805
Qy	1081	GluHisIleAsnIleCysGluValLeuAsnAlaThrGluMetThrCysGlnAlaProAla	1100
Db	3806	GAGCACATCAATATCTGTGAGGTTCTGAACGCTACTGAGATGACCTGTCTCAGGCGCCGCC	3865
Qy	1101	LeuAlaLeuGlyProAspHisGlnSerAspLeuThrGluArgProGluGluPheGlyPhe	1120
Db	3866	CTCGCTCTGGGTCTCTGACCAAGTCCAGCTGACCGAGAGGCCGAGGAGTTTGGCTTC	3925
Qy	1121	IleLeuAspAsnValGlnSerLeuLeuIleLeuAsnLysThrAsnPheThrTyrrPro	1140
Db	3926	ATCCTGCACACGTCGAGTCCCTGCTCATCCTCAACAGACCAACTTCACCTACTATCCC	3985
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Db	3986	AAACCGGTGTTTGAAGGCTTTTGGTCCCTCAGGAATCCTGGAGCTCAAGCTGGCACGCC	4045
Qy	1161	IleIleLeuLysGlyLysAsnLeuIleProProValAlaGlyGlyAsnValLysLeuAsn	1180
Db	4046	ATCATCTTAAGGCAAGAACCTGATCCCGCTGTGCTGGGGCAACGTCAGCTGAAC	4105
Qy	1181	TyrThrValLeuValGlyLysProCysThrValThrValSerAspValGlnLeuLeu	1200



Db 4106 TACACTGTGCTGGTGGGAGAACCGTGCACCGTGACCGTGTCAGATGCTCCAGCTGCTC 4165  
QY 1201 CysGluSerProAsnLeuIleGlyArgHisLysValMetAlaValGlyGlyMetGlu 1220  
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Db 4346 AAACGCAAGTCCCGGAAAGTGACCTCACGCTGAAGCGGTGCAGATGCAGATGCACAC 4405  
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Db 4766 GCCACTGATGTGTGAAGCAGCTGCTGGCGGACCTCATTGACAAGAACCTGGAGAGCAAG 4825  
QY 1421 AsnHisProLysLeuLeuLeuArgArgThrGluSerValAlaGluLysMetLeuThrAsn 1440  
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QY 1441 TrpPheThrPheLeuLeuTyrLysPheLeuLysGluCysAlaGlyGluProLeuPheSer 1460  
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QY 1481 AlaArgTyrSerLeuSerGluAspLysLeuIleArgGlnIleAspTyrLysThrLeu 1500  
Db 5006 GCCCGCTACTCTTGGCAGGACACAGCTCATCCGACGACGATGATGACTACAAACCCCTG 5065  
QY 1501 ValLeuSerCysValSerProAspAsnAlaAsnSerProGluValProValLysIleLeu 1520  
Db 5066 GTCTGTGAGCTGTGTGAGCCAGCAATGCCAACAGCCCGAGGTCCCGATTAAGATCTTC 5125  
QY 1521 AsnCysAspThrIleThrGlnValLysGluLysIleLeuAspAlaIlePheLysAsnVal 1540  
Db 5126 AACTGTGACACCATCACTCAGGTCAAGGAGAAATCTGTGATGCCATCTCAAGATGTG 5185  
QY 1541 ProCysSerHisArgProLysAlaAlaAspMetAspLeuThrArgGlnGlySerGly 1560

Db 5186 CTTTGTCTCCACCGCGCCAAAGCTGCAGATATGATCTGGAGTGGCGACAAGGAGTGGG 5245  
QY 1561 AlaArgMetIleLeuGlnAspGluAspIleThrThrLysIleGluAsnAspTyrLysArg 1580  
Db 5246 CCAAGGATGATCTTTGCAAGGATGAAGACATCACCAAGGATTTGAGATGATTGGAAGCGA 5305  
QY 1581 LeuAsnThrLeuAlaHisTyrGlnValProAspGlySerValValAlaLeuValSerLys 1600  
Db 5306 CTGAACACACTGGCCCACTACACAGTGCAGATGTTTCCGTGGTGGCATTAGTGTCCAAG 5365  
QY 1601 GlnValThrAlaTyrAsnAlaValAsnAsnSerThrValSerArgThrSerAlaSerLys 1620  
Db 5366 CAGGTGACAGCTATAACGAGTAGTAACCTCCACCTCTCCAGGACTCTCAGCAAGTAAA 5425  
QY 1621 TyrGluAsnMetIleArgTyrThrGlySerProAspSerLeuArgSerArgThrProMet 1640  
Db 5426 TATGAATAACATGATCCGGTACACGCGCAGCCCGCAGACGCTCCGCTCAGGACACCTATG 5485  
QY 1641 IleThrProAspLeuGluSerGlyValLysMetTrpHisLeuValLysAsnHisGluHis 1660  
Db 5486 ATCACTCTGACCTGGAGAGTGGAGTCAAGATGTGGCACCTTAGTGAAGAACCCAGACAC 5545  
QY 1661 GlyAspGlnLysGluLysAspArgGlySerLysMetValSerGluIleTyrLeuThrArg 1680  
Db 5546 GGAGACCAAGAGAGGGGACCGGGGAGCAGATGTGTCTGAAATCTACCTGACCCGGA 5605  
QY 1681 LeuLeuAlaThrLysGlyThrLeuGlnLysPheValAspAspLeuPheGluThrIlePhe 1700  
Db 5606 CTCTGTGGCCACTAAGGCGACACTGCAGAAAGTTTGTGATGACCTCTTTGACCATCTTC 5665  
QY 1701 SerThrAlaHisArgGlySerAlaLeuProLeuAlaIleLysTyrMetPheAspPheLeu 1720  
Db 5666 AGCAGGCGACACCTGGCTGTGCCCTGTGCCCATCAAGTACATGTTTGACTTCTGT 5725  
QY 1721 AspGluGlnAlaAspLysHisGlyIleHisAspProHisValArgHisThrTrpLysSer 1740  
Db 5726 GATGAGCAGGCTGATAAATGATGCAATCATGACCGCAGCCTCGCCATCATCTGAAGAGC 5785  
QY 1741 AsnCysLeuProLeuArgPheTrpValAsnMetIleLysAsnProGlnPheValPheAsp 1760  
Db 5786 AATTGCTTCCCTGAGGTTTTGGGTCAACATGATCAAGAACCCGAGTTTGTGTTGAC 5845  
QY 1761 IleHisLysAsnSerIleThrAspAlaCysLeuSerValValAlaGlnThrPheMetAsp 1780  
Db 5846 ATCCATAGAAGACAGCATCACAGACGCTGCTCTCTGTGGTGGCTCAGACCTTCATGGAC 5905  
QY 1781 SerCysSerThrSerGluHisArgLeuGlyLysAspSerProSerAsnLysLeuLeuTyr 1800  
Db 5906 TCTTGTCTCCAGTCAGAGCACCGCTGGCAAGACTCGCCCTCCAAAGCTGCTGTAT 5965  
QY 1801 AlaLysAspIleProSerTyrLysAsnTrpValGluArgTyrTyrSerAspIleGlyLys 1820  
Db 5966 GCCAAGGACATCCCGCAGCTACAAGATTTGGGTGGAGAGGTATTACTCAGACATAGGGAAG 6025  
QY 1821 MetProAlaIleSerAspGlnAspMetAsnAlaTyrLeuAlaGluGlnSerArgMetHis 1840  
Db 6026 ATGCCAGCCATCAGCGACCAAGACATGAACGCATACCTGGCTGAGCATCCCGATGGAC 6085  
QY 1841 MetAsnGluPheAsnThrMetSerAlaLeuSerGluIlePheSerTyrValGlyLysTyr 1860  
Db 6086 ATGAATGAGTTCAACACCATGAGTGCATCTCTCAGATCTTCTCTATGTGGCATAATAC 6145  
QY 1861 SerGluGluIleLeuGlyProLeuAspHisAspAspGlnCysGlyLysGlnLysLeuAla 1880  
Db 6146 AGCGAGGAGATCTTGGACCTCTGGACCCACGACGACCATGTGGGAAGCAGAACTGGCC 6205  
QY 1881 TyrLysLeuGluGlnValIleThrLeuMetSerLeuAspSer 1894  
Db 6206 TACAACTAGAACCAAGTCAATAACCTCTATGAGCTTAGACAGC 6247

RESULT 3

US-10-175-523-95

; Sequence 95, Application US/10175523

Publication No. US20030096264A1  
 GENERAL INFORMATION:  
 APPLICANT: Brockman, Jeffrey  
 APPLICANT: Evans, David  
 APPLICANT: Hook, Derek  
 APPLICANT: Klimczak, Leszek  
 APPLICANT: Laeng, Pascal  
 APPLICANT: Palfreyman, Michael  
 APPLICANT: Rajan, Prichi  
 TITLE OF INVENTION: MULTI-PARAMETER HIGH THROUGHPUT SCREENING ASSAYS (MPHTS)  
 FILE REFERENCE: 3235/LJ795-US3  
 CURRENT APPLICATION NUMBER: US/10/175,523  
 CURRENT FILING DATE: 2002-06-18  
 PRIOR APPLICATION NUMBER: US 60/299,151  
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 PRIOR FILING DATE: 2002-01-18  
 PRIOR APPLICATION NUMBER: US 60/361,834  
 PRIOR FILING DATE: 2002-03-04  
 NUMBER OF SEQ ID NOS: 197  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO 95  
 LENGTH: 6730  
 TYPE: DNA  
 ORGANISM: Mus musculus  
 FEATURE:  
 NAME/KEY: misc feature  
 LOCATION: (1)..(6730)  
 OTHER INFORMATION: where n may be a or g or c or t/u, unknown, or other

US-10-175-523-95

Alignment Scores:

Pred. No.: 0 Length: 6730  
 Score: 6765.00 Matches: 1268  
 Percent Similarity: 80.24% Conservative: 239  
 Best Local Similarity: 67.52% Mismatches: 357  
 Query Match: 15 Indels: 14  
 DB: 15 Gaps: 8

US-09-964-956-13 (1-1896) x US-10-175-523-95 (1-6730)

QY	25	LeuLeuThrArgGlnProAlaProLeuSerGlnLysGlnArgSerPheValThrPheArg	44
DB	628	CTGCTAGCTCGTGGACCAAGATATGCTCAG-----TACAGCACTTCCAC	675
QY	45	GlyGluProAlaGlu---GlyPheAsnHisLeuValValAspGluArgThrGlyHisIle	63
DB	676	TCTGAGATCGTGACTGGACTTTCAACCATTTGACTGTACACCGAAGAACAGGGGCTGTG	735
QY	64	TyrLeuGlyAlaValAsnArgIleTyrLysLeuSerSerAspLeuLysValLeuValThr	83
DB	736	TATGTGGGGCTATCAATGCTGTACAAAGTTGACTGGCAACCTCACCATCCAGGTGGCT	795
QY	84	HisGluThrGlyProAspGluAspAsnProLysCysTyrProArgIleValGlnThr	103
DB	796	CACAGACAGGCGCAGAGAGACACAGGCTTCTACCCACCCCTCATTTGTACAGCCC	855
QY	104	CysAsnGluProLeuThrThrThrAsnAsnValAsnLysMetLeuLeuLeuAspTyrLys	123
DB	856	TGCAGTGAAGTCTTACACTACCAACCAATGTCACAACTACTGATCATTTGACTACTCT	915
QY	124	GluAsnArgLeuLeuAlaCysGlySerLeuTyrGlnGlyIleCysLeuLeuLeuArgGlu	143
DB	916	GAGATTCGCTCTGCTGCTGCGGAAGCTCTACCAAGGTGTTTGAAGCTCTCGGACTA	975
QY	144	GluAspLeuPheLysLeuGlyGluProTyrHisLysLysGluHisTyrLeuSerGlyVal	163

DB	976	GATGACCTCTTCATCCTGGTGGAGCCATCCACAAGAGAACTACTTGTCTCAGTGT	1035
QY	164	AsnGluSerCysValPheGlyValIleValSerTyrSerAsnLeuAspLysLeu	183
DB	1036	AATAAGACAGGACCATGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1095
QY	184	PheIleAlaThrAlaValAspGlyLysProGluTyrPheProThrIleSerArgLys	203
DB	1096	TTTATCGGCACTCTGTGATGCAAGCAGCAGTACTTCTCCCTACTCTGTCCAGCGCAAG	1155
QY	204	LeuThrLysAsnSerGluAlaAspGlyMetPheAlaTyrValPheHisaspGluPheVal	223
DB	1156	CTGCCCGTGGACCTGAGTCTTCAGCAATGCTGGACTATGAGCTCCACAGTGAATTGTG	1215
QY	224	AlaserMetIleLysIleProSerAspThrPheThrIleIleProAspPheAspIleTyr	243
DB	1216	TCCTCCTCATCAAGATTCCTCTGACACCTGAGCCTGTCTCTCCTCCTCCTCCTCCTC	1275
QY	244	TyrValTyrGlyPheSerSerGlyAsnPheValTyrPheLeuThrLeuGlnProGluMet	263
DB	1276	TACATCTATGGCTTTGCCAGTGGGGTGTGTCTACTTTCTCCTGCTCCAGCGAGAG---	1332
QY	264	ValSerProProGly-----SerThrThrLysGluGlnValTyrThrSerLysLeu	280
DB	1333	---ACCCCTCAGGCGATGCCATCAATTCAGCTGGAGACCTCTCTATATCTCAAGAAAT	1389
QY	281	ValArgLeuCysLysGluAspThrAlaPheAsnSerTyrValGluValProIleGlyCys	300
DB	1390	GTGCGTCTCTGCAAGATGACCCCAAGTTCCATCTCTATGTGTCTCTGCTCTTGTGCTGC	1449
QY	301	GluArgSerGlyValGluTyrArgLeuLeuGlnAlaAlaTyrLeuSerLysAlaGlyAla	320
DB	1450	ACAGTGTGGGTGGATATGCTCTCTGAGGAGCTTACTTGCAGGCGGAGAA	1509
QY	321	ValLeuGlyArgThrLeuGlyValHisProAspAspLeuLeuPheThrValPheSer	340
DB	1510	GCTTAGCTCAGGCTTCAACATCAGCAGCGAAGATGTCTGTGCTCCATCTTTTTC	1569
QY	341	LysGlyGlnLysArgLysMetLysSerLeuAspGluSerAlaLeuCysIlePheIleLeu	360
DB	1570	AAGGGCAGAGCAGTACACACCCCTGATGACTGCTCTGCTCTGCTCTGCTCTGCTCTG	1629
QY	361	LysGlnIleAsnAspArgIleLysGluArgLeuGlnSerCysTyrArgGlyGluGlyThr	380
DB	1630	CGGGCCATCAACTTGCAATCAAGGAGCGTGTGAGTCTCTGCTCTGCTCTGCTCTGCTCT	1689
QY	381	LeuAspLeuAlaTrpLeuLysValLysAspIleProCysSerSerAlaLeuLeuThrIle	400
DB	1690	TTGGAGCTCAACTGGCTGTGGGAAAGGATGTGAGTGCACCAAGCGGCTGTGCCAATC	1749
QY	401	AspAspAsnPheCysGlyLeuAspMetAsnAlaProLeuGlyValSerAspMetValArg	420
DB	1750	GATGATAACTTCTGCGGCTGGACATCAACAGCCTCTGGAGGCTCCACTCTGTGGAG	1809
QY	421	GlyIleProValPheThrGluAspArgAspArgMetThrSerValIleAlaTyrValTyr	440
DB	1810	GGACTGACCTGTATACCAAGGAGCGGCTGACCTGTGCTGTGCTGTGCTGTGCTGTGCT	1869
QY	441	LysAsnHisSerLeuAlaPheValGlyThrLysSerGlyLysLeuLysLysIleArgVal	460
DB	1870	AATGGCTACAGTGTGTTTGTGGGAGTAAAGTGGCAGCTGAAGAGATTCAGCT	1929
QY	461	AspGlyProArgGlyAsnAlaLeuGlnTyrGluThrValGlnValVal---AspProGly	479
DB	1930	GATGGTCCCCCATCGTGGGGTCCAGTATGAGATGTCTGTGTGTGTGTGTGTGTGTGTGT	1989
QY	480	ProValLeuArgAspMetAlaPheSerLysAspHisGluGlnLeuTyrIleMetSerGlu	499
DB	1990	CCATCTCTCGGAGCATGGCTTCTCCATCAATCAGCTATACCTATATGTGTGTGTGTGTGT	2049
QY	500	ArgGlnLeuThrArgValProValGluSerCysGlyGlnTyrGlnSerCysGlyGluCys	519
DB	2050	AGACAGTCCACAGGCTCCTGTGTAATCATGTGAACAGTATACCACTTGTGTGTGTGTGTGT	2109

QY 520 LeuGlySerGlyAspProHisCysGlyTyrCysValLeuHisAsnThrCysThrArgLys 539  
Db 2110 CTAAGCTCAGGGAGTCTCACTGTGGCTGGTGGCCCTGCACACATGTCTCCCGAGA 2169  
QY 540 GluArgCysGluArgSerLysGluProArgArgPheAlaSerGluMetLysGlnCysVal 559  
Db 2170 GACAAATGCCAACGGGCTCGGAAGCAAAATCGAATTTGCTCCAGATATCAACCCAGTGCATG 2229  
QY 560 ArgLeuThrValHisProAsnAsnIleSerValSerGlnTyrAsnValLeuValLeu 579  
Db 2230 AGCCTTGAGGTACACCCCNACAGCATCTCTGTGCATCACAGCCGGCTGCTCAGCCCTG 2289  
QY 580 GluThrTyrAsnValProGluLeuSerAlaGlyValAsnCysThrPheGluAspLeuSer 599  
Db 2290 GTTGTGAATGATGCTCCCAACCTCTCTGAAGGTATATGCTGTGCTTTGGGAATCTGACT 2349  
QY 600 GluMetAspGlyLeuValValGlyAsnGlnIleGlnCysTyrSerProAlaAlaLysGlu 619  
Db 2350 GAGGTGAGGACAGGTATCTGGAGGTCAAGTCACTGCATCTCACCTGGACCCAGGAT 2409  
QY 620 ValProArgIleIleThrGluAsnGlyAspHisValValGlnLeuGlnLeuLysSer 639  
Db 2410 GTCCCT--GTCACTCCCTCTGGATCAAGACTGGTGTGGCCCTAGAGCTGCAGCTGAGATCC 2466  
QY 640 LysGluThrGlyMetThrPheAlaSerThrSerPheValPheTyrAsnCysSerValHis 659  
Db 2467 AAAGAGACAGGAAGATCTTTGTGCAGACCCGAATCAAGTTCTATACTGCAGTGCCAC 2526  
QY 660 AsnSerCysLeuSerCysValGluSerProTyrArgCysHisTyrCysLysTyrArgHis 679  
Db 2527 CAACGTGCTGTCTGTGTAAACAGCGCCTTCGCTGCCATGGTGCAGATACCGTAAC 2586  
QY 680 ValCysThrHisAspProLysThrCysSerPheGlnGluGlyArgValLysLeuProGlu 699  
Db 2587 CTCGTGCACATGATGACCCCACTACTGTTCCTTCCAGGAAGCAGGATCAATGTTTCAGAG 2646  
QY 700 AspCysProGlnLeuArgValAspLysIleLeuValProValGluValIleLysPro 719  
Db 2647 GACTGTCCCAAGCTCGTCCCAAGGAGGAGATCTGTATCCAGTGGGGAAGTAACCA 2706  
QY 720 IleThrLeuLysAlaLysAsnLeuProGlnProGlnSerGlyGlnArgGlyTyrGluCys 739  
Db 2707 ATCACCTTAAAGGCCGGAACCTCCCGCCAGCCAGCTCGGCCAGCGAGCTACGAGTGT 2766  
QY 740 IleLeuAsnIleGlnGlySerGluArgValProAlaLeuArgPheAsnSerSerSer 759  
Db 2767 GTGCTCAGANTCAAGGGCTGTCCACGGGTCTCTGCCCTGCGTTTCAACAGTTCCAGT 2826  
QY 760 ValGlnCysGlnAsnThrSerTyrSerTyrGluGlyMetGluIleAsnAsnLeuProVal 779  
Db 2827 GTGCAGTGCACCAACAGCTCTACAGTATGATGGATGGACATCAGCAACCTAGCAGTG 2886  
QY 780 GluLeuThrValValTyrAsnGlyHisPheAsnIleAspAsnProAlaGlnAsnLysVal 799  
Db 2887 GACTTTGCTGTAGTATGAATGGCAACTTCATTATTGACAACTTCAGACCTCAGGACCTGAAAGTA 2946  
QY 800 HisLeuTyrLysCysGlyAlaMetArgGluSerCysGlyLeuCysLeuLysAlaAspPro 819  
Db 2947 CATCTACAAGTGTGCAGCCAGCGGAAAGCTGTGTCTCTGCCCTCAAGGCTGACCA 3006  
QY 820 AspPheAlaCysGlyTyrCysGlnGlyProGlyGlnCysThrLeuArgGlnHisCysPro 839  
Db 3007 AAGTTTCAGTGTGGTGTGGTGGAGCGCAGATGTACCTTCCACAGCACTGCCCC 3066  
QY 840 AlaGlnGluSerGlnTyrLeuLeuLeuSerGlyAlaLysSerLysCysThrAsnProArg 859  
Db 3067 AGCACTTCTAGCCCCCTGCTGACTGGTCCAGCCACAATGCAAGTGTTCACACCCCAA 3126  
QY 860 IleThrGluIleIleProValThrGlyProArgGluGlyGlyThrLysValThrIleArg 879  
Db 3127 ATCAGAGATTTTGCAGATATCAGGACCACTGAAGAGGGGACTCGTGTGACCATCAT 3186

QY 880 GlyGluAsnLeuGlyLeuGluPheArgAspIleAlaSerHisValLysValAlaGlyVal 899  
Db 3187 GCGCGTGAACCTGGCTGGCTGACTTCTCTGAGATTGCTCACCATTGTGCAGTGGCTGGAGTG 3246  
QY 900 GluCysSerProLeuValAspGlyTyrIleProAlaGlnGlnIleValCysGluMetGly 919  
Db 3247 CCTGCACCATCTCCAGGGGAATACATCATCGCTGAGCAGATCGTCTGTGAGATGGC 3306  
QY 920 GluAlaLysProSerGlnHisAlaGlyPheValGluIleCysValAlaValCysArgPro 939  
Db 3307 CATGCCGTTATAGGTACACATCTGGCTGTGGCCCTGTGCATTTGGGAATGCAAGCA 3366  
QY 940 GluPheMetAlaArgSerSerGlnLeuTyrTyrPheMetThrLeuThrLeuSerAspLeu 959  
Db 3367 GAGTTTCATGACCAAGTCCACAGCAGTATCTTTTGTGAATCTCTGTGTGTGCATCTC 3426  
QY 960 LysProSerArgGlyProMetSerGlyGlyThrGlnValThrIleThrGlyThrAsnLeu 979  
Db 3427 AGCCCGATCCCGGAGCACAGTCAAGGTACCATGGTGACCATCACAGGCCATTAACCTT 3486  
QY 980 AsnAlaGlySerAsnValValMetPheGlyLysGlnProCysLeuPheHisArgArg 999  
Db 3487 GGTGTCTGGAGCAGTGTGGCAGTGTACCTGGGCAATCAGACTGTGAATTTCTATGGGAG 3546  
QY 1000 SerProSerTyrIleValCys--AsnThrThrSerSerAspGluValLeuGluMetLys 1018  
Db 3547 TCAATGAATGAGATTGTATGTGTTTCACCCCCATCATCCAATGGACTAGGACCATCTC 3606  
QY 1019 ValSerValGlnValAspArgAlaLysIleHisGlnAspLeuValPheGlnTyrValGlu 1038  
Db 3607 GTCTCCGTGAGTGTGCAGAGCCCGGTGGATAGCAGTCTGCAGTTTCGAGTATATAGAT 3666  
QY 1039 AspProThrIleValArgIleGluProGluTyrSerIleValSerGlyAsnThrProIle 1058  
Db 3667 GACCCACGGGTCAACAGTATTGAGCCAGTGGAGTATCAGTAGTGGGCACACACCCCTA 3726  
QY 1059 AlaValTyrGlyThrHisLeuAspLeuIleGlnAsnProGlnIleArgAlaLysHisGly 1078  
Db 3727 ACCATCACAGGCTTCAACTTGGATTGATTCAGGAGCCAGGTCGAGTCAAAATTAAT 3786  
QY 1079 GlyLysGluHisIleAsnIleCysGluValLeuAsnAlaThrGluMetThrCysGlnAla 1098  
Db 3787 GGCAAGAAATCTGTCAATGTATGCAGAGTGGTAACACACACCCTCACCTGTCTGGCA 3846  
QY 1099 ProAlaLeuAlaLeuGlyProAspHisGlnSerAspLeuThrGluArgProGluPhe 1118  
Db 3847 CCTCTCTGACCCAGTGACTTACCGCCAGGTCTGGACACTGTGTGAACGGCCAGATGATTT 3906  
QY 1119 GlyPheIleLeuAspAsnValGlnSerLeuLeuIleLeuAsnLysThrAsnPheThrTyr 1138  
Db 3907 GGATTTCTCTTTAACAATGTTCAATCTCTTACTCATCTATAACGACCAAGGTTCATCTAC 3966  
QY 1139 TyrProAsnProValPheGluAlaPheGlyProSerGlyIleLeuGluLeuLysProGly 1158  
Db 3967 TACCCCAACCCACGTTTGAACCTGCTCAGCCCCACTGGAATCTTGGATCAGAAGCCAGC 4026  
QY 1159 ThrProIleIleLeuLysGlyLysAsnLeuIleProProValAlaGlyGlyAsnValLys 1178  
Db 4027 TCACCCATCATCTGAAGGGCAAAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 4083  
QY 1179 LeuAsnTyrThrValLeuValGluLysProCysThrValThrValSerAspValGln 1198  
Db 4084 CTCACCTACACAGTAATGATGTGAGAGACACCTTGTACAGTCACTGTCTGTCTGAGACACAG 4143  
QY 1199 LeuLeuCysGluSerProAsnLeuIleGlyArgHisLysValMetAlaArgValGlyGly 1218  
Db 4144 CTGCTTTGTGAACCTCCCAACCTCAGGCGCAGCAAGGTCTATGCTTCACTGTGGCGGG 4203  
QY 1219 MetGluTyrSerProGlyMetValTyrIleAlaProAspSerProLeuSerLeuProAla 1238  
Db 4204 ATGGTGTCTCTCACTGTGGTCCCGTGGAGCTATCTCGAGAGCTGTGTGACCTTGCAGCC 4263  
QY 1239 IleValSerIleAlaValAlaGlyGlyLeuLeuIleIlePheIleValAlaValLeuIle 1258

Db 4264 ATCATCAGCATCGAGCTGGTGAAGCCCTCTTTATCATCGTCATCATTTGCTCATC 4323  
QY 1259 AlaTyrLysArgLysSerArgLysSerLeuThrLeuLysArgLeuGlnMetVal 1278  
Db 4324 GCTTACAGCGCAAGTCTAGGAAATGACCTCACTCAAGCGCTCCAAATGCAATG 4383  
QY 1279 AspAsnLeuSerArgValAlaLeuGluCysLysGluAlaPheAlaGluLeuGlnThr 1298  
Db 4384 GACAACTGGAGTCCAGGGTGCCTGGAGTCAAGGAAGCTTTTCGGAGCTTCAGACA 4443  
QY 1299 AspIleHisGluLeuThrSerAspLeuAspGlyAlaGlyIleProPheLeuAspTyrArg 1318  
Db 4444 GACATCAATGAGCTTAACAGTACTGGATCGATCAGGAATCCCTTACCTGAGCTACCGT 4503  
QY 1319 ThrTyrThrMetArgValLeuPheProGlyIleGluAspHisProValLeuArgAspLeu 1338  
Db 4504 ACCTATGCCATGAGAGTCTGTTCAGGCACTTGAGGACCCCTGTTCTCGGGAAGCTG 4563  
QY 1339 GluValProGlyTyrArgGlnGluArgValGluLysGlyLeuLysLeuPheAlaGlnLeu 1358  
Db 4564 GAGGTACAGGAAATGAGCAGCAGCAGCGTGGAGAAAGCCCTGAAACTCTTCGCCAGCTT 4623  
QY 1359 IleAsnAsnLysValPheLeuLeuSerPheIleArgThrLeuGluSerGlnArgSerPhe 1378  
Db 4624 ATCAACAACAGAGTGTCTTGCTGACCTTCATCCGTACACTGGAACTACAGCGCAGCTTC 4683  
QY 1379 SerMetArgAspArgGlyAsnValAlaSerLeuIleMetThrValLeuGlnSerLysLeu 1398  
Db 4684 TCCATGCGAGACCGTGGGAACCTGGCTCTCTCATCATGACAGCGCTTCAGGGTCCGCTA 4743  
QY 1399 GluTyrAlaThrAspValLeuLysGlnLeuLeuAlaAspLeuIleAspLysAsnLeuGlu 1418  
Db 4744 GAATATGCCATGATGTCTCAAGCAGCTGCTCTCTGACCTCATTTGACAAAGACCTGGAG 4803  
QY 1419 SerLysAsnHisProLysLeuLeuLeuArgThrGluSerValAlaGluLysMetLeu 1438  
Db 4804 AACAAAGAACCCCAAGCTGCTCTCGCAGAGCTAGTCTGTGCGCGAGAGATGCTG 4863  
QY 1439 ThrAsnTyrPheThrPheLeuLeuTyrLysPheLeuLysGluCysAlaGlyLysProLeu 1458  
Db 4864 ACTAAGTGTGTGCTTTCTTACACAAGTTCCTGAAGAGTGTGCTGGGAAACCACTC 4923  
QY 1459 PheSerLeuPheCysAlaIleLysGlnMetGluLysGlyProIleAspAlaIleThr 1478  
Db 4924 TTCATGCTATCTGTGCAATCAAGCAGCAGATGGAAGGCGCCCATTTGACCTATTACT 4983  
QY 1479 GlyGluAlaArgTyrSerLeuSerGluAspLysLeuIleArgGlnGlnIleAspTyrLys 1498  
Db 4984 GGTGAGGCCCGATACTCCCTGAGTGAAGACAAGCTCATCCGGCAGCAGATCGAGTATAG 5043  
QY 1499 ThrLeuValLeuSerCysValSerProAspAsnAlaAsnSerProGluValProValLys 1518  
Db 5044 ACTCTGATCTGACTGTGTCAACCTGACATGAGAACAGCCGAGATGCCAGTGAAG 5103  
QY 1519 IleLeuAsnCysAspThrIleThrGlnValLysGluLysIleLeuAspAlaIlePheLys 1538  
Db 5104 GTACTAAACTGTGACACCATCACTCAAGTCAAGGAGAGATCCTCGATGCCGTATATAAG 5163  
QY 1539 AsnValProCysSerHisArgProLysAlaAlaAspMetAspLeuGluTyrArgGlnGly 1558  
Db 5164 AATGTCCTTACTCCAGCGGCCCAAGGCTGTGGATGATGATGAGTGGCGCCCAAGGC 5223  
QY 1559 SerGlyAlaArgMetIleLeuGlnAspGluAspIleThrLysIleGluAsnAspTyr 1578  
Db 5224 CGGATTCAGCAGTGTGTTCAGGACGAGCAATACCAACAAATAGAGGGTCACTGG 5283  
QY 1579 LysArgLeuAsnThrLeuAlaHisTyrGlnValProAspGlySerValValAlaLeuVal 1598  
Db 5284 AAGCGCTTAAACACTGATGATTAACAGGTGTGACAGATCCGTCGTGGCTCTGGT 5343  
QY 1599 SerLysGlnValThrAlaTyrAsnAlaValAsnAsnSerThrValSerArgThrSerAla 1618

Db 5344 CCTAAGCAGACCTCTCTTACAAATCCCTGCTGCTGCGAGCATCTCTCGACATCCATT 5403  
QY 1619 SerLysTyrGluAsnMetIleArgTyrThrGlySerProAspSerLeuArgSerArgThr 1638  
Db 5404 AGCAGATATGACTCTCTCTTCCAGTATACAGAGGAGCCAGACAGCTCCGGTCCCGGTC 5463  
QY 1639 ProMetIleThrProAspLeuGluSerGlyValLysMetTrpHisLeuValLysAsnHis 1658  
Db 5464 CCCATGATCAACCCAGACTTGGAGAGGGTGTCAAGTTTGGCATCTGCTGAGATCTACTTG 5523  
QY 1659 GluHisGlyAspGlnLysGluGlyAspArgGlySerLysMetValSerGluIleTyrLeu 1678  
Db 5524 GACCATGTGTACAGAGGAGGGTGCAGCGGGCAGCAAAATGGTGTCTGAGATCTACTTG 5583  
QY 1679 ThrArgLeuLeuAlaThrLysGlyThrLeuGlnLysPheValAspAspLeuPheGluThr 1698  
Db 5584 ACCGGCTTCTAGCCACCAAGGCACTCCGCAAAATTTGGACGACTGTTTGAGACC 5643  
QY 1699 IlePheSerThrAlaHisArgGlySerAlaLeuProLeuAlaIleLysTyrMetPheAsp 1718  
Db 5644 TTGTTGACGACTGTGACCGGGTAGTGTCTCTCCCTAGCCATCAAGTACATGTTTGTAT 5703  
QY 1719 PheLeuAspGluGlnAlaAspLysHisGlyIleHisAspProHisValArgHisThrTrp 1738  
Db 5704 TTCTGTGATGAGCAGCAGCAGACAGATATCCAGCACACAGATGTGGGACACACTGG 5763  
QY 1739 LysSerAsnCysLeuProLeuArgPheTrpValAsnMetIleLysAsnProGlnPheVal 1758  
Db 5764 AAAAGCAACTGCTTCCACTTCGTTCTGGTGAATGTATCAAGAACCTCAATTGTGA 5823  
QY 1759 PheAspIleHisLysAsnSerIleThrAspAlaCysLeuSerValValAlaGlnThrPhe 1778  
Db 5824 TTTTGACATCCCAAGGGCAGCATCACAGATGCTGCTCTCTGTGTAGCCACAGCTTT 5883  
QY 1779 MetAspSerCysSerThrSerGluHisArgLeuGlyLysAspSerProSerAsnLysLeu 1798  
Db 5884 ATGGACTCTCTGTTCCCATCAGAGCCAGCTAGGCAAGGACTCACCTTCCAAAGCTG 5943  
QY 1799 LeuTyrAlaLysAspIleProSerTyrLysAsnTyrValGluArgTyrTyrSerAspIle 1818  
Db 5944 CTCTATGCCAAGGATATCCCTCAGTTATAGAACTGGGTAGAAAGATCTATGACAGATT 6003  
QY 1819 GlyLysMetProAlaIleSerAspGlnAspMetAsnAlaTyrLeuAlaGluGlnSerArg 1838  
Db 6004 GCCAAGCTCCAGCCATAGTAGCAAGATATGAATGCTTACCTCGCGAGAGCTCCCGC 6063  
QY 1839 MetHisMetAsnGluPheAsnThrMetSerAlaLeuSerGluIlePheSerTyrValGly 1858  
Db 6064 CTGCATGCTACAGAGTTCAATATGCTGAGCGCCCTCAACAGAGATCTACTCATATGACG 6123  
QY 1859 LysTyrSerGluGluIleLeuGlyProLeuAspHisAspGlnCysGlyLysGlnLys 1878  
Db 6124 AAGTACAGTGGAGGCTCATCGGGCAGCTAGACAGAGATGAACAGGCCGACGCAACGA 6183  
QY 1879 LeuAlaTyrLysLeuGlnValIleThrLeuMetSerLeuAspSerAsnLys 1896  
Db 6184 CTGCGCTTACAGGTGGAGCATCTCATCAAGCCATGTCTCATAGAGAGCTGAAAG 6237

RESULT 4

US-10-312-352-70  
; Sequence 70, Application US/10312352  
; Publication No. US20040053824A1  
; GENERAL INFORMATION:  
; APPLICANT: INCYTE GENOMICS, INC.; TANG, Y. Tom  
; APPLICANT: YUE, Henry; AZIMZAI, Yalda  
; APPLICANT: HE, Ann; BATRA, Sajeev  
; APPLICANT: LO, Terence P.; NGUYEN, Darniel B.  
; APPLICANT: BURRILL, John D.; MARCUS, Gregory A.  
; APPLICANT: ZINGLER, Kurt A.; GANDHI, Ameena R.  
; APPLICANT: LAU, Preeti G.; KEARNEY, Liam  
; APPLICANT: BURFORD, Neil; YAO, Monique G.  
; APPLICANT: CHAWLA, Narinder K.; ELLIOT, Vicki S.  
; APPLICANT: ARVIZU, Chandra S.; KHAN, Farrah A.

131 GlySerLeuTyrGlnGlyIleCysLysLeuLeuArgLeuGluAspLeuPheValLeuGly 151  
552 GGCAGCGCCCTCCAGGCACTCTCCAGTCTCTCGGCTCGGAGTCTCTCAACTGGGT 611  
151 GluProTyrHisLysLysGluHisTyrLeuSerGlyValAsnGluSerGlySerValPhe 170  
612 GAGCCACACACCGTAAGGAGCACTACCTGTCTCAGCGTGCAGAGGACGACGACATGGCG 671  
171 GlyValIleValSer-----TyrSerAsnLeuAspAspLysLeuPheIleAlaThrAla 188  
672 GCGTGTCTCATTCGCGGGCCACCGGGCCAGGGCCAGCCAGCTCTTCGTGGGCAACCC 731  
189 ValAspGlyLysProGluTyrPheProThrIleSerSerArgLysLeuThrLysAsnSer 208  
732 ATCGATGGCAAGTCCGAGTACTTCCGACACACTGTCCAGCGCTCGGCTCATGTGCCAACGAG 791  
209 GluAlaaspGlyMetPheAlaTyrValPheHisaspGluPheValAlaSerMetIleLys 228  
792 GAGATCCGACATGTTGGCTTCGTGTACCCAGGATGAGTTGTGTATCATCAGACTCAAG 855  
229 IleProSerAspThrPheThrIleIleProAspPheAspIleTyrTyrValTyrGlyPhe 248  
852 ATCCCTTCGGACACGCTGTCCAAAGTTCGCGGCTTTCGACATCTACTATGTGTACAGTTC 911  
249 SerSerGlyAsnPheValTyrPheLeuThrLeuGln-----ProGluMetValSerPro 266  
912 CGCAGCAGCAGGTTTGTCTACTACTTCAGCTCAGCTGCAGCTAGACACAGCTGACCTCGCT 971  
267 ProGlySerThrThrLysGluGlnValTyrThrSerLysLeuValArgLeuCysLysGlu 286  
972 -----GATGCGCGCGCGAGCACTTCTTCACTGTCAGTCCAAAGATCGTGGGTCTGTGGAC 1022  
287 AspThrAlaPheAsnSerTyrValGluValProIleGlyCysGluArgSerGlyValGlu 306  
1026 GACCCCAATCTACTCTGACGTTGAGTTCCTCCATTTGGCTGGAGCAGCGGGTGTGGAG 1081  
307 TyrArgLeuLeuGlnAlaIleTyrLeuSerLysAlaGlyAlaValLeuGlyArgThrLeu 326  
1086 TACCGCTGTGTGAGGATGCTACTCTGAGCGCGCGCGCGCTGCCCTGCCCCACAGCTG 1144  
327 GlyValHisProAspAspLeuLeuPheThrValPheSerLysGlyGlnLysArgLys 346  
1146 GGCTGGCTGAGGACGAGGACGCTGTTCACTGTGTTGCCACGGCCAGGAACCGC 1201  
347 MetLysSerLeuAspGluSerAlaLeuCysIlePheIleLeuLysGlnIleAsnAspArg 366  
1206 GTGAAGCCACCAAGGAGTCAAGCACTGTGCTCTTCACTGCTCAGGCGCCATCAAGGAGAG 1261  
367 IleLysGluArgLeuGlnSerCysTyrArgGlyGluGlyThrLeuAspLeuAlaTrpLeu 386  
1266 ATTGAAGAGCGCATCCAGTCTCTGCTACCGTGGTGAGGGCAAGCTCTCCCTCGCGTGG 1321  
387 LysValLysAspIleProCysSerSerAlaLeuLeuThrIleAspAsnPheCysGly 406  
1326 CTCACAGGAGCTGGGCTGCATCACTCACTCCCGCTGCAGATCATCACTTCTCGCGG 1381  
407 LeuAspMetAsnAlaProLeuGlyValSerAspMetValArgGlyIleProValPheThr 426  
1386 CAGACTTCAACAGCCCTTGGGGGCAACAGTCACTCATTGAGGGGACGCCCTGTTCG 1441  
427 GluAspArgAspArgMetThrSerValIleAlaTyrValTyrLysAsnHisSerLeuAla 446  
1446 GACAAGGATGATGCTGACGCGCGTGCCTATGACTATTCGGGGCCGCACTGTGGTA 1501  
447 PheValGlyThrLysSerGlyLysLeuLysLysIleArgValAsp-----GlyProArg 464  
1506 TTCGCGGCACCGAAGTGGCGCATCCGCAAGATCTGTTGGTGCCTCTCAACACCCCGT 1561  
465 GlyAsn---AlaLeuGlnTyrGluThrValGlnValValAspProGlyProValLeuArg 483  
1566 GCGCGGCTGCGCTGGCTACGAGCGTGTGCGCCAGAGGCGAGCCCATCTCTCGCA 1621

QY		484	AspMetalAlaPheSerLysAspHisGluClnLeuTyrIleMetSerGluArgGlnLeuThr	503
DB		1626	GACTCGCTCTTCACGCCCAACACCACAGTACCTCTACCCATGCAGGAAGACAGGTGACG	1685
QY		504	ArgValProValGluSerCysGlyGlnTyrGlnSerCysGlyGluCysLeuGlySerGly	523
DB		1686	CGGTGGCTGTGGAGAGCTGTGCAGTACACATCTCTGTGAGCTGTCTGGGGTGACCG	1745
QY		524	AspProHisCysGlyTyrCysValLeuHisAsnThrCysThrArgLysGluAraCysGlu	543
DB		1746	GACCCCACACTGTGCTGTGTCTCTGCACAGCATCTGCTCGCGCGCGGACGCTGTGAG	1805
QY		544	ArgSerLysGluProArgAtgPheAlaSerGluMetLysGlnCysValArgLeuThrVal	563
DB		1806	CGACGACGAGCCCCGCGTTTCTGCGGAGCTCTGCAGTGTGTGACGTACCTGTG	1865
QY		564	HisProAsnAsnIleSerValSerGlnTyrAsnValLeuLeuValLeuGluThrTyrAsn	583
DB		1866	CAGCCCCGCAATGTGTCTGTCCACCATGTCCAGGTCCCACTTGTGTCTGCAGGCTGGAAC	1925
QY		584	ValProGluLeuSerAlaGlyValAsnCysThrPheGluAspLeuSerGluMetAspGly	603
DB		1926	GTGCTGACCTCTCAGCTGGCGGTCAACTGTCTCTCGAGGACTTCACGGAATCTGAGAGC	1985
QY		604	LeuValValGlyAsnGlnIleClnCysTyrSerProAlaLysGluValProArgIle	623
DB		1986	GTCTGGAGGATGCGCGGATCCACTGCGCTCACCTCCGCGCGGAGGTGGCGCCATC	2045
QY		624	IleThrGluAsnGlyAspHisHISValValGlnLeuGlnLeuLysSerLysGluThrGly	643
DB		2046	ACGCGGGGCCAGGAGAGCACAGCGGTGGTGAACCTTCACCTAAAGTCCAAGSAGACAGGG	2105
QY		644	MetThrPheAlaSerThrSerPheValPheTyrAsnCysSerValHisAsnSerCysLeu	663
DB		2106	AAGAAGITTTGGTCTGTGGACTTCGTCTTCTACAACCTGCAGGTCCACCACTCTGCCTG	2165
QY		664	SerCysValGluSerProTyrArgCysHisTrpCysLysTyrArgHisValCysThrHis	683
DB		2166	TCCTGTGTCAACGGCTCCTTTCCCTGCACCTGTGTGCAATAACGCCACGTGTGCACACAC	2225
QY		684	AspProLysThrCysSerPheGlnGluGlyArgValLysLeuProGluAspCysProGln	703
DB		2226	AACGTGCTGACTGCGCTTCTCGAGGGCGGTGTCAAGTGTCTGAGGACTGCCACAG	2285
QY		704	LeuLeuArgValAspLysIleLeuValProValGluValIleLysProIleThrLeuLys	723
DB		2286	ATCTGCGCTCCACGCAGATCTACGTGCAGTGGAGTGTGTAACCCATCACTCCCTGGCC	2345
QY		724	LalysAsnLeuProGlnProGlnSerGlyClnhargGlyTyrGluCysIleLeuAsnIle	743
DB		2346	GCACGGACCTTGCCACAGCCACATGCAGCGCAGGTGGATAGTGTGCTTCCACATC	2405
QY		744	GlnGlySerGluGlnArgValProAlaLeuArgPheAsnSerSerValGlnCysGln	763
DB		2406	CCGGCAGCCCCGCGGTGTCCACGCCCTGCGCTTCAACAGCTCCACCTGCAGTGCCAG	2465
QY		764	AsnThrSerTyrSerTyrGluGlyWetGluIleAsnAsnLeuProValGluLeuThrVal	783
DB		2466	AATTCTCTGTACTCCTACGAGGGAAACGATGTACGCACTGCCAGTGAACCTGTCTAGTC	2525
QY		784	ValTyrAsnGlyHisPheAsnIleAspAsnProAlaGlnAsnLysValHisLeuTyrLys	803
DB		2526	GTGTGGAACGGCACTTTGTCTATTGCACACCCACAGAACATCCAGGCGCACTCTACAG	2585
QY		804	CysGlyAlaMetArgGluSerCysGlyLeuCysLeuLysAlaAspProAspPheAlaCys	823
DB		2586	TGCCCGGCCCTCGCGAGAGGTGGCGCTCTGCTCAAGSCCGACCCGCGCTTCGAGTGC	2645
QY		824	GlyTyrCysGlnGlyProGlyGlnCysThrLeuArgGlnHisCysProAlaGln--Glu	842
DB		2646	GGATGGTGGTGGCGAGCGCGCTGTCTCTCTGGACACCACTCGCTCGCTCGCGACACCT	2705
QY		843	SerGlnTrpLeuGluLeuSerGlyAlaLysSerLysCysThrAsnProArgIleThrGlu	862

[illegible]

Db 3783 TGCAGAGCGCCCACTTCACTGGGCGACGACACAGGTTCAGGTGCGGGCAGGCTGCTTCGAG 3842  
Qy 1221 TyrSerProGlyMetValTyrIleAlaProAspSerProLeuSerLeuProAlaIleVal 1240  
Db 3843 TTCTCGCGAGGACATCGAGCTGTACTCGACAGCCTGTGTGACGCTGCTGCCTGCCAATTGTG 3902  
Qy 1241 SerIleAlaValAlaGlyGlyLeuLeuIlePheIleValAlaValLeuIleAlaTyr 1260  
Db 3903 GGCATTGGCGAGCGGGGTCTCTGCTGCTGTCTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 3962  
Qy 1261 LysArgIysSerArgGlySerAspLeuThrLeuIysArgLeuGlnMetGlnMetAspAsn 1280  
Db 3963 AAGGCGCAAGTCACGAGATGCTGACCGCACACTCAAGCGGTGTCAGCTCCAGATGGACAAC 4022  
Qy 1281 LeuGlnSerArgValAlaLeuGlnCysIysGluAlaPheAlaGluLeuGlnThrAspIle 1300  
Db 4023 CTGAGATCCCGGTGGCCCTCGAATGCAAGAACCCCTTTGAGAGCTGCAGACAGATC 4082  
Qy 1301 HisGluLeuThrSerAspLeuAspGlyAlaGlyIleProPheLeuAspTyrArgThrTyr 1320  
Db 4083 CACGAGCTGACCAATGACTGGACGGTGGCGCATCCCTTCTTCTTACTACCGGACATAT 4142  
Qy 1321 ThrMetArgValLeuPheProGlyIleGluAspHisProValLeuArgAspLeuGluVal 1340  
Db 4143 GCCATGGGGTGGCTTCTTCCGGATCGAGACCACTGCTGTCTCAAGGAGATGGAGGTG 4202  
Qy 1341 ProGlyTyrArgGlnGluArgValGluIysGlyLeuIysLeuPheAlaGlnLeuIleAsn 1360  
Db 4203 -----CAGGCCAATGTGGAGAGTCCGTGACACTGTTCGGCGAGCTGCTACC 4250  
Qy 1361 AsnIysValPheLeuLeuSerPheIleArgThrLeuGlnSerGlnArgSerPheSerMet 1380  
Db 4251 AAGAAGCACTTCCTGCTGACCTTCATCGCACTGTCGAGGACACAGCGACGCTTCTCCATG 4310  
Qy 1381 ArgAspArgGlyAsnValAlaSerLeuIleMetThrValLeuGlnSerLysLeuGluTyr 1400  
Db 4311 CGCAACCGCGGAATGTGGCTCTCTCATATGACGCGCCCTGACAGGCGAGATGGATATAC 4370  
Qy 1401 AlaThrAspValLeuLeuGlnLeuLeuAlaAspLeuIleAspLysAsnLeuGluSerLys 1420  
Db 4371 GCCACAGCGTGTCTCAAGCACTGCTTCCACCTCATCGAGAGAAGAACCTGGAGAGCAAG 4430  
Qy 1421 AsnHisProLysLeuLeuLeuArgThrGluSerValAlaGluLysMetLeuThrAsn 1440  
Db 4431 AACCAACCAAGCTGCTACTGCGCGGACTGAGTGGTGGGAGAGAGATGCTAACTAAC 4490  
Qy 1441 TrpPheThrPheLeuLeuTyrLysPheLeuLysGluCysAlaGlyGluProLeuPheSer 1460  
Db 4491 TGGTTCACTTCTTGTATAAGTTCTCAAGGAGTGGCTGGGAGCGGCTGTTCTATG 4550  
Qy 1461 LeuPheCysAlaIleLysGlnMetGlnLysGlyProIleAspAlaIleThrGlyGlu 1480  
Db 4551 CTGTACTCGCCCATCAAGCAGATGGAGAGGCGCCCATTTGACGCCATCACCGGGTGAG 4610  
Qy 1481 AlaArgTyrSerLeuSerGluAspLysLeuIleArgGlnGlnIleAspTyrLysThrLeu 1500  
Db 4611 GCACGCTACTCTCTGAGTGAGGACAAAGCTCATCCGGCAGCAGATTGACTACAGACACTG 4670  
Qy 1501 ValLeuSerCysValSerProAspAsnAlaAsnSerProGluValProValLysIleLeu 1520  
Db 4671 ACCCTGAATGTGTGAACCTTGAATGAGATGACCTGAGTGGAGTGGCGGGTGAAGGGCTG 4730  
Qy 1521 AsnCysAspThrIleThrGlnValLysGluLysIleLeuAspAlaIlePheLysAsnVal 1540  
Db 4731 GACTGTGACGGTCACCGAGCCAGAGAGAGTGTCTGGACGCTGCTTACAGGGGGTG 4790  
Qy 1541 ProCysSerHisArgProLysAlaAlaAspMetAspLeuGluTyrArgGlnGlySerGly 1560  
Db 4791 CCTACTCCAGCGGCCCAAGCGCGGACATGGACCTGGAGTGGCGCGGCGCGGCGCATG 4850  
Qy 1561 AlaArgMetIleLeuGlnAspGluAspIleThrThrLysIleGluAsnAspTyrLysArg 1580  
Db 4851 GCGCGCATCATCTCTGACGAGGAGGACGTCCACCAAGATTGACACGATTGGAAGAGG 4910

Qy 1581 LeuAsnThrLeuAlaHisTyrGlnValProAspGlySerValValAlaLeuValSerLys 1600  
Db 4911 CTGAACACACACTGGCTCACTTACAGGTGACAGCGGCTCTCGTGGTGGCACTGGTGGCCCAAG 4970  
Qy 1601 GlnValThrAlaTyrAsnAlaValAsnAsnSerThrValSerArgThrSerAlaSerLys 1620  
Db 4971 CAGAGCTGCGCTACAACTCTCCAACTCTCCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCT 5027  
Qy 1621 TyrGluAsnMetIleArgTyrThrGlySerProAspSerLeuArgSerArgThrProMet 1640  
Db 5028 TAGGAGAGCATGCTCGCACCGCCAGCAGCCCGCAGCAGCTGCGTGGCGCAGCCCATG 5087  
Qy 1641 IleThrProAspLeuGluSerGlyValLysMetTrpHisLeuValLysAsnHisGluHis 1660  
Db 5088 ATCAGCCCGCAGCTGGAGAGCGCACCAAGCTGTGGCACCTGTGTGAAGAACCCAGCACAC 5147  
Qy 1661 GlyAspGlnLysGluGlyAspArgGlySerLysMetValSerGluIleTyrLeuThrArg 1680  
Db 5148 CTGGACAGCGTGGAGGTGACCGCGCAGCAAGATGGTCTCGAGATCTACTTGCACGCG 5207  
Qy 1681 LeuLeuAlaThrLysGlyThrLeuGlnLysPheValAspAspLeuPheGluThrIlePhe 1700  
Db 5208 CTACTGGCCCAACGAGGACACTGCGAAGTTTGTGGACGACTGTGTGAGCACTTCTTC 5267  
Qy 1701 SerThrAlaHisArgGlySerAlaLeuProLeuAlaIleLysTyrMetPheAspPheLeu 1720  
Db 5268 AGCAGGCGCACCGGGCTCAGCCTGCGCTGGCATCAAGTACATGTTGACTTCTCTG 5327  
Qy 1721 AspGluGlnAlaAspLysHisGlyIleHisAspProHisValArgHisThrTrpLysSer 1740  
Db 5328 GATGAGCAGCGCGACAGCAGATCCAGATGTCAGCTGCGGCCACACCTCGGAAGAGC 5387  
Qy 1741 AsnCysLeuProLeuArgPheTrpValAsnMetIleLysAsnProGlnPheValPheAsp 1760  
Db 5388 AACTGCT 5447  
Qy 1761 IleHisLysAsnSerIleThrAspAlaCysLeuSerValValAlaGlnThrPheMetAsp 1780  
Db 5448 ATTCAAGAAGACGATCATCGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5507  
Qy 1781 SerCysSerThrSerGluHisArgLeuGlyLysAspSerProSerAsnLysLeuLeuTyr 1800  
Db 5508 TCTGCT 5567  
Qy 1801 AlaLysAspIleProSerTyrLysAsnTrpValGluArgTyrTyrSerAspIleGlyLys 1820  
Db 5568 GCCAAGGACATCCCAACTACAAAGAGCTGGGTGGAGGTACTATGACACATCGCCAAG 5627  
Qy 1821 MetProAlaIleSerAspGlnAspMetAsnAlaTyrLeuAlaGluGlnSerArgMetHis 1840  
Db 5628 ATGCCAGCCATCAGCGACCCAGACATGAGTGGGTATCTGGCTGAGGAGTCCCGGCTGAC 5687  
Qy 1841 MetAsnGluPheAsnThrMetSerAlaLeuSerGluIlePheSerTyrValGlyLysTyr 1860  
Db 5688 CTGAGCCAGTTCAACAGCATGAGCGCTTGCACGAGATCTACTCTTACATCACCAGATAC 5747  
Qy 1861 SerGluGluIleLeuGlyProLeuAspHisAspAspGlnCysGlyLysGlnLysLeuAla 1880  
Db 5748 AAGGATGAGATCTGCGACGCCCTGGAGAGGATGAGCGCGCGCGCGCGCGCGCGCGCGCGCG 5807  
Qy 1881 TyrLysLeuGluGlnValIleThrLeuMetSerLeuAspSer 1894  
Db 5808 AGCAAGCTGGAGCAGGTGGTGGACAGCATGGCCCTGAGCAGC 5849

## RESULT 5

US-10-087-684-31  
; Sequence 31, Application US/10087684  
; Publication No. US20040029116A1  
; GENERAL INFORMATION:  
; APPLICANT: Edinger, Shlomit R.  
; APPLICANT: MacDougall, John R.  
; APPLICANT: Millet, Isabelle



	QY	91	AspAsnProLysCysTyrProProArgIleValGlnThrCysAsnGluProLeuThrThr	110
	Dd	347	GACAAAGAGAATGTCTACCGCGCCGCCAGCGTCAGTCTGGCCCCCACGGCTGGGCAGT	406
	QY	111	ThrAsnAsnValAsnLysMetLeuLeullelAspTyrLysGlUAsnArgLeulleAlaCys	130
	Dd	407	ACTGACAACGTCACCAAGAGTGCTGTCTGGACTATGCCGTAAACCGCTGTCTGGCCTGT	466
	QY	131	GlySerLeuTyrgInGlylleCyslysLeuleuAargLeuGluAspLeuPheLysLeuGly	150
	Dd	467	GGCAGCGCTCCAGGGCATCTGCAGATTCTTCGCTCGCATCTTTCAAATGGGT	526
	QY	151	GluProTyrHisLysValSergHistrLeuSergLyValAsnGluSergGlyserValPhe	170
	Dd	527	GAGCCACACCACCGTAAGAGCACTACTGTCTCAGCGTGCAGGAGGAGGAGCATGTGCG	586
	QY	171	GlyValIleValSer-----TyrSerAsnLeuAspAspLysLeuPheIleAlaThrAla	188
	Dd	587	GGCGTGCTCATITGCCGGGCCACCGGGCCAGGGCCAGGCTCTTCGTGGGCCACACC	646
	QY	189	ValAspGlyLeuProGluTyrPheProthrIleSerSerArgLysLeuThrLysAsnSer	208
	Dd	647	ATCGATGGCAAGTCCGAGTACTTCCCACACTGTCCAGCGTCGCTCATGTGGCCAACGAG	706
	QY	209	GluAlaAspGlyMetPheAlaTyrValPheHisAspGluPheValAlaSerMetIleLys	228
	Dd	707	GAGGATGCCGATGTCGCTTCGTTACACAGTAGATTGTGTATCATCAGCTCAAG	766
	QY	229	IleProSerAspThrPheThrIleleProAspPheAspileTyrTyrValTyrGlyPhe	248
	Dd	767	ATCCCTTCGACACGCTGCCAAGTTCGCGGCTTTGACATCTACTATGTGTACAGCTTC	826
	QY	249	SerSerGlyAsnPheValTyrPheLeuThrLeuGln-----ProGluMetValSerPro	266
	Dd	827	CGCAGGACAGTTTTGCTTACTACCTCAGCTGCAGTAGACACACAGCTGACCTGCCT	886
	QY	267	ProGlySerThrThryesGluGlnValTyrThrSerLysLeuValArgLeyCysLysGlu	286
	Dd	887	-----GATGCCCGCCGAGCACTTCTTCAGCTGCCAAGATCGTGGCGTCTGTGTGGAC	940
	QY	287	AspThrAlaPheAsnSerTyrValGluValProileGlyCysgluarGsserGlyValGlu	306
	Dd	941	GACCCCAANTTCTCTGTACGTTGAGTTCCTTCATTCGCTGCAGCAGGCGGTGTGGAG	1000
	QY	307	TyrArgLeuLeuGlnAlalaTyrIeuSerLysAlaGlyAlaValleuglyArgThrLeu	326
	Dd	1001	TACCGCTGTCAGGATGCCCTACTCTGAGCCGCGCGCGCTGCCCCGCCAACCACTG	1060
	QY	327	GlyValHisProAspAspLeuLeuPheThrValPheSerLysGlyGlinLysArgLys	346
	Dd	1061	GGCTTGCTGAGGACGAGACGTGCTGTTCACTGTGTTCCGCCAGGCCAGAGAACCOC	1120
	QY	347	MetLysSerLeuAppGluSerAlalaLeuCysIlePheIleLeuLysGlnIleAsnAspArg	366
	Dd	1121	GTGAAGCCCAAGAGGTGAGCACTGTCCCTGTTCCAGCTCAGGGCCATCAAGGAGAAG	1180
	QY	367	IleLysGluArgLeuGlnSerCystVsrArgGlyGluGlyThrLeuAspLeuAlatrpLeu	386
	Dd	1181	ATTAAGGAGGCATCCAGTCTCTACTACCGTGTGTAGGGCAAGCTCTCCCTGCCGTGGCTG	1240
	QY	387	LysValLysAspIleProCysSerSerAlaLeuLeuthrIleAspAspAnPheCysGly	406
	Dd	1241	CTCAACAGAGGTGGGTGTCATACTCGCCCCCTGCAGATCGATCAGCACTTCTGCGGG	1300
	QY	407	LeuAspMetAsnAlaproLeuGlyValSerAspMetValArgglyIleProValPheThr	426
	Dd	1301	CAGGACTTCAACAGCCCCCTGGGGGCACAGTCACCATTGAGGGAGCGCCCCCTGTCGTG	1360
	QY	427	GluAspArgAspArgMetThrSerValIleAlaTyrValTyrLysAsnHisSerLeuAla	446
	Dd	1361	GACAAGGATGATGGCTGACCGCGGTGGCTGCCTATGACTATCCGGGGCGGCATCTGGTA	1420



447 PheValGlyThrLysSerGlyLysLeuLysLysIleArgValAsp-----GlyProArg 464  
1421 TTCCCGGCGACGCGAAGTGGCGGCATCGCAGATCTCGTGGACCTCTCAAAACCCCGGT 1480  
465 GlyAsn---AlaLeuGlnTyrGluThrValGlnValValAspProGlyProValLeuArg 483  
1481 GCGCGCGCTGCGCTGGCTACAGAGCGTCTGGCCCGAGGAGCGCCCATCTCGCA 1540  
484 AspMetAlaPheSerLysAspHisGlnLeuTyrIleMetSerGluArgGlnLeuThr 503  
1541 GACCTGCTCTCAGCCCCAACCAACAGTACTCTACGCCATGACCGAGAGCAGGTGACG 1600  
504 ArgValProValGluSerCysGlyGlnTyrGlnSerCysGlyGluCysLeuGlySerGly 523  
1601 CGGTGCTGCTGGAGAGTGTGTGTCAGTACACGCTGCTGAGCTGTGTGGGTACCG 1660  
524 AspProHisCysGlyTyrCysValLeuHisAsnThrCysThrArgLysGluArgCysGlu 543  
1661 GACCCCTACTGTGCTGTGTGTCTGACAGCATGTCTCGCGGGGAGCCCTGTGAG 1720  
544 ArgSerLysGluProArgArgPheAlaSerGlnMetLysGlnCysValArgLeuThrVal 563  
1721 CGAGCAGCAGCGCCCGACGCTTGTGCGGACCTGTGTCAGTGTGTGACGCTGACTGTG 1780  
564 HisProAsnAsnIleSerValSerGlnTyrAsnVal---LeuLeuValLeuGluThrTyr 582  
1781 CAGCCCGCAATGTGTGTCTCACCATGTCCAGGTCCCGAGTGTGTGTGCGCCCTGG 1840  
583 AsnValProGluLeuSerAlaGlyValAsnCysThrPheGluAspLeuSerGluMetAsp 602  
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603 GlyLeuValValGlyAsnGlnIleGlnCysTyrSerProAlaAlaLysGluValProArg 622  
1901 AGCGTCTGGAGGATGGCGGATCCACTGCGCTCACCTCCGCGGAGGTGGCGCC 1960  
623 IleIle-----ThrGluAsnGlyAspHisValValGlnLeuGlnLeuLysSerLys 640  
1961 ATCAGCGGGCGGAGGAGGAGACCGCGGTGTGTGAATCTACTTAAAGTCCAG 2020  
641 GluThrGlyMetThrPheAlaSerThrSerPheValPheTyrAsnCysSerValHis--- 659  
2021 GAGACAGGGAAGTGTGCGTCTGTGACTTCGCTTCTTCTACAACTGCAGCGTCCACAG 2080  
660 AsnSerCysLeuSerCysValGluSerProTyrArgCysHisTyrCysLysTyrArgHis 679  
2081 TCGAGTGCCTGCTCTGTCTCAACGCTCCTTCTGCTCCACTGTGTGCAATACCGCAC 2140  
680 ValCysThrHisAspProLysThrCysSerPheGlnGluGlyArgValLysLeuProGlu 699  
2141 GTGTGCACACACACGTGCTGACTGCGCTTCTGAGGCGCGGTGTCAAGCTGTCTGAG 2200  
700 AspCysProGlnLeuLeuArgValAspLysIleLeuValProValGluValIleLysPro 719  
2201 GACTGCCACAGATCTGCGCTCCACGAGATCTACGTGCGAGTGGAGTGGTAAACCC 2260  
720 IleThrLeuLysAlaLysAsnLeuProGlnProGlnSerGlyArgGlyTyrGluCys 739  
2261 ATCACCTTGGCGCGACCGAACTGCGCACAGCCACAGCCACAGTCAGGCGAGTATGAGTGC 2320  
740 IleLeuAsnIleGlnGlySerGluGlnArgValProAlaLeuArgPheAsnSerSerSer 759  
2321 CTCCTTCCATCCCGGCGAGCCCGCGGTGTGACCGCCCTGCGCTTCAACAGCTTCCAGC 2380  
760 ValGlnCysGlnAsnThrSerTyrGlyGlyMetGluIleAsnAsnLeuProVal 779  
2381 CTGCAAGTCCCAATCTCTGACTCTTACGAGGGAACGATGTGACGCGACTGCGCACTG 2440  
780 GluLeuThrValValTyrAsnGlyHisPheAsnIleAspAsnProAlaGlnAsnLysVal 799  
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800 HisLeuTyrLysCysGlyAlaMetArgGluSerCysGlyLeuLysAlaAspPro 819

2501 CACCTCTACAAGTGGCGCGCTCGCGAGAGCTGGCGCTCTGCTCAAGCGCCACCG 2560  
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2561 CGCTTCGAGTGGGATGTGTGCGCGAGCCCGCTGCTCTCCCTGCGACACCACTCGCT 2620  
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859 ArgIleThrGluIleProValThrGlyProArgGluGlyGlyThrLysValThrIle 878  
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879 ArgGlyGluAsnLeuGlyLeuGluPheArgAspIleAlaSerHisValLysValaLagly 898  
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QY 1494 GlnIleAspTyrLysThrLeuValLeuSerCysValSerProAspAsnAlaAsnSerPro 1513  
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QY 1831 AlaTyrLeuAlaGluGlnSerArgMetHisMetAsnGluPheAsnThrMetSerAlaLeu 1850  
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QY 1889 LeuMetSerLeuAspSer 1894  
Db 5780 ACGATGCCCTGAGCAGC 5797

RESULT 6  
US-10-218-779-31  
Sequence 31, Application US/10218779  
Publication No. US2004002922A1  
GENERAL INFORMATION:  
APPLICANT: Edinger, Shiomit  
APPLICANT: MacDougall, John  
APPLICANT: Millet, Isabelle  
APPLICANT: Ellerman, Karen  
APPLICANT: Stone, David  
APPLICANT: Gerlach, Valerie  
APPLICANT: Grosse, William  
APPLICANT: Alsobrook II, John  
APPLICANT: Lepley, Denise  
APPLICANT: Rieger, Daniel  
APPLICANT: Burgess, Catherine  
APPLICANT: Casman, Stacie  
APPLICANT: Spytke, Kimberly  
APPLICANT: Boldog, Ferenc  
APPLICANT: Li, Li  
APPLICANT: Padigaru, Muralidhar  
APPLICANT: Mishra, Vishnu  
APPLICANT: Patturajan, Meera  
APPLICANT: Shenoy, Suresh  
APPLICANT: Rastelli, Luca  
APPLICANT: Tchernev, Velizar  
APPLICANT: Vernet, Corine  
APPLICANT: Zerhusen, Bryan  
APPLICANT: Malyankar, Uriel  
APPLICANT: Guo, Xiaojia  
APPLICANT: Miller, Charles  
APPLICANT: Gangoli, Esha  
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same  
FILE REFERENCE: 21402-214  
CURRENT APPLICATION NUMBER: US/10/218,779  
CURRENT FILING DATE: 2002-08-14  
PRIOR APPLICATION NUMBER: 60/253,834  
PRIOR FILING DATE: 2000-11-29  
PRIOR APPLICATION NUMBER: 60/250,-926  
PRIOR FILING DATE: 2000-11-30  
PRIOR FILING DATE: 2000-11-30  
PRIOR APPLICATION NUMBER: 60/264,180  
PRIOR FILING DATE: 2001-01-25  
PRIOR APPLICATION NUMBER: 60/313,656  
PRIOR FILING DATE: 2001-08-20  
PRIOR APPLICATION NUMBER: 60/327,456  
PRIOR FILING DATE: 2001-10-05  
NUMBER OF SEQ IDS NOS: 216  
SOFTWARE: Patent In Ver. 2.1  
SEQ ID NO 31  
LENGTH: 5895  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-218-779-31

Alignment Scores:  
Pred. No.: 0 Length: 5895  
Score: 6267.50 Matches: 1214  
Percent Similarity: 77.33% Conservative: 260  
Best Local Similarity: 63.69% Mismatches: 397  
Query Match: 62.74% Indels: 35  
DB: 13 Gaps: 23

US-09-964-956-13 (1-1896) x US-10-218-779-31 (1-5895)

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Db 1661 GACCCCACTGTGGCTGT 1720  
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Qy	1155	LeuLysProGlyThrProIleLeuLysGlyLysAsnLeuLeuProProValAlaGly	1174
Db	3578	CTGAAGGCCAGCTCCCACTCATCTCTCAAGGGCGGAACCTCTTGGCACCT--GCACCC	3634
Qy	1175	GlyAsnValLysLeuAsnTyThrValLeuValGlyGlyLysProCysThrValThrVal	1194
Db	3635	GGCACTCCGACTCAACTACAGGTGCTCATCGGCTCCACACCTGTACCTCACCGTG	3694
Qy	1195	SerAspValGlnLeuLeuCysGlySerProAsnLeuIleGlyArgHisLysValMetAla	1214
Db	3695	TCGGAGACGCAACTGCTGTGGAGGCCCAACCTCACTGGGACGACAAAGGTCACGGTG	3754
Qy	1215	ArgValGlyGlyMetGluTySerProGlyMetValTyrlleAlaProAspSerProLeu	1234
Db	3755	CGTGAGGTGGCTTCGAGTTCTCGCCAGGACACTGCAGGTGTACTCGGACAGCCTGCTG	3814
Qy	1235	SerLeuProAlaIleValSerIleAlaValAlaGlyLeuLeuIleIlePheIleVal	1254
Db	3815	ACGCTGCTGCCATTGTGGCARTTGGCGGAGGGGGGTCTCTGTCTGGTGCATCGTG	3874
Qy	1255	AlaValLeuIleAlaTyLysArgLysSerArgGluSerAspLeuThrLeuLysArgLeu	1274
Db	3875	GCRTGTGCTATCGCTCAAGCGCACTCAAGAGTGTCTACCGCACACCTCAAGCGGCTG	3934
Qy	1275	GlnMetGlnMetAspAsnLeuGluSerArgValAlaLeuGluCysLysGluAlaPheAla	1294
Db	3935	CAGCTCAGATGGACACCTGGAGTCCGGTGGCCCTCGAATGCAAGGAAGCCTTTGCA	3994
Qy	1295	GluLeuGlnThrAspIleHisGluLeuThrSerAspLeuAspGlyAlaGlyIleProPhe	1314
Db	3995	GAGCTGCAGACAGACATCCAGACTGACCAATGACCTGGACGGTGGCGGCATCCCTTC	4054
Qy	1315	LeuAspTyArgThrTyThrMetArgValLeuPheProGlyIleGluAspHisProVal	1334
Db	4055	CTTGACTACCGGACATATGCAATGCGGGTGCTCTTCTCGGATCGAGGACACCTGTG	4114
Qy	1335	LeuArgAspLeuGluValProGlyTyArgGlnGluArgValGluLysGlyLeuLysLeu	1354
Db	4115	CTCAAGAGATGGAGGTA-----CAGGCCAATGTGGAGAAGTCGCTGACACTG	4162
Qy	1355	PheAlaGlnLeuIleAsnAsnLysValPheLeuLeuSerPheIleArgThrLeuGluSer	1374
Db	4163	TTGGGGCAGCTGCTGACCAAGACACTTCTGTGTGACCTTCACTCCGACGCTGGAGGCA	4222
Qy	1375	GlnArgSerPheSerMetArgAspGlyAsnValAlaSerLeuIleMetThrValLeu	1394
Db	4223	CAGCGAGCTTCTCCATGGCGGACCGCGGGAATGTGGCTCGCTCATCATGCGGCCCTG	4282
Qy	1395	GlnSerLysLeuGluTyAlaThrAspValLeuLysGlnLeuLeuAlaAspLeuIleAsp	1414
Db	4283	CAGGGCGAGATGGAATACGCCACAGGGGTGTCTAAGCAGCTGCTTTCCGACCTCATCG	4342
Qy	1415	LysAsnLeuGluSerLysAsnHisProLysLeuLeuArgArg---ThrGluSerVal	1433
Db	4343	AAGAACTGGAGACAGAACACCCCAAGCTGTACTTGGCCCGGCCCAACTGAGTCGGTG	4402
Qy	1434	AlaGluLysMetLeuThrAsnTrrPheThrPheLeuLeuTyrlsPheLeuLysGluCys	1453
Db	4403	GCAGAGAAGATGCTAACTGAATGTGGTTCACCTTCCTTTGTAATAAGTTCCTCAAGGATGC	4462
Qy	1454	AlaGlyGluProLeuPheSerLeuPheCysAlaIleLysGlnGlnMetGluLysGlyPro	1473
Db	4463	GCTGGGGAGCGCTGTTTCATGCTGTACTGTCGCCCATCAAGCAGCAGATGGAGAGGGCCCC	4522
Qy	1474	IleAspAlaIleThrGlyGluAlaArgTySerLeuSerGluAspLysLeuIleArgGln	1493

Db	4523	ATTGACCCCATCAGGGTGAGGACGCGTACTCCTCGAGTGAGGACAAGCTCATCCGGCAG	1513
Qy	1494	GlnIleAspTyrLysThrLeuValLeuSerCysValSerProAspAsnAlaAsnSerPro	1513
Db	4583	CAGATTGACTACAAGACACTGACCCGTGAACCTGTGTGAACCCCTGAGAATGAGATGCACCT	4642
Qy	1514	GluValProValLysIleLeuAenCysAspThrIleThrGlnValLysGluLysIleLeu	1533
Db	4643	GAGGTGCGGTGAAGGGCGTGTGATGTGACACGGTCAACCCAGGCCAAGGAGAGAGCTGCTG	4702
Qy	1534	AspAlaIlePheLysAenValProCysSerHisArgProLysAlaAlaAspMetAspLeu	1553
Db	4703	GACGCTGCCCTACAAGGGCGTGCCCTACTCCAGCGGCCCAAGCGCGGACATGGACCTG	4762
Qy	1554	GluTrpArgGlnGlySerGlyAlaArgMetIleLeuGlnAspGluAspIleThrThrLys	1573
Db	4763	GAGTGGCGCCAGGGCCGATCGGGCGCATCATCTCGAGGACGAGACGTCACCAACAAG	4822
Qy	1574	IleGluAenAspTrpLysArgLeuAenThrLeuAlaHisTyrGlnValProAspGlySer	1593
Db	4823	ATTGACAACGATTGGAAGAGCTGACACACTGGCTCATCAACGGGTGACAGCGGGTCC	4882
Qy	1594	ValValAlaLeuValSerLysGlnValThrAlaTyrAsnAlaValaAsnAenSerThrVal	1613
Db	4883	TCGGTGGCATGTGGTCCCAAGACAGACGCTCGCGCTACAACATCTCCAACCTCTCCACCTTC	4942
Qy	1614	SerArgThrSerAlaSerLysTyrGluAenMetIleArgTyrThrGlySerProAspSer	1633
Db	4943	ACCAAG---TCCCTCAGCATATCAGAGCATCTCGCGACGGCCAGACGCCCGACAGC	4999
Qy	1634	LeuArgSerArgThrProMetIleThrProAspLeuGluSerGlyValLysMetTrpHis	1653
Db	5000	CTGGCTCGCGCAGCCCATGATCAGCCCGACTCGAGAGCGCCACCAAGCTGTGGCAC	5059
Qy	1654	LeuValLysAenHisGluHisGlyAspGlnLysGluGlyAspArgGlySerLysMetVal	1673
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Qy	1674	SerGluIleTyrLeuThrArgLeuLeuAlaThrLys---GlyThrLeuGlnLysPheVal	1692
Db	5120	TCGGAGATCTTACITGACACGGCTACTGGCCACCAAGCAGGGCACACTGCAGAAAGTTGTG	5179
Qy	1693	AspAspLeuPheGluThrIlePheSerThrAlaHisArgGlySerAlaLeuProLeuAla	1712
Db	5180	GACGACCTGTTTGAGACCATCTTCAGCACGGCACCGGGGCTCAGCCCTCGCGCTGGCC	5239
Qy	1713	IleLysTyrMetPheAspPheLeuAspGluGlnAlaAspLysHisGlyIleHisAspPro	1732
Db	5240	ATCAAGTACATGTTTGCATCTCTCGATGACAGCGCCGACCAAGCACCAGATCCACGATCT	5299
Qy	1733	HisValArgHisThrTrpLysSerAsnCys---LeuProLeuArgPheTrpValAsnMet	1751
Db	5300	GACGTGGCCACACCTGGAAGAGCAACTGCAGACGCTGCCCTCGCGCTCTCGGTGAACCTG	5359
Qy	1752	IleLysAenProGlnPheValPheAspIleHisLysAenSerIleThrAspAlaCysLeu	1771
Db	5360	ATCAAGAACCACAGTTTGTGTTCGATTCACAAGAACAGCATCAGGACGCTGCTGTTG	5419
Qy	1772	SerValValAlaGlnThrPheMetAspSerCysSerThrSerGluHisArgLeuGlyLys	1791
Db	5420	TCGGTGTGGCCAGACCTTCATGCACTCTCGTCTCCACCTCTGAGCAACAAGCTGGGCAAG	5479
Qy	1792	AspSerProSerAenLysLeuLeuTyrAlaLysAspIleProSerTyrLysAenTrpVal	1811
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Qy	1812	Glu---ArgTyrTyrSerAspIleGlyLysMetProAlaIleSerAspGlnAspMetAsn	1830
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222 PheValAlaSerMetIleLysIleProSerAspThrPheThrIleIleProAspPheAsp 241  
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; Sequence 313, Application US/09964824A  
; Patent No. US20020102531A1  
; GENERAL INFORMATION:  
; APPLICANT: Horrigan, Stephen  
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu  
; FILE OF INVENTION: Seta  
; FILE REFERENCE: 689290-73  
; CURRENT APPLICATION NUMBER: US/09/964,824A  
; PRIOR FILING DATE: 2001-09-27  
; PRIOR APPLICATION NUMBER: US/60/236,033  
; PRIOR FILING DATE: 2000-09-28  
; PRIOR APPLICATION NUMBER: US/60/236,032  
; PRIOR FILING DATE: 2000-09-28  
; PRIOR APPLICATION NUMBER: US/60/236,028  
; PRIOR FILING DATE: 2000-09-28  
; NUMBER OF SEQ ID NOS: 583  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 313  
; LENGTH: 6252  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
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Alignment Scores:  
Pred. No.: 3,08e-269 Length: 6252  
Score: 2580.00 Matches: 654  
Percent Similarity: 50.63% Conservative: 344  
Best Local Similarity: 33.18% Mismatches: 713  
Query Match: 25.83% Indels: 260  
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QY 44 ArgGlyGluProAlaGluGlyPheAsnHisLeuValValAspGluArgThrGlyHisIle 63  
Db 95 CGCAGCGAG-----AAAGAGCTGAACCACTGCTGTGGATGAGGCTCAGCGCGTGTG 148  
QY 64 TyRLeuGlyAlaValAsnArgIleTyRLeuSerSerAspLeuLysValLeuValThr 83  
Db 149 TACTTGGGGCGGTGAATGCTCTACAGCTGGATGCGAAGCTGCGCTGAGCGAGCAG 208  
QY 84 HisGluThrGlyProAspGluAspAsnProLysCysTyRProProArgIleValGlnThr 103  
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759 SerValGlnCysGlnAsnThrSerTyrSerTyrGluGlyMetGluIleAsnAsn----- 776  
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2207 AACGAGAGCTGCCCTGACCTCTACGTCAAGTCTTACGGCAAG---AATATGCAC--- 2260  
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2261 -----AGCAAGTCCATGTGACCTCTACAACTGCTCTTTGGCGGAGGACTGC 2311  
812 GlyLeuLysLeuLysAlaAspProAspPheAlaCysGlyTrpCysGlnGlyProGlyGln 831  
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Db	4406	AGCGTATCGTGAGGACGAG---GGAGTGGAGCGCATCCCGGTGAAGGTCTCTCACTGT	4462
QY	1523	AspThrIleThrGlnValIysGluIysIleLeuAspAlaIlePheIysAsnValProCys	1542
Db	4463	GACACCATCTCCAGGTCAAGGAGAAATCATTTGACCGAGTGTACCGTGGGACGCCCTGC	4522
QY	1543	SerHisArgProIysAlaAlaAspMetAspLeuGluTrpArgGlnGlySerGlyAlaArg	1562
Db	4523	TCTGCTGCGCCAGGCCACACAGCGTGTCTGGAGTGGCTCCGGGCTCCACAGCGCAG	4582
QY	1563	MetIleLeuGlnAspGluAspIleThrThrIysIleGluAsnAspTrpIysArgLeuAsn	1582
Db	4583	---ATCCTCTCGGACCTGACCTGACGTCACACAGCGGAGGGCGGTGGGAAGCGCGTCAAC	4639
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QY	1663	GlnIysGluGlyAspArgGlySer-----LysMetValSerGlu	1675
Db	4808	GAGGCAAGTCCAAGAGAGCGCGTGAAGAGAGGCGGACGAAGGCCCATCCCGAG	4867
QY	1676	IleTyrLeuThrArgLeuAlaThrIysGlyThrLeuGlnIysPheValAspAspLeu	1695
Db	4868	ATTACTCTGACGGGTCTCTCAGTCAAGGGCACACTGCAGAGTTGTGGCAACATTC	4927
QY	1696	PheGluThrIlePheSerThrAlaHisArgGlySerAlaLeuProLeuAlaIleLysTyr	1715
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QY	1716	MetPheAspPheLeuAspGluGlnAlaAspLysHisGlyIleHisAspProHisValArg	1735
Db	4979	TTCTTCGCATCTCTGCAGCAGGAGGAGAGACCAACATCCAGATGAAGACACCATC	5038
QY	1736	HisThrTriPlysSerAsnCysLeuProLeuArgPheTrpValAsnMetIleLysAsnPro	1755
Db	5039	CACATCTGAAGAAGCAACAGCTTACCGCTCCGCTTCTGGGTGAACATCTCTCAAGAACCC	5098
QY	1756	GlnPheValPheAspIleHisIysAsnSerIleThrAspAlaCysLeuSerValValala	1775
Db	5099	CACCTTCATCTTTGACGTGATGTCCACAGAGTGGTGGAGCGCTCGTGTGAGTCATCGCG	5158
QY	1776	GlnThrPheMetAspSerCysSerThrSerGluHisArgLeuGlyLysAspSerProSer	1795
Db	5159	CAGACCTTCATGATGCCTGCACGCGCACGGAGCATAAAGTGAGCGCGATTCTCCAGC	5218
QY	1796	AsnIysLeuLeuTyrAlaIysAspIleProSerTyrIysAsnTrpValGluArgTyrTyr	1815
Db	5219	AACAAGCTGTGTACGCCAAGGAGATCTCCACTCAAGAAGATGTGTGGAGGATTACTAC	5278
QY	1816	SerAspIleGlyLysMetProAlaIleSerAspGlnAspMetAsnAlaTyrLeuAlaGlu	1835
Db	5279	AAGGGATCCGGCAGATGGTGCAGGTGACGCACCGACCATGAACACACACCTGGCGAG	5338
QY	1836	GlnSerArgMetHisMetAsnGluPheAsnThrMetSerAlaLeuSerGluIlePheSer	1855
Db	5339	ATTTCGGGCGCACACGAGACTCCTTGAAACACCTCTGTGCATCTCCACAGCTCTACCAA	5398
QY	1856	TyrValGlyIysTyrSerGluGluIleLeuGlyProLeuAspHisAspAspGlnCysGly	1875



Db 5399 TACACGAGAGTACTATGACGAGATCATCAATGCTTGGAGGAGGATCTCTGCGCCAG 5458  
Qy 1876 LysGlnLysLeuAlaTyrLysLeuGluVal 1886  
Db 5459 AAGATGAGCTGGCTTCCGCTGCAGAGATT 5491

RESULT 8

US-09-930-213-254  
; Sequence 254, Application US/09930213  
; Publication No. US20030170625A1  
; GENERAL INFORMATION:  
; APPLICANT: ROSENTHAL, ANDRE  
; APPLICANT: HINZMANN, BERND  
; APPLICANT: SCHAFFER, REINHARD  
; APPLICANT: ZUBER, JOHANNES  
; APPLICANT: TCHER-NITSE, OLEG  
; APPLICANT: GRIPS, MARTIN  
; APPLICANT: HELLMER, MARTIN  
; APPLICANT: SCHMITZ, ANNE-CHANTAL  
; APPLICANT: SERS, CHRISTINE  
; TITLE OF INVENTION: DETECTION OF DIFFERENTIAL GENE EXPRESSIONS  
; FILE REFERENCE: ALBRE-14  
; CURRENT APPLICATION NUMBER: US/09/930,213  
; CURRENT FILING DATE: 2001-01-31  
; PRIOR APPLICATION NUMBER: DE 10004102.7  
; PRIOR FILING DATE: 2000-01-31  
; NUMBER OF SEQ ID NOS: 885  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 254  
; LENGTH: 6252  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-930-213-254

Alignment Scores:  
Pred. No.: 3,086-269 Length: 6252  
Score: 2580.00 Matches: 654  
Percent Similarity: 50.63% Conservative: 344  
Best Local Similarity: 33.18% Mismatches: 713  
Query Match: 25.83% Indels: 260  
DB: 10 Gaps: 61

US-09-964-956-13 (1-1896) x US-09-930-213-254 (1-6252)

Qy 24 ThrLeuLeuThrArgGlnProAlaProLeuSerGlnLysGlnArgSerPheValThrPhe 43  
Db 35 ACCCTGCTGGCCTGCTGGGCGCAGGTGCCAGCCTGAGCCCGCCGCAAGCTGGACTTCTTC 94  
Qy 44 ArgGlyGluProAlaGluGlyPheAsnHisLeuValValAspGluArgThrGlyHisIle 63  
Db 95 CGCAGCGAG-----AAGAGCTGACCCACTGGCTGGATGAGGCTCAGGCGTGGTG 148  
Qy 64 TyrLeuGlyAlaValAsnArgIleTyrLysLeuSerAspLeuLysValLeuValThr 83  
Db 149 TACCTGGGGGGGTGAATGCCCTTACCAGCTGGATGGGAAGCTGCAGCTGGAGCAGCAG 208  
Qy 84 HisGluThrGlyProAspGluAspAsnProLysCysTyrProArgIleValGlnThr 103  
Db 209 GTGGCCAGCGGGCCCGCCCTGGACCAAGAGTGCACGCCGCCCATCGAGCCAGCCAG 268  
Qy 104 CysAsnGluProLeuThrThrThrAsnAsnValAsnLysMetLeuLeuLeuAspTyrLys 123  
Db 269 TGCCATGAG---GCTGAGATGACTGACAATGTCACACAGCTGCTGCTGCTGCACTCC 325  
Qy 124 GluAsnArgLeuLeuAlaCysGlySerLeuTyrGlnGlyIleCysLysLeuLeuArgLeu 143  
Db 326 AGGAAGCGCCTGGTGGAGTGGCGGAGCCCTCTTCAAGGGGATCTGCGCTCTGCGGCCCTG 385  
Qy 144 GluAsp-----LeuPheLysLeuGlyGluProTyrHisLysLysGluHisTyrLeuSer 161  
Db 386 AGCAACATCTCCCTCCGCTGTTCTACGAGGACGCGAGGAGAAAGTCTTCTGCGGCC 445

Qy 162 GlyValAsnGluSerGlySerValPheGlyValIleValSerTyrSerAsnLeuAspAsp 181  
Db 446 ACCAATGATGAGGGCGTGCACACAGTGGGCTGGTGGAGCTCCACGGTCTCTGGTGGTAC 505  
Qy 182 LysLeuPheLeuAlaThrAlaValAspGlyLysProGluTyrPheProThrIleSerSer 201  
Db 506 CGCGTCTGCTTTGTGGGCAAGGCAATGGGCCACACAGCAGCGCATCATCGTGGACACT 565  
Qy 202 ArgLysLeuThrLysAsnSerGluAlaAspGlyMetPheAlaTyrValPheHisAspGlu 221  
Db 566 CGGTGTTGGACCGACTGACAGCAGGAGGCGCTTGAAGCTCACAGCACCACGCCACC 625  
Qy 222 PheValAlaSerMetIleLysIleProSerAspThrPheThrIleIleProAspPheAsp 241  
Db 626 TACAAGGCGCGCTACCTGTCCACCAACACACAGCAGTTTC----- 664  
Qy 242 IleTyrTyrValTyrGlyPheSerSerGlyAsnPheValTyrPheLeuThrLeuGlnPro 261  
Db 665 -----GTGGCGCCTTCAGAGCGCCCTAGCTCTTCTTGTCTTCTCAGCAGCAG 715  
Qy 262 GluMetValSerProGlySerThrThrLysGluGlnValTyrThrSerLysLeuVal 281  
Db 716 GACAAG---CACCGCGCCCGGAACCGCAG-----CTGTGGCA 751  
Qy 282 ArgLeuCysLysGluAspThrAlaPheAsnSerTyrValGluValProIleGlyCysGlu 301  
Db 752 CGCATGTGCAGAGAAGACCCCACTACTCTCTACCTGGAGATGAGCTGAGTGGCGG 811  
Qy 302 ArgSerGlyValGluTyrArgLeuLeuGlnAlaTyrLysLeuSerLysAlaGlyAlaVal 321  
Db 812 GACCCCGACATCCAC-----GCCGCTGCTTT-----GCCACCTGC 847  
Qy 322 LeuGlyArgThrLeuGlyValHisProAspAspLeuLeuPheThrValPheSerLys 341  
Db 848 CTGGCGCCTCGCTGGCTGGCTGGCTGGAGGGTGTATATGTGTCTTCTCAGAGA 907  
Qy 342 GlyGlnLysArgLysMetLysSerLeuAspGluSerAlaLeuCysIlePheIleLeuLys 361  
Db 908 GACAGC-----CGGAGCAGTGGGGCGCGTGGCGCTCTGCTGTCTCCGCTGGAC 961  
Qy 362 GlnIleAsnAspArgIleLysGluArgLeuGlnSerCysTyrArgGlyGluGlyThrLeu 381  
Db 962 AAGGTGCAGCCCAAGATGAGGCCAACCGCAACGCTGTATAC-----ACAGGACCCCG 1015  
Qy 382 AspLeuAlaTyrLeuLysValLys-----AspIleProCysSerSerAlaLeu 397  
Db 1016 GAGCCCGTGACATCTTCTACAGCCCTTCCAGCGGATATCCAGTGGCGGCCGCGG 1075  
Qy 398 LeuThrIleAspAspAsnPhe---CysGlyLeuAsp---MetAsnAlaProLeuGlyVal 415  
Db 1076 CGCGGCTCCAGCAAGAGCTTCCATGTGGCTGGAGCAGCTGCCCTACCGCTGGGCAG 1135  
Qy 416 SerAspMetValArgGlyIleProValPheThrGluAspArgAspArgMetThrSerVal 435  
Db 1136 CGGAGCGGCTCAGAGGACAGCGCGTGGCTGGAGGCGCTGAGCTGAGCTCAGCGCGTG 1195  
Qy 436 IleAlaTyrValTyrLysAsnHisSerLeuAlaPheValGlyThrLysSerGlyLysLeu 455  
Db 1196 ACGGTCCGCGCCGAGAACCAACACACACTGTGTCTTCTGGCACCTCTGATGCGCGATC 1255  
Qy 456 LysLysIleArgValAspGlyProArgGlyAsnAlaLeuGlnTyrGluThrValGlnVal 475  
Db 1256 CTCAGGTGTACCTCACC---CCAGATGGCACCTCTCAGAGTACACTCTATCTCTGTG 1312  
Qy 476 ValAspProGlyProValLeuArgAspMetAlaPheSerLysAspHisGluGlnLeuTyr 495  
Db 1313 GAGATAACAGAGAGTCAAGCGCAGCTGGTACTCTCTGGAGACCTGGGCGACCTGTAC 1372  
Qy 496 IleMetSerGluArgGlnLeuThrArgValProValGluSerCysGlyGlnTyrGlnSer 515  
Db 1373 GCCATGCCAGACAGAGTGTTCGGCTGCGCGTGCAGAGTGCCTGAGTACCGCAGC 1432  
Qy 516 CysGlyGluCysLeuGlySerGlyAspProHisCysGlyTyrCysValLeuHisAsnThr 535

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Db 1433 TCACCCAGTGCAGCGGACTCCAGGACCCCTACTCGGCTGTGTGCTGCGAGGACGA 1492
QY 536 CysThrArgLysGluArgCysGluArgSerLysGluProArgArgPheAla---SerGlu 554
Db 1493 TCACCCGAGCGCGAGTGTCCGGCGGCGAGGAGCCAGCCACTGCTGTGAGCCGA 1552
QY 555 MetLysGlnCysValArgLeuThr---ValHisProAsnAsnIleSer---ValSerGln 572
Db 1553 AGCAAGTGTGCTGTGCGCGCTACACGAGCGCCAGCCAGCCACAGAAACATGAGCGCGCGGCCAG 1612
QY 573 TyrAsnValLeuLeuValLeuGluThrTyrAsnValProGluLeuSerAla-----Gly 590
Db 1613 GGGGAGGTGCAGCTACCGTCAAGCC---CTCCCTGCGCTGAGGAGGAGACGAG 1666
QY 591 ValAsnCysThrPheGluAspLeuSerGluMetAspGlyLeuValValGlyAsnGlnIle 610
Db 1667 TTGCTGTGCTGCTTTTGGGAGTGCAGCGCCAGCCAGCCCGCGCGTGGAGGGCGAGCCGCTC 1726
QY 611 GlnCysTyrSerProAlaAlaLysGluValProArgIleIleThrGluAsnGly---Asp 629
Db 1727 ATCTGCACTCCCAAGAGC-----ATCCCC-----GTCACACCCCGGCGGACGAG 1774
QY 630 HisHisValValGlnLeuGlnLeuLysSerLysGluThrGlyMetThrPheAlaSerThr 649
Db 1775 CACGTGGCGGTGACCATCCAGCTCTCTTAGACGAGCAACATCTTCTCCTCAGCTCTAC 1834
QY 650 SerPheValPheTyrAsnCysSerValHisAsnSer-----CysLeu 663
Db 1835 CAGTACCCCTCTACAGCTCGCGCCAGCCAGCCAGTGCCTGCGCCACATGGAGGACG 1894
QY 664 SerCysValGluSerProTyrArgCysHisTyrCysLysTyrArgHisValCysThrHis 683
Db 1895 TCCTCGTGAGCAACCGCTGGACCTGCGAGTGGACCTGCTACACAGTGCAGGAG 1954
QY 684 ---AspProLysThrCysSerPheGlnGluGly-----ArgValLysLeuProGluAsp 700
Db 1955 GCTTCGCCCAACCCCT-----GAGGACGCGCATCGCTCGCCGACATGGAGGACG 2005
QY 701 CysProGlnLeuLeuArgValAspLysIleLeuValProValGluValIleLysProIle 720
Db 2006 TGTCCCGAGTCTCTGGGACCCAGCCCTGCTGTGATCCCATGACACGAGACAGATGTG 2065
QY 721 ThrLeuLysAlaLysAsnLeuProGlnProGlnSerGlyGlnArgGlyTyrGluCysIle 740
Db 2066 AACTTCCAGGGCAAGAACTGGAC-----2089
QY 741 LeuAsnIleGlnGlySerGluGlnArgValProAla-----LeuArgPheAsnSerSer 758
Db 2090 ---ACGGTGAAGGGTCTCTCCCTGCAGCTGGCGAGTACTGTGCTCAAGTTATGGAGCCG 2146
QY 759 SerValGlnCysGlnAsnThrSerTyrSerTyrGluGlyMetGluIleAsnAsn-----776
Db 2147 GTGACCATGCAGGAATCTGGGACCTTCGCTTTCGAGCCCAAGCTGTCCACGATGCC 2206
QY 777 -----LeuProValGluLeuThrValThrValProValPheAsnIleAspAsn 793
Db 2207 AACGAGAGCGTCCCTGCAGCTCTACGCTCAAGTCTTACGCAAG---AATATCGAC---2260
QY 794 ProAlaGlnAsnLysValHis-----LeuTyrLysCysGlyAlaMetArgGluSerCys 811
Db 2261 -----AGCAAGCTCCATGTGACCTCTACACTGCTCTTGGCGCGAGCGACTGC 2311
QY 812 GlyLeuLysLeuLysAlaAspProAspPheAlaCysGlyTyrCysGlnGlyProGlyGln 831
Db 2312 AGCCTGTGCGCGCGCTTAACCCGACTACAGGTGTGCTGTGCGGGGCGCAGAGCAGG 2371
QY 832 CysThrLeuArgGlnHisCysProAlaGlnGluSerGlnTyrLeuGluLeuSerGlyAla 851
Db 2372 TCGGTGTATGAGCCCTGTGC-----AACACC 2398
QY 852 LysSerLysCysThrAsnProArgIleThrGluIleIleProValThrGlyProArgGlu 871
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QY 1210 HisLys-----ValMetAlaArgVal 1216  
Db 3482 CCCAAGCGGCGGCAAGAACAGACACACACACCAACCTGCCGAGTTCATTGTGAAGTTC 3541  
QY 1217 GlyGlyMetGluTyrSerProGlyMetValTyrIle-----AlaProAsnSerPro 1233  
Db 3542 GGCTCTCGCGAGTGGTGGTGGCGCGGTGAGTACGACACACGCGGTGAGCGAGCTGCCG 3601  
QY 1234 LeuSerLeu-----ProAlaIleValSerIleAlaValAlaGly 1246  
Db 3602 CTCAGCTCATCTTGGCTGCTCATCGTGCCTCATGTGTGCTGCTGCTGCTGCTGCTGCT 3658  
QY 1247 GlyLeuLeuIleIlePheIleValAlaValLeuLeuLeuAlaTyrLysArgLysSerArgGlu 1266  
Db 3659 -----GTCTACTGCTACTGGAGGAAGACGACGAG 3688  
QY 1267 SerAspLeuThrLeuLysArgLeuGlnMetGlnMetAspAsnLeuGluSerArgValAla 1286  
Db 3689 GCCGAACGAGATGAGAAATCAAGTCCAGCTGGAGGCGCTGGAGGAGCGTGGCG 3748  
QY 1287 LeuGluCysLysGluAlaPheAlaGluLeuGlnThrAspIleHisGluLeuThrSerAsp 1306  
Db 3749 GACCGCTGCAAGAAAGAAATTCACAGACCTGATGATCGAGATGGAGGACCAACAGCAC 3808  
QY 1307 LeuAspGlyAlaGlyIleProPheLeuAspTyrArgThrTyrThrMetArgValLeuPhe 1326  
Db 3809 GTGCAGGCGCGGATCCCCGTGCTGAGCTCAAGACCTACACCGCGGCTCTTCTTC 3868  
QY 1327 -----ProGlyIleGluAspHisProValLeuArgAspLeuGluValProGly 1342  
Db 3869 CTGCGCTCCAAAGGACGGCGAAGAGCGTGTATGATACCGGCAAGCTGGACATCCCTGAG 3928  
QY 1343 TyrArgGlnGluArgValGluLysGlyLeuLysLeuPheAlaGlnLeuIleAsnAsnLys 1362  
Db 3929 CCGCGCGCGCGGTGGAGACGCCCTCTACAGTTCCTCAACCTGCTGAACAGCAAG 3988  
QY 1363 ValPheLeuLeuSerPheIleArgThrLeuGluSerGlnArgSerPheSerMetArgAsp 1382  
Db 3989 TCTTCTCTCATCAATTCATCCACACCTCGAGAACCAAGCGGGAGTCTCGCGCGCGCC 4048  
QY 1393 ArgGlyAsnValAlaSerLeuIleMetThrValLeuGlnSerLysLeuGluTyrAlaThr 1402  
Db 4049 AAGGCTTACTTCGGCTCCCTGCTGACGGTGGCGCTGACCGGAACTGGAGTACTACACG 4108  
QY 1403 AspValLeuLysGlnLeuAlaAspLeuIleAspLysAsnLeuGluSerLysAsnHis 1422  
Db 4109 GACATCATGCACGCTCTTCTTGAGCTCTCTGGAGCAGTACGTGGTGGCCAAAGAAC--- 4165  
QY 1423 ProLysLeuLeuArgArgThrGluSerValAlaGluLysMetLeuThrAsnTyrPhe 1442  
Db 4166 CCCAAGCTGATGCTGCGCAGGCTGAGACTGTGGTGGAGAGGATGCTGTCCAACCTGGATG 4225  
QY 1443 ThrPheLeuLeuTyrLysPheLeuLysGluCysAlaGlyGluProLeuPheSerLeuPhe 1462  
Db 4226 TCCATCTCGCTGACCACTACTCAAGACAGTGGCGGGAGCCCTGTACAGCTCTTC 4285  
QY 1463 CysAlaIleLysGlnMetGluLysGlyProIleAspAlaIleThrGlyGluAlaArg 1482  
Db 4286 AAGGCCATCAACATCAGTGGAAAGGCGCGGTGGATGCGGTACAGAAAGGCCCAAG 4345  
QY 1483 TyrSerLeuSerGluAspLysLeuIleArgGlnIleAspTyrLysThrLeuValLeu 1502  
Db 4346 TACACTCTCAACGACCGGGCTGCTGGGGATGATGGAGTACGACACCCCTGACGGTG 4405  
QY 1503 SerCysValSerProAspAsnAlaAsnSerProGluValProValLysIleLeuAsnCys 1522  
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QY 1523 AspThrIleThrGlnValLysGluLysIleLeuAspAlaIlePheLysAsnValProCys 1542  
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QY 1543 SerHisArgProLysAlaAlaAspMetAspLeuGluTyrArgGlnGlySerGlyAlaArg 1562  
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QY 1563 MetIleLeuGlnAspGluAspIleThrThrLysIleGluAsnAspTyrLysArgLeuAsn 1582  
Db 4583 ---ATCCTCTCGACACTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGAC 4639  
QY 1583 ThrLeuAlaHisTyrGlnValProAspGlySerValAlaLeuValSerLysGlnVal 1602  
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Db 4727 GACCTG-----CCTGGGAGCGCCATGCCCTC----- 4753  
QY 1643 ProAspLeuGluSerGlyValLysMetTyrPheLysLeuValLysAsnHisGluHisGlyAsp 1662  
Db 4754 -----CTGGAGGAGAGAACCGGTGTGGCACCTGTGTGGCGCCGACCGGAGGTGGAC 4807  
QY 1663 GlnLysGluGlyAspArgGlySer-----LysMetValSerGlu 1675  
Db 4808 GAGGCAAGTCCCAAGAGAGCGAGCGTGAAGAGAGAGGAGCGGACGAGCCATCACCAG 4867  
QY 1676 IleTyrLeuThrArgLeuLeuAlaThrLysGlyThrLeuGlnLysPheValAspAspLeu 1695  
Db 4868 ATCTACTCTGACGCGGTCTCTCAGTCAAGGCGACACTGCAGCAGTTGTGGACAACCTTC 4927  
QY 1696 PheGluThrIlePheSerThrAlaHisArgGlySerAlaLeuProLeuAlaIleLysTyr 1715  
Db 4928 TTCAGAGCGTCTCGCGCTGGGAC-----GCGTGGCCACTGTCAGTCAAGTAC 4978  
QY 1716 MetPheAspPheLeuAspGluGlnAlaAspLysHisGlyIleHisAspProHisValArg 1735  
Db 4979 TTCCTCGACTCTCTGACGAGCAGCAGAGAGAGAGCAACATCCAGGATGAAGACCACTC 5038  
QY 1736 HisThrTyrLysSerAsnCysLeuProLeuArgPheTyrValAsnMetIleLysAsnPro 1755  
Db 5039 CACATCTGGAAGACGAGACAGTTCACGCTCCGCTTCTGGTGAACATCTCTCAAGAACCCC 5098  
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QY 1816 SerAspIleGlyMetProAlaIleSerAspGlnAspMetAsnAlaTyrLeuAlaGlu 1835  
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QY 1876 LysGlnLysLeuAlaTyrLysLeuGluGlnVal 1886

5701 TCAGCTGTTGGACCGGACTGACAGCAGGAGCGCTTTGAAGCCTACACGAGCAGCCAC 5642
221 uPheValAlaSerMetIleLysIleProSerAspThrPheThrIleIleProAspPhe 241
5641 CTAAAGCGCGCTACTGTCACCAACACACAGCAGTTTC----- 5602
241 pIleTyTyValTyArgPheSerSerGlyAsnPheValTyPheLeuThrLeuGlnPr 261
5601 -----GTGGCGGCTTCGAGGAGCGCCCTACGTCCTCTTTGCTTCAACAGCA 5552
261 oGluMetValSerProGlySerThrThrLysGluGlnValTyThrSerLysLeuVa 281
5551 GGACAAAG---CACCCGCGCCGGAACCGCACG-----CTGCTGGC 5516
281 lArgLeuCysGluAspThrAlaPheAsnSerTyValGluValProIleGlyCysGl 301
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301 uArgSerGlyValGluTyArgLeuLeuGlnAlaTyArgLeuSerLysAlaGlyAlaVa 321
5455 GGACCCCGACATCCAC-----GCCGTGCTTT-----GCCACCTG 5420
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5419 CCTGGCGCTCTCGTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 5360
341 sGlyGlnLysArgLysMetLysSerLeuAspGluSerAlaLeuCysIlePheIleLeuLy 361
5359 AGACAGC-----CGGAGCAGTGGGGGCGCGGCTCTGCTGCTGCTGCTGCTGCTG 5306
361 sGlnIleAsnAspArgIleLysGluArgLeuGlnSerCysTyArgGlyGluGlyThrLe 381
5305 CGAGTGCAGCGCCAGATGAGGCCAACCGACCGCTGTTC-----ACAGGCACCG 5252
381 uAspLeuAlaTrpLeuLysValLys-----AspIleProCysSerSerAlaLe 397
5251 GGAGCGCGGTGACATCTTACAGCCCTTCCACGGCGATATCCAGTGGCGCGCCACGC 5192
397 uLeuThrIleAspAsnPhe---CysGlyLeuAsp---MetAsnAlaProLeuGlyVa 415
5191 GCCGGCTCCAGCAAGAGCTTCCATGTGCTGGAGCACCTGCCCTACCGCTGGCGAG 5132
415 lSerAspMetValArgGlyIleProValPheThrGluAspArgAspArgMetThrSerVa 435
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435 lIleAlaTyValTyLysAsnHisSerLeuAlaPheValGlyThrLysSerGlyLysLe 455
5071 GACGTCGCCCGCCGAGAACACACACTGTGCTTTCTGGGCACTCTCATGAGCCCGAT 5012
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4954 GGAGATAAACAGAGAGTCAAGCGCGACCTGTGTCTGTGAGACCTGGGAGCGCTGTA 4895
495 rIleMetSerGluArgGlnLeuThrArgValProValGlnSerCysGlyGlnTyGlnSe 515
4894 GCCATGACCCAGACAGAGGTGTCCGGCTCCGGTCCGAGAGTCCCTGAGTACCCGAC 4835
515 rCysGlyGluCysLeuGlySerGlyAspProHisCysGlyTrpCysValLeuHisAsnTh 535
4834 CTGACCCAGTCCCGGAGTCCAGGACCCCTACTGCGGCTGTGTGCTGCTGCGAGGAG 4775
535 rCysThrArgLysGluArgCysGluArgSerLysGluProArgArgPheAla---SerGl 554
4774 ATGCACCCGAGGCGGAGTGTCCGGGCGCGAGAGCCAGCCAGCTGGCTGTGGAGCGG 4715
554 uMetLysGlnCysValArgLeuThr---ValHisProAsnAsnIleSer---ValSerGl 572

Db Qy Db Qy Db Qy Db Qy Db Qy Db Qy Db Qy Db Qy Db Qy Db Qy Db Qy Db Qy Db Qy
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221 uPheValAlaSerMetIleLysIleProSerAspThrPheThrIleIleProAspPhe 241
5641 CTAAAGCGCGCTACTGTCACCAACACACAGCAGTTTC----- 5602
241 pIleTyTyValTyArgPheSerSerGlyAsnPheValTyPheLeuThrLeuGlnPr 261
5601 -----GTGGCGGCTTCGAGGAGCGCCCTACGTCCTCTTTGCTTCAACAGCA 5552
261 oGluMetValSerProGlySerThrThrLysGluGlnValTyThrSerLysLeuVa 281
5551 GGACAAAG---CACCCGCGCCGGAACCGCACG-----CTGCTGGC 5516
281 lArgLeuCysGluAspThrAlaPheAsnSerTyValGluValProIleGlyCysGl 301
5515 AGCATGTGCAGAGAGACCCCACTACTCTCTACCTGGAGATGAGCTGCAGTCCG 5456
301 uArgSerGlyValGluTyArgLeuLeuGlnAlaTyArgLeuSerLysAlaGlyAlaVa 321
5455 GGACCCCGACATCCAC-----GCCGTGCTTT-----GCCACCTG 5420
321 lLeuGlyArgThrLeuGlyValHisProAspAspLeuLeuPheThrValPheSerLy 341
5419 CCTGGCGCTCTCGTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 5360
341 sGlyGlnLysArgLysMetLysSerLeuAspGluSerAlaLeuCysIlePheIleLeuLy 361
5359 AGACAGC-----CGGAGCAGTGGGGGCGCGGCTCTGCTGCTGCTGCTGCTGCTG 5306
361 sGlnIleAsnAspArgIleLysGluArgLeuGlnSerCysTyArgGlyGluGlyThrLe 381
5305 CGAGTGCAGCGCCAGATGAGGCCAACCGACCGCTGTTC-----ACAGGCACCG 5252
381 uAspLeuAlaTrpLeuLysValLys-----AspIleProCysSerSerAlaLe 397
5251 GGAGCGCGGTGACATCTTACAGCCCTTCCACGGCGATATCCAGTGGCGCGCCACGC 5192
397 uLeuThrIleAspAsnPhe---CysGlyLeuAsp---MetAsnAlaProLeuGlyVa 415
5191 GCCGGCTCCAGCAAGAGCTTCCATGTGCTGGAGCACCTGCCCTACCGCTGGCGAG 5132
415 lSerAspMetValArgGlyIleProValPheThrGluAspArgAspArgMetThrSerVa 435
5131 CGCGAGCGGCTCAGAGCGCAGCGCTGCTGCGAGCGTGGAGCGCTGAACCTCAGCGCGT 5072
435 lIleAlaTyValTyLysAsnHisSerLeuAlaPheValGlyThrLysSerGlyLysLe 455
5071 GACGTCGCCCGCCGAGAACACACACTGTGCTTTCTGGGCACTCTCATGAGCCCGAT 5012
455 uLysLysIleArgValAspGlyProArgGlyAsnAlaLeuGlnTyArgLeuValGlnVa 475
5011 CCTCAGGTGTACCTCACC---CCAGATGGCACCTCTCAGAGTACGACTCTATCTTGT 4955
475 lValAspProGlyProValLeuArgAspMetAlaPheSerLysAspHisGluGlnLeuTy 495
4954 GGAGATAAACAGAGAGTCAAGCGCGACCTGTGTCTGTGAGACCTGGGAGCGCTGTA 4895
495 rIleMetSerGluArgGlnLeuThrArgValProValGlnSerCysGlyGlnTyGlnSe 515
4894 GCCATGACCCAGACAGAGGTGTCCGGCTCCGGTCCGAGAGTCCCTGAGTACCCGAC 4835
515 rCysGlyGluCysLeuGlySerGlyAspProHisCysGlyTrpCysValLeuHisAsnTh 535
4834 CTGACCCAGTCCCGGAGTCCAGGACCCCTACTGCGGCTGTGTGCTGCTGCGAGGAG 4775
535 rCysThrArgLysGluArgCysGluArgSerLysGluProArgArgPheAla---SerGl 554
4774 ATGCACCCGAGGCGGAGTGTCCGGGCGCGAGAGCCAGCCAGCTGGCTGTGGAGCGG 4715
554 uMetLysGlnCysValArgLeuThr---ValHisProAsnAsnIleSer---ValSerGl 572

Db 5459 AAGATGCACCTGGCCCTCCGCTGACAGCAGATT 5491
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US-10-276-774-838/c
; Sequence 838, Application US/10276774
; Publication No. US20040053245A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NO. US20040053245A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-030
; CURRENT APPLICATION NUMBER: US/10/276,774
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 09/496,914
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 2700
; SOFTWARE: Custom
; SEQ ID NO 838
; LENGTH: 6329
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-276-774-838
Alignment Scores:
Pred. No.: 9,366-265 Length: 6329
Score: 2639.00 Matches: 652
Percent Similarity: 50.43% Conservative: 343
Best Local Similarity: 33.05% Mismatches: 716
Query Match: 25.42% Indels: 262
DB: 13 Gaps: 61
US-09-964-956-13 (1-1896) x US-10-276-774-838 (1-6329)
Qy 24 ThrLeuLeuThrArgGlnProAlaProLeuSerGlnLysGlnArgSerPheValThrPhe 43
Db 6232 ACCCTGCTGGCCCTGCTGGCGAGCGTGCAGCTGAGCGCCCGCAGCTGACCTCTTC 6173
Qy 44 ArgGlyGluProAlaGluGlyPheAsnHisLeuValValAspGluArgThrGlyHisIle 63
Db 6172 CGCAGCGAG-----AAAGAGCTGAACCCACCTCGCTGTGATGAGCGCTCAGCGCTGTG 6119
Qy 64 TyLeuGluValAlaValAsnArgIleTyLysLeuSerSerAspLeuLysValLeuValThr 83
Db 6118 TACCTGGGCGCGTGAATGCCCTCTACAGCTGGATGCGAGCTGAGCTGAGCGAGCGAG 6059
Qy 84 HisGluThrGlyProAspGluAspAsnProLysCysTyProProArgIleValGlnThr 103
Db 6058 GTGCCACAGCGCGCGCTCTGGAGCAACAGAGTGCACGCGCGCCATCAGCGCCAGCCAG 5999
Qy 104 CysAsnGluProLeuThrThrThrAsnAsnValAsnLysMetLeuLeuLeuLeuLys 123
Db 5998 TGCCATGAG---GCTGAGATGACTGACATGTCAACAGCTGTGCTGTGCTGACCCCTCC 5942
Qy 124 GluAsnArgLeuIleAlaCysGlySerLeuTyArgGlnGlyIle-CysLysLeuLeuArgLe 143
Db 5941 AGGAAACGCTGTGTGGAGTCCGGGAGCTTCTTAAGGGCATCTCGCTGCTGCGCGCTC 5882
Qy 143 uGluAsp-----LeuPheLysLeuGlyGluProTyHisLysLysGluHisTyLysLeu 161
Db 5881 GAGCAACATCTCCCTCCGCTGTCTTACAGAGAGCGCGCGGAGAGAGTCTTCTGCTGCG 5822
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Qy 181 pLysLeuPheIleAlaThrAlaValAspGlyLysProGluTyPheProThrIleSerSe 201
Db 5761 CCGCGTGTCTGTTGTGGGCAAGGCAATGGGCCACACAGCAACCGGATCATCTGAGCAC 5702
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1684	Db	AG---ATCCTGTGGACCTGGACCTGAGCGTACACAGCGGAGGCGCGTGAAGCGCGTCA	1628
1582	QY	snThrLeuAlaHisTyrGlnValProAspGlySerValValAlaLeuValSerLysGlnV	1602
1627	Db	ACACCCATTGACACTACATATGTCGGGATGGAGCCACCTCATCTG-----	1581
1602	QY	alThrAlaTyrAsnAlaValAsnAsnSerThrValSerArgThrSerAlaSerLysTyrG	1622
1580	Db	-----TCCAAGTGGGGGTCTCCACAGCCCGGAGCAGACGCCAGC	1541
1622	QY	luAsnMetIleArgTyrThrGlySerProAspSerLeuArgSerArgThrProMetIle	1642
1540	Db	AGNACCTG-----CCTGGGGAGCGCCATGCCCCC-----	1512
1642	QY	hrProAspLeuGluSerGlyValLysMetTrpHisLeuValLysAsnHisGluHisGlyA	1662
1511	Db	-----CTGGAGGAGGAGAACCGGGTGTGCACCTGTGCGCGCCACGACGAGGTGG	1460
1662	QY	spGlnLysGluGlyAspArgGlySer-----LysMetValSerG	1675
1459	Db	ACGAGGCGAAGTCCAAGAGGCGCGTGAAGAGAGGAGCGGACGAGAGGCCATCACCG	1400
1675	QY	luIleTyrLeuThrArgLeuLeuAlaThrLysGlyThrLeuGlnLysPheValAspAspL	1695
1399	Db	AGATCTACCTGACGCGCTGCTCTCAGTCAAGGGCACACTGCAGCAGTTTGTGCACAAC	1340
1695	QY	euPheGluThrIlePheSerThrAlaHisArgGlySerAlaLeuProLeuAlaIleLysT	1715
1339	Db	TCTTCCAGACGCTGCTGGCGCTCGGCGAC-----GCGGTGCCACCTGCAGTCAAGT	1289
1715	QY	YrMetPheAspPheLeuAspGluGlnAlaAspLysHisGlyIleHisAspProHisValA	1735
1288	Db	ACTTCTCGACTTCCTGGACGAGCGAGCGAGAGACCAACATCCAGGATCAAGACACCA	1229
1735	QY	rgHisThrTrpLysSerAsnCysLeuProLeuArgPheTrpValAsnMetIleLysAsnP	1755
1228	Db	TCCACATCTGGAGAGCAACAGTTTACCGCTCCGGTTCTGGGTGAACATCTCTCAAGAACC	1169
1755	QY	roGlnPheValPheAspIleHisLysAsnSerIleThrAspAlaCysLeuSerValValA	1775
1168	Db	CCCACTTCATTTTGACGTGCATGTCCAGAGTGGTGGACGCTCGCTGCAGTCAATCG	1109
1775	QY	laGlnThrPheMetAspSerCysSerThrSerGluHisArgLeuGlyLysAspSerProS	1795
1108	Db	CGCAGACCTTCATGGATGCTGCAGCGCACGAGCATAAAGCTGAGCGCGGATTCCTCCA	1049
1795	QY	erAsnLysLeuLeuTyrAlaLysAspIleProSerTyrLysAsnTrpValGluArgTyrT	1815
1048	Db	GCACAAAGCTGCTGACGCGAGGAGATCTCCACCTACAAGAAGATGTGGAGGATTACT	989
1815	QY	YrSerAspIleGlyLysMetProAlaIleSerAspGlnAspMetAsnAlaTyrLeuAlaG	1835
988	Db	ACAAAGGGATCCGGCAGATGGTGCAGGTCCAGCGACCGAGCATGAACACACACACCTGC	929
1835	QY	luGlnSerArgMetHisMetAsnGluPheAsnThrMetSerAlaIleuSerGluIlePheS	1855
928	Db	AGATTCCCGGGCGCACACGGACTCCTTGAACACCCCTCGTGGCACTCCACAGCTCTACC	869
1855	QY	erTyrValGlyLysTyrSerGluGluIleLeuGlyProLeuAspHisAspAspGlnCysG	1875
868	Db	AATACACGCAAGAGTACTATGACGAGATCATCAATGCCCTTGGAGGAGGATCCTCCGCC	809
1875	QY	lyLysGlnLysLeuAlaTyrLysLeuGluGlnVal	1886
808	Db	AGAAATGTCAGCTGGCGCTTCCGCGCTGCAGCAGATT	774

US-10-240-425-350  
; Sequence 350, Application US/10240425  
; Publication No. US20040033502A1  
; GENERAL INFORMATION:  
; APPLICANT: Williams, Amanda

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; APPLICANT: Boland, Joseph F.
; APPLICANT: Lord, Reginald V.
; APPLICANT: Alvarez, Chris
; APPLICANT: Wetzel, Jon C.
; APPLICANT: Scherf, Uwe
; APPLICANT: Vockley, Joseph G.
; TITLE OF INVENTION: Gene Expression Profiles in Esophageal Tissue
; FILE REFERENCE: 44921-5026
; CURRENT APPLICATION NUMBER: US/10/240,425
; CURRENT FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: PCT/US01/09847
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 60/193,446
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 1588
; SOFTWARE: PatenIn Ver. 2.1
; SEQ ID NO 350
; LENGTH: 6754
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20040033502A1 AB014520
; US-10-240-425-350

Alignment Scores:
Pred. No.:      8,88e-258          Length:      6754
Score:           2475.50          Matches:     650
Percent Similarity: 48.64%        Mismatches:   334
Best Local Similarity: 32.13%      Indels:       749
Query Match:     24.78%           Gaps:         293
DB:              13               Gaps:         59

US-09-964-956-13 (1-1896) x US-10-240-425-350 (1-6754)

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Db    286 CGTGTGTCCTCGGGGGCGCGCGCGCGCGCCCTGGAGATCGAGCGTGCTCCCTCG 345

QY    32  ProLeuSerGlnLysGlnArgSerPheValThrPheArgGlyGluProAlaGluGlyPhe 51
      |||||
Db    346 CCCAGCCCCACC-----

QY    52  AsnHisLeuValValAspGluArgThrGlyHisIleTyrlEuGlyAlaValAsnArgIle 71
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db    358 AACAACTTCGCCCTCGACGCGCGCGCGGGACCGTGACTGGCGGCCTCAACCGCCCTC 417

QY    72  TyrLysLeuSer--SerAspLeuLysValLeuValThrHisGluThrGlyProAspGlu 90
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Db    418 TATCAGTCTCGGGCGCACCTGAGCTGAGCGCCGAGCGCGCGCGCGCGCGCTGCC 477

QY    91  AspAsnProLysCyseTyrrProProArgIleValGln---ThrCysAsnGluProLeuThr 109
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db    478 GACAGCCCGCTGTGTCAAGCTCCGACAGTGGCGGAGGCGCTCGTCGACGACCGCGCGCG 537

QY    110 ThrThrAsnValAsnLysMetLeuLeuIleAspTyrLysGluAsnArgLeuIleAla 129
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db    538 CTCACGGACCACTAACACAAGATCTCGAGCTGGACCCCGCGCGCGCGCGCTGGTAGTCGTG 597

QY    130 CysGlySerLeuTyrdIngIleCysLysLeuLeuArgLeuGluAspLeuPheLysLeu 149
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Db    598 TGGGGGTCCATCTACACAGGCTTCTGCGAGTGGCGCGCGGGGTAAACATCTCGGCGCGT 657

QY    150 GlyVLuProTyTHisLysLysGluHisTyrlEuserglyValAsnGluSerGlySerVal 169
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QY    170 PheGlyValIleValSerTyrrSerAsnLeuAsp-----
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Db    718 CTGAACGTGGCGCCAACACACCGGCTCCACCGTGGGCTAGTTCGTCCCTCCCGCG 777

QY    181 -----AspLysLeuPheIleAlaThrAlaValAspGlyLysProGluTyrr 195
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1795 CACCAGATGGCGAGGTGAAGTGCCTCCCTGCAACGTGCACCTCCACTGTGGGAGTGC 1854  
520 LeuGlySerGlyAspProHisCysGlyTyrCysValLeuHisAsnThrCysThrArgLys 539  
1855 GTGGGTGGCGGAGCGCTACTCTGCGGTGGTGGCTGGAGCGCGTGCACCTTGACG 1914  
540 GluArgCysGluArgSerLysGluProArgArgPheAlaSerGluMetLys----- 556  
1915 CAGGACTGCACCAATTCAGCGAGCAGCAGCATTTCTGGACCATGGCAGCGGCGCCAGC 1974  
557 GlnCysValArgLeuThrValHisProAsnAsnLysSerValSerGln---TyrAsnVal 575  
1975 CGCTGCTCCTGACCGCTCTGCTCCGAGATCGATGCGCCAGGAGTACCCAGC 2034  
576 LeuLeuValLeuGluThrTyrAsnValProGluLeuSerAla---GlyValAsnCysThr 594  
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595 Phe-----GluAspLeuSerGluMetAspGlyLeuValValGlyAsnGlnLe 610  
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611 GlnCysTyrSerProAlaAlaLysGluValProArgLleLeuThrGluAsnGlyAspHis 630  
2155 GCTACTGCACCTCTCGCGAGGACCATGTTTCGCGCTTCCCGCCCAACCCAGGACAC 2214  
631 HisValValGlnLeuGlnLysSerLysGluThrGlyMetThrPheAlaSerThrSer 650  
2215 -----GTGACTGTGTGATGCTGTGGGTCAATGGCGGAACATCGTCAAGGCCAAT 2268  
651 PheValPheTyrAsnCysSer-----ValHisAsnSerCysLeuSer 664  
2269 TTCACCATCTACGACTCGAGCGCCTGCACAAAGTGTACCCCGCACACAGCTGTACCA 2328  
665 CysValGluSerProTyrArgCysHisTyrCysLysTyrArgHisValCysThrHisasp 684  
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685 ProLysThrCysSerPheGlnGluGlyArgValLysLeuProGluAspCysProGlnLeu 704  
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2725 TGTGCATGGGAGCCCGACTGTTCCAGTGCCTGGCGCGGAAGACCTGGGTCACTG 2784  
823 CysGlyTyrCysGlnGlyProGlyGlnCysThrLeuArgGlnHisCysProAlaGlnGlu 842  
2785 TGCATGTGAGTGTATGCC-----TGCCGCTGCGGGG-----CCTCTGAG--- 2826  
843 SerGlnTrpLeuGluLeuSerGlyAlaLysSerLysCysThrAsnProArgLysThrGlu 862

2827 -----CCCATGCTGGCACC-----TGCCCCCGCCCCAGATCCGCGG 2865  
863 IleileProValThrGlyProArgGluGlyThrLysValThrLysLeuArgGlyGluAsn 882  
2866 ATTGAGCCCTGAGTGGCCGTGGACGGTGGACCTCTGCTCACCATCCGAGGAAGAAC 2925  
883 LeuGlyLeuGluPheArgAspLysLeuHisValLysValAlaGlyValGluCysSer 902  
2926 CTGGCGCGGGCTCAGTACGTGGCCACCGCGGTGATTTGGTGTGGCTGTGAG 2985  
903 ProLeuValAspGlyTyrProAlaGluGlnLeuValCysGluMetGlyGluAlaLys 922  
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3043 CCAGGACCACTCTCAGTGTGGTGGACCGTG-----AACGCTCTTAGGAG 3087  
943 AlaArgSerSerGlnLeuTyrTyrPheMetThrLeuThrLeuSerAspLeuLysProSer 962  
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963 ArgGlyProMetSerGlyThrGlnValThrLysLeuThrGlyThrAsnLeuAsnLysGly 982  
3148 ATGGGCCCCAAGCCCGGGGACACAGGATCACCATTCATGGGAATGACTCTCATGTAGGC 3207  
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3322 TGTGTGGCTTCAGCGCTCGGGCTCGGCGACGACCGCACTCCTCTGTGTACATGCAG 3381  
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1170 ProProValAlaGlyGlyAsnValLysLeuAsnTyrThrValLeuValGlyGluLysPro 1189  
3799 -----GGGCTCCAGAGTACAGTACCGGGTCAAGTGAAGTCAAGTAAAGC 3843  
1190 CysThrValThrValSerAspValGlnLeuLysCysGluSerProAsn----- 1205



Db 3844 TGGGACATCCAGATTGCTCTGACAGAATCATCCACTGCTCGGTCAACAGTCCCTGGGC 3903  
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 Db 4903 ATGACACCCGACGCTGACACAGGTCAAGAGAGAGATCTCTGGAGGCTTCTCCAGAAT 4962

Qy 1540 ValProCysSerHisArgProLysAlaAlaAspMetAspLeuGluTrpArgGlnGlySer 1559  
 Db 4963 GTGCGCTACTCCAGTGGCGGTGCGAGAGAGCTGCACCTTGAGTGTTCGCTCCAGC 5022  
 Qy 1560 GlyAlaArgMetIleLeuGlnAspGluAspIleThrTyrLysIleGluAsnAspTrpLys 1579  
 Db 5023 ACACAGAGCTACATCTCTGGGACCTGCGACACCTCAGTGTGGAGAGCGCGCGCAAG 5082  
 Qy 1580 ArgLeuSerThrLeuAlaHisTyrGlnValProAspGlySerValValAla-----Leu 1597  
 Db 5083 AAGCTTAAACGCTGGCCCATACAGATCCCTAGAGTGGCTCCCTGGCCCATGAGTCTC 5142  
 Qy 1598 ValSerLysGlnValThrAlaTyrAsnAlaValAsnAsnSerThrValSerArgThrSer 1617  
 Db 5143 ATAGACAAGAAG-----GACAAACACCTGGCGGAGTGAAT 5178  
 Qy 1618 AlaSerLysTyrGluAsnMetIleArgTyrThrGlySerProAspSerLeuArgSerArg 1637  
 Db 5178 ----- 5178  
 Qy 1638 ThrProMetIleThrProAspLeuGluSerGlyValLysMetTrpHisLeuVal----- 1655  
 Db 5179 -----GACTTGGACACA---GAGAAGTATTTCCATTTGCTGCTGCT 5217  
 Qy 1656 -----LysAsnHisGluHisGlyAspGlnLysGluGlyAsp 1667  
 Db 5218 ACGGACGAGCTGGCGGAGCCCAAGAGTCTCACCGGAGAGCCATCGCAAG----- 5268  
 Qy 1668 ArgGlySerLysMetValSerGluIleTyrLeuThrArgLeuLeuAlaThrLysGlyThr 1687  
 Db 5269 -----AAGTGTCTCCCGAAATCTACCTGACCGCTGCTCTCCACCAAGGACAG 5319  
 Qy 1688 LeuGlnLysPheValAspAspLeuPheGluThrIlePheSerThrAlaHisArgGlySer 1707  
 Db 5320 TTGCAGAAAGTTCTGGATGACCTGTCAAGGCCATTCTGAGTATC-----CGTGAAGAC 5373  
 Qy 1708 AlaLeuProLeuAlaIleLysTyrMetPheAspPheLeuAspGluGlnAlaAspLysHis 1727  
 Db 5374 AAGCCCCACCTGGCTGTCTAGTACTTTTCACCTCTCTGGAGAGAGCTGAGAGAGG 5433  
 Qy 1728 GlyIleHisAspProHisValArgHisThrTrpLysSerAsnCysLeuProLeuArgPhe 1747  
 Db 5434 GGAATCTCCGACCCCGACACACCTACATCTGGAAGACCAACACAGCTTCTCTCCGGTTC 5493  
 Qy 1748 TrpValAsnMetIleLysAsnProGlnPheValPheAspIleHisLysAsnSerIleThr 1767  
 Db 5494 TGGGTGAACATCTCGAAGACCCCGAGTTTGTCTTTGACATCGACAGACAGACCATC 5553  
 Qy 1768 AspAlaCysLeuSerValValAlaGlnThrPheMetAspSerCysSerThrSerGluHis 1787  
 Db 5554 GAGCGCTGCTTCAGTATCGCGCAGCGCTTCATCGACGCTGCTCATCTCTGACCTG 5613  
 Qy 1788 ArgLeuGlyLysAspSerProSerAsnLysLeuLeuTyrAlaLysAspIleProSerTyr 1807  
 Db 5614 CAGCTGGGCAAGGATTCGCCAACCAACAGCTCTCTACGCCAAGGAGATTCCTGAGTAC 5673  
 Qy 1808 LysAsnTrpValGluArgTyrTyrSerAspIleGlyLysMetProAlaIleSerAspGln 1827  
 Db 5674 CGGAAGATCTGTCAGCGCTACTACAAGCAGATCCAGGACATGACGCGCTCAGCGAGCAA 5733  
 Qy 1828 AspMetAsnAlaTyrLeuAlaGluGlnSerArgMetHisMetAsnGluPheAsnThrMet 1847  
 Db 5734 GAGATGAATGCCCATCTGCGCGAGAGTTCGAGGAATACCAAGATGAGTTCACACCAAT 5793  
 Qy 1848 SerAlaLeuSerGluIlePheSerTyrValGlyLysTyrSerGluGluIleLeuGlyPro 1867  
 Db 5794 GTGGCCATGGCAGAGATTTATAGTACCCCAAGAGGTATCGCGCGAGATCATGGCCGC 5853  
 Qy 1868 LeuAspHisAspAspGlnCysGlyLysGlnLysLeuAlaTyrLysLeuGlnValIle 1887  
 Db 5854 CTGGAGGCCAACCCCGCGGAGGACACAACTGACAGCACAAAGTTTGGAGCGGTGTG 5913

181	QY	-----AspLysLeuPheIleAlaThrAlaValAspGlyLysProGluTyr	195
778	Db	::::: :::	837
196	QY	Phe-----ProthrIleSer	200
838	Db	TTCCTCCCGCAACCGCAGCTGGAGACCACCGCTTCGAGAACACGCCCGCAGATCGCC	897
201	QY	SerArgLysLeuThrLysAsnSerGluAlaAspGlyMetPheAlaTyrValPheHisAsp	220
898	Db	ATCCGCTCCCTGGACACCGCGCGGCACCTGGCCAAGCTCTTCACCTTCGACCTCAAC---	954
221	QY	GluPheValAlaSerMetIleLysIleProSerAspThrPheThrIleIleProaspPhe	240
955	Db	-----CCCTCCGAC-----GACAAC	969
241	QY	AspIleTyrTyrtValTyrGlyPheSerSerGlyAsnPheValTyrPheLeuThr-----	258
970	Db	ATCCTCAAAGATCAAGCAGGGGCCAAGAGCAGACAAGCTGGGTCTCGTAGCGGCTTC	1029
259	QY	LeuGlnProGluMetValSerProProdyserThrThr-----	271
1030	Db	CTGCACCCGCTCC---GACCCCGCGCGGTGCACAGTCTACGCGTACTGCGGTCAAC	1086
272	QY	-----LysGluGlnValTyrThrSerLysLeuValArgLeuCys	284
1087	Db	ACGAGGCGCGCGGCGCACAGAGAGCCAGCGGAGCGTGCTGCGCGCATCTGC	1146
285	QY	LysGluAspThrAla-----PheAsnSerTyrValGluValPro	297
1147	Db	CTGCCCCACGGCGCGGCGACGCCAAGAAGCTCACCGAGTCTCTACATCCAGTTGGCC	1206
298	QY	IleGlyCysGluArgSeirGlyValGluTyrArgLeuLeuGlnAlaAlaTyrLeuSerLys	317
1207	Db	-----TTGCATGTCGGCGCGCGCGGC	1230
318	QY	AlaGlyAlaValLeuGlyArgThrLeuGlyValHisProAspAspLeuLeuPheThr	337
1231	Db	CSCGCGACCTCTACAGCGCGCTGTGTGCGGTCTCCAGCCCGGAGCGCGGTCTTTGCT	1290
338	QY	ValPheSerLysGlyGlnLysArgLysMetLysSerLeuAspGluSerAlaLeuCysIle	357
1291	Db	GTCTTCGAGCGCCCACGGGTCCCGCGCGCGCGCTGTCTCGGCGCATCTCGGCC	1350
358	QY	PheIleLeuLysGlnIleAsnAspargileLysGluArgLeuGlnSerCystyrArgGly	377
1351	Db	TTCCGCTTCGCGACGTGCGAGCCGCCATCCGAGCTGCGCGCACCGCCTGCTT-CGTGA	1409
378	QY	GluGlyThrLeu-----AspLeuAlaTrpLeuLysValLysAspIlePro	392
1410	Db	ACCGCGCGCCG-ACGTGTGGCGGTCTCGACAGCGTGTGTGAGGACACGGGACCGGCT	1468
393	QY	CysSerSerAlaLeu-----LeuThrIleAspAspAsnPheCysgly---LeuAsp	408
1469	Db	CGAGGCGCAAG-CTCAACATCCAGCTCCAGCCAGACGACTGACTGTGAGTGCTCAC	1527
409	QY	MetAsnAlaProLeuGlyValSerAspMetValArgGlyIleProvalPheThrGluAsp	428
1528	Db	CTTCAGCACCCCGCTCTCCATCTCGACGCCCTCGAAAGGCCACCCCGGTGTCCGC-	1581
429	QY	ArgAspArgMetThrSerValIleAlaTyrValTyrLysAsnHisSerLeuAlaPheVal	448
1582	Db	GCCTCGGCGCTACCTTCGTGGCCGTGGCCAGCGTCAACAATAACACGGGTCTCTCG	1641
449	QY	GlyThrLysSerGlyLysLeuLysLysIleArgValAspGlyProArgGlyAsnAlaLeu	468
1642	Db	GCACCGTCAACGGGAGGTTCTCAAGATCAACCTGAAC-----	1680
469	QY	GlnTyrGluThrValGlnValAlaAsp-----ProGlyPro	480
1681	Db	-----GAGATCATCAGGTGTGAGACGCGCGGTGTGACTGTGGCCTATTGGGAGGCC	1734
481	QY	ValLeuArgAspMetAlaPheSer---LysAspHisGluGlnLeuTyrIleMetSerGlu	499

2785	Db	TGATGTGGAGTGTATGGC-----TGCGCGCTGCGGGGG-----CCTCTCGAG---	282
843	Qy	SerGlnTrpLeuGluLeuSerGlyAlaLysSerLysCysThrAsnProArgIleThrGlu	862
2827	Db	-----CCATGTGGTGCCACC-----TGCCCGCCCGCCAGATCCGCGCG	2865
863	Qy	IleIleProValThrGlyProArgGluGlyGlyThrLysValThrIleArgGlyGluAsn	882
2866	Db	ATTGAGCCCTGTAGTGGCCGTTGGACGGTGGACCTGTGTGACCATCCGAGGAGGAC	2925
883	Qy	LeuGlyLeuGluPheArgAspIleAlaSerHisValLysValAlaGlyValGluCysSer	902
2926	Db	CTGGCGCGCGGCTCAGTGACGTGGCCACCGCGTGTGGATTGGTGTGGCCCTGTGAG	2985
903	Qy	ProLeuValAspGlyTyrIleProAlaGluGlnIleValCysGluMetGlyGluAlaLys	922
2986	Db	CCACTGCTGACAGATACAGGTGTGGAGAGATCGTGTGTCTCAGAGGCCAGCC---	3042
923	Qy	ProSerGlnHisAlaGlyPheValGluIleCysValAlaValCysArgProGluPheMet	942
3043	Db	CCAGGACCACTCTCAGGTGGTGACCGTG-----AACGCCCTTAAGGAG	3087
943	Qy	AlaArgSerGlnLeuTyrTyrPheMetThrLeuThrLeuSerAspLeuLysProSer	962
3088	Db	GGCAAGTCCCGGGACCCCTTCTCTCAGTGTGCCCCGTGTGCTCACTCCCTGGAGCCCTAC	3147
963	Qy	ArgGlyProMetSerGlyGlyThrGlnValThrIleThrGlyThrAsnLeuAsnAlaGly	982
3148	Db	ATGGCCCCCAAGCGCGGGGACCAGATCACCATCCATGGGATGACCTCCATGTAGGC	3207
983	Qy	SerAsnValValValMetPheGly---LysGlnProCysLeuPheHisArgArgSerPro	1001
3208	Db	TCCGAGTCCAGGTCTCTGGTGAACGACACAGACCCCTGCACGAGCTGATCGCAGAT	3266
1002	Qy	SerTyrIleValCysAsnThrThrSerSerAspGluValLeuGluMetLysValSerVal	1021
3268	Db	ACCAGATCGCCTGC-----ACCATGCTGAGGGGGCCCTGCCGGTCCGGTGCCTGTG	3322
1022	Qy	GlnVal-----AspArgAlaLysIleHisGlnAspLeuValPheGlnTyrValGlu	1038
3322	Db	TGTGTGCGCTTCGAGCGTCGGGGCTGCGTGACGCAACCTCACCTTCTGGTACATGCAG	3388
1039	Qy	AspProThrIleValArgIleGluProGluTrpSerIleValSerGlyAsnThrProfile	1055
3382	Db	AACCGGTCATCACGGGCATCAGTCCCGCGCAGCCCTGTGTCAGTGGCGGAGGACCATC	3443
1059	Qy	AlaValTrpGlyThrHisLeuAspLeuIleGlnAsnProGlnIleArgAlaLysHisGly	1078
3442	Db	ACAGTGGCTGTGAGCGTTTCCACATGCTGCAGAAATGTCTCATGGCCGCTCCACCACAT	3507
1079	Qy	GlyLysGluHisIleAsnIleCysGluValLeuAsnAlaThrGluMetThrCysGlnAla	1098
3502	Db	GGCCGGGAGCCC---ACCGCTCTGAAGGTCTCAACTCCACCCCTCATCACTGCCCGTCC	3555
1099	Qy	ProAlaLeuAlaLeuGlyProAspHisGlnSerAspLeuThrGluArgProGluGluPhe	1111
3559	Db	CCCGGGCGCTTGAGCAACGCATCAGCGCCAGTGGNCTTCTCATCAATGGCGGCGCTAC	3611
1119	Qy	GlyPheIleLeuAspAsnValGlnSerLeuLeuIleLeu-----Asn	1133
3619	Db	GCAGACGAGGTGCTGTGGCTGAGGAGGTACTTGGACCCCGGAGGAGCCACGCGGGCAGC	3677
1133	Qy	LysThrAsnPheThrTyrProAsnProValPheGluAlaPheGlyProSerGlyIle	1155
3679	Db	AGGTTCCGCTGGACTACTCTCCCAACCCACAGTTCTCTACGGCCCAAGGAGGAGAGTGG	3733
1153	Qy	LeuGluLeuLysProGlyThrProfileIleLeu-----LysGlyLys	1166
3739	Db	ATCAAGCACCCCGGGGAGGCTCTCACCTCGTTATCCACGTGACGACCAACAAAGGG---	3799
1167	Qy	AsnLeuIleProProValAlaGly-----GlyAsnValLysLeuAsn	1188
3796	Db	-----GCCGGGAAGGAGCAGCAGCTCGGGGCTCCAGAGTCCAGAGTCCAGAG	3833

1181	QY	TyThrValLeuValGlyGluLysProCysThrValThrValSerAspValGlnLeuLeu	1200
3838	Db	TACCGGTCAAGATAGGCCAAGTAAGCTGCAGATCCAGATTGTCTCTGCAGAGAAATCATC	3897
1201	QY	CysGluSerProAsn-----LeuIleGlyArgHisLeuValMetAlaArg	1215
3898	Db	CACTGCTCGGTCAACAGAGTCCTGGCGGCGGTGGGCGAGCTGCCCATCACATCCAG	3957
1216	QY	ValGlyGlyMetGluTySerProGlyMetValTyIleAlaProAspSerProLeuSer	1235
3958	Db	GTAGGAACCTTCAACAGACCCATCCGCACATCGAGCTGGGGGGGCGAGC-----GAG	4008
1236	QY	LeuProAlaIleValSerIleAlaValAlaGlyGlyLeuLeuIleIlePheIleValAla	1255
4009	Db	ACGGCCATCATCGTGTCCATCGTATCGACGCTCTGCTGCTCTCGTCTCGGTGGTGGCC	4068
1256	QY	ValLeuIleAlaTyrlsArgLysSerArgGluSerAspLeuThrLeuLysArgLeuGln	1275
4069	Db	----CTGTTCTGTTCTGTACCAAGAGCCGACGTGCTGAGCGTTACTGCGCAAGACGCGTG	4125
1276	QY	MetGlnMetAspAsnLeuGluSerArgValAlaLeuGluCysLysGluAlaPheAlaGlu	1295
4126	Db	CTGCAGATGGAGAGATGAATCTCAGATCCGAGAGGAAATCCGCAAAAGGCTTCGCTGAG	4185
1296	QY	LeuGlnThrAspIleHisGluLeuThrSerAspLeuAsp--GlyAlaGlyIleProPhe	1314
4186	Db	CTGCAGACAGACATGACAGATCTCACCAGGAGCTGAACCGAGCCAGCGGATCCCTTC	4245
1315	QY	LeuAspTyArgThrTyThrMetArgValLeuPhePro-----	1327
4246	Db	CTGGAGTATAAGCACTTCGTGACCGGCACCTTCTTCCGCAAGTGTTCCTCCTTATGAA	4305
1328	QY	-----GlyIleGlu	1330
4306	Db	GAGCGTTAGCTGCTGCCCTCCAGACCCTCACTCCAGGGCAGCTCCAGGCACAGGAA	4365
1331	QY	AspHisProValLeuArgAspLeuGluValProGlyTyArgGlnGluArgValGluLys	1350
4366	Db	ACCCACCCCACTGCTGGAGAGTGGAGATTCCTGAGAGCTGCGGCCCAACATGGGAAGAG	4425
1351	QY	GlyLeuLysLeuPheAlaGlnLeuIleAsnLysValPheLeuLysPheIleArg	1370
4426	Db	GGAAATAGCTGTGTTCTCCTACTACTCGACACACAGACCTTCTCATGCTTTGTGCCAC	4485
1371	QY	ThrLeuGluSerGlnArgSerPheSerMetArgAspArgGlyAsnValAlaSerLeuIle	1390
4486	Db	CGCTGGAGCAGCAGAAAGCACTTCGGTGGCCGACAGTGCAGCTCGCTCGCTGCTG	4545
1391	QY	MetThrValLeuGlnSerLysLeuGluTyAlaThrAspValLeuLysGlnLeuAla	1410
4546	Db	ACCATCGCGCTGCACGGCAAGCTGGAGTACTACACAGCATCATGAAGAGCTGTGTGTG	4605
1411	QY	AspLeuIleAspLysAsnLeuGluSerLysAsnHisProLysLeuLeuArgArgThr	1430
4606	Db	GACCTCATTTAGTGCCTCG-----GCCGCCAAGAACCCCAAGCTCATGTGCGGGGCACA	4659
1431	QY	GluSerValAlaGluLysMetLeuThrAsnTyrPheThrPheLeuLeuTyrlsPheLeu	1450
4660	Db	GAGTCTGTGGTGGAGAAGATGCTCACCACATGGATGTCATCTGCATGTACAGCTGTCTG	4719
1451	QY	LysGluCysAlaGlyGluProLeuPheSerLeuPheCysAlaIleLysGlnGlnMetGlu	1470
4720	Db	CGGGAGCGGTGGGGGAGGCATCTTCTCGCTGCTGTGTGCCATCAAGCAGCAATCAAC	4779
1471	QY	LysGlyProIleAspAlaIleThrGlyGluAlaArgTyrlsSerLysSerGluAspLysLeu	1490
4780	Db	AAGGGCTCCATCGAGCCCATCACGGCAAGGCCGCTACACACTCAATGAGGAGTGGCTG	4839
1491	QY	IleArgGlnGlnIleAspTyrlsThrLeuValLeuSerCysValSerProAspAsnAla	1510
4840	Db	CTGCGGGAGAACATCAGAGCCCAAGCCCGGAACCTGTAAAC---GTGCTCTCCAGGCGTGT	4895

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Db      5848 AGGTATCGCGCCGAGATATGCGCGCTGGAGGCAACCCACCGCGCGGAGACAA 5907
Qy      1879 LeuAlaTyrLysLeuGluGlnValIleThrLeuMet 1890
Db      5908 CTGCAGCAAGATTTCAGCAGGTGGTGGCTTTGATG 5943

RESULT 12
US-10-087-192-1943
; Sequence 1943, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: CANCER
; FILE REFERENCE: 529452000122
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1943
; LENGTH: 6340
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-087-192-1943

Alignment Scores:
Pred. No.:      5,21e-248      Length:      6340
Score:          2385.50
Percent Similarity: 47.70%
Best Local Similarity: 31.89%
Query Match:    23.88%
Indels:         341
Gaps:           13

US-09-964-956-13 (1-1896) x US-10-087-192-1943 (1-6340)
Qy      52 AsnHisLeuValValAspGluArgThrGlyHisIleTyrLeuGlyAlaValAsnArgIle 71
Db      34 AACAACTTCGCTGGAGCGCGCGGGGACCGGTGTACCTGGCGCGGTCAACCGCTC 93
Qy      72 TyrLysLeuSer---SerAspLeuLysValLeuValThrHisGluThrGlyProAspGlu 90
Db      94 TATCAGCTGTGGGCGCGCAACCTGAGCTGGAGCGCGGCGCGCGCGCGCGCGCGCG 153
Qy      91 AspAsnProLysCysTyrProArgIleValGln---ThrCysAsnGluProLeuThr 109
Db      154 GACAGCCCGCTGTGTACCGCTCCGAGCTCCGAGCGCTCGTGGCAGCACCGCGCGCG 213
Qy      110 ThrThrAsnValAsnLysMetLeuLeuIleAspTyrLysGluAsnArgLeuIleAla 129
Db      214 CTCACGGACAACTACAAAGATCTCGAGTGGACCCCGCGCGCGCGCGCGCGCGCG 273
Qy      130 CysGlySerLeuTyrGlnGlyIleCysLysLeuLeuArgLeuGluAspLeuPheLysLeu 149
Db      274 TGGCGCGCGCTG----- 285
Qy      150 GlyGluProTyrHisLysLysGluHisTyrLeuSerGlyValAsnGluSerVal 169
Db      286 -----CTCGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 315
Qy      170 PheGlyValIleValSerTyrSerAsnLeuAspLysLeuPheIleAlaThrAlaVal 189
Db      316 AGTCCTCTTCCTCCCGCAACCGCGCTGGAGGACCAACCGCTTC----- 360
Qy      190 AspGlyLysProGluTyrPheProThrIleSerSerArgLysLeuThrLysAsnSerGlu 209
Db      361 -----GAGAACACGCGCGCGAGATCGCCATCGCTCCCTGGACACGCGCGCGGAC 408

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Qy      210 AlaAspGlyMetPheAlaTyrValPheHisAspGluPheValAlaSerMetIleLysIle 229
Db      409 CTGCGCAAGCTCTTCACCTTCGACCTCAAC----- 438
Qy      230 ProSerAspThrPheThrIleIleProAspPheAspIleTyrTyrValTyrGlyPheSer 249
Db      439 CCTCCCGAC-----GACAACTATCTCAAGATCAAGCAGCGCGCGCGCAAG 480
Qy      250 SerGlyAsnPheValTyrPheLeuThr-----LeuGlnProGluMetValSerProPro 267
Db      481 GAGCAGCACAAGCTGGGCTTGTGAGCGCTTCTCTGCACCGCTCC---GACCCCGCGCGCG 537
Qy      268 GlySerThrThr----- 273
Db      538 GGTGCACAGTCTCTACGGGTACTCTGGCGCTCAACAGCAGGCGCGCGCGCGCGCGCAAGGAG 597
Qy      274 GlnValTyrThrSerLysLeuValArgLysCysLysGluAspThrAlaPheAsnSerTyr 293
Db      598 AGCCAGCGCGGAGCGCTCTGGCGCGCATCTGC----- 630
Qy      294 ValGluValProIleGlyCysGluArgSerGlyValGluTyrArgLeuLeuGlnAlaAla 313
Db      631 -----CTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 675
Qy      314 TyrLeuSerLysAlaGlyAlaValLeuGlyArgThrLeuGlyValHisProAspAspAsp 333
Db      676 TACATCCAC-----CGCTGGTGTCTGGTCTTCCCGCGCGCGCGCGCGCGCGCGCG 714
Qy      334 LeuLeuPheThrValPheSerLysGlyGlnLysArgLysMetLysSerLeuAspGluSer 353
Db      715 CGGCTCTTTGTCTTTCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 774
Qy      354 AlaLeuCysIlePheIleLeuLysGlnIleAsnAspArgIleLysGluArgLeuGlnSer 373
Db      775 GCACCTTCGCGCTTTCGCGCTTCGCGCGAGCTGCGAGCGCGCGCGCGCGCGCGCGCGCG 834
Qy      374 CysTyrArgGlyGluGlyThrLeu-----AspLeuAlaTrpLeuLysVal 388
Db      835 TGCCTT-CGTGAAACCGCGCGCGCG-ACGTGTGGCGGTCTCGACAGCGTGTGTGCGAGGCA 892
Qy      389 LysAspIleProCysSerSerAlaLeu-----LeuThrIleAspAsnAspPheCys 405
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Qy      406 Gly---LeuAspMetAsnAlaProLeuGlyValSerAspMetValArgGlyIleProVal 424
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Qy      425 PheThrGluAspArgAspArgMetThrSerValIleAlaTyrValTyrLysAsnHisSer 444
Db      1012 TTCCGC-----GCCCGCGCGCTCACCTCCGTCGCGCGCGCGCGCGCGCGCGCGCG 1065
Qy      445 LeuAlaPheValGlyThrLysSerGlyLysLysLysIleArgValAspGlyProArg 464
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Qy      465 GlyAsnAlaLeuGlnTyrGluThrValGlnValValAsp----- 477
Db      1117 -----GAGAGCATGCGAGTGTGTGAGCAGCGCGCGGTGTGTGTGTGTGTGTGTGT 1158
Qy      478 ---ProGlyProValLeuArgAspMetAlaPheSer---LysAspHisGluGlnLeuTyr 495
Db      1159 TATGGGAGCGCGTGCACCATGTCTCAGTTTGACCCAGCAGAGCTCCGGTACCTTTTAC 1218
Qy      496 IleMetSerGluArgGlnLeuThrArgValProValGluSerCysGlyGlnTyrGlnSer 515
Db      1219 CTGATGATCCCAACACCATGAGTGGAGGTGCGCGCGCTGCAACGTCGACTCCACC 1278
Qy      516 CysGlyGluCysLeuGlySerGlyAspProHisCysGlyTyrCysValLeuHisAsnThr 535
Db      1279 TGTGGGACTGTGGTGGTGGCGGAGCGCTACTCGCGCTGTGTGTGTGTGTGTGTGTGTGT 1338
Qy      536 CysThrArgLysGluArgCysGluArgSerLysGluProArgArgPheAlaSerGluMet 555

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Db 1339 TGCACCTTGGACGAGGAGTCCACCAATTCAGCCAGCAGCAGATTTCCTGGACCGAGTCCAGC 1398  
 Qy 556 Lys-----GlnCysValArgLeuThrValHisProAsnAsnIleSerValSerGln 572  
 Db 1399 GAGGCCCCAGCGGTGCTGCGCATGACCTGCTGCTCCGAGATCGATGTCGCCAG 1458  
 Qy 573 ---TyrAsnValLeuLeuValLeuThrTyrAsnValProGluLeuSerAla---Gly 590  
 Db 1459 GAGTACCCAGGCGATGCTGAGATCTCGGCGCAGCTGCGCCAGCTCAGTGGCATGGAG 1518  
 Qy 591 ValAsnCysThrPhe-----GluAspLeuSerGluMetAspGlyLeuValVal 606  
 Db 1519 ATGGCTGTGATATGGGAACAACATCCGCACTGTGGCTCGGTCGCCAGCCCTGCTTT 1578  
 Qy 607 GlyAsnGlnIleGlnCysTyrSerProAlaAlaLysGluValProArgIleIleThrGlu 626  
 Db 1579 GGTCAACCAAGTTCCTACTGCAACCTCTCGCGAGGACAGTTTCGCGCTTCCCCCCC 1638  
 Qy 627 AsnGlyAspHisHisValValGlnLeuGlnLeuLysSerLysGluThrGlyMetThrPhe 646  
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 Qy 647 AlaSerThrSerPheValPheTyrAsnCysSer-----ValHisAsn 660  
 Db 1693 GTCAGGCGCAATTCACCATCTACGACTGAGCGCAGCTGCACAGGTATACCCCAACA 1752  
 Qy 661 SerCysLeuSerCysValGluSerProTyrArgCysHisTyrCysLysTyrArgHisVal 680  
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 Qy 681 CysThrHisAspProLysThrCysSerPheGlnGluGlyArgValLysLeuProGluAsp 700  
 Db 1813 TGTGTTTCAACCACTGCTGCGGAGGCTTCCACCAACCCAGCAGC-----CCTCAGGAC 1869  
 Qy 701 CysProGlnLeuLeuArgValAspLysIleLeuValProValGluValIleLysProIle 720  
 Db 1870 TGCCCCCGAGCCTCTCTACCCCTGCGACCGGTGCTACGGGTGCTCCCGCAGACATC 1929  
 Qy 721 ThrLeuLysAlaLysAsnLeuProGlnProGlnSerGlyGlnArgGlyTyrGluCysIle 740  
 Db 1930 CTGGTGCCTCTGCGCAACACTGCCTTTTTCAGGCTGCA-----GCCCTGAGTGTAGT 1983  
 Qy 741 LeuAsnIleGlnGlySerGluGlnArgValProAlaLeuArgPheAsnSerSerVal 760  
 Db 1984 TTT-----GGCTGGAGGAGATCTTCGAGGCTGTGGTCAATGACTCTGTGTA 2034  
 Qy 761 GlnCys-----GlnAsnThrSerTyrSerTyrGluGlyMetGluLeuAsnLeuProVal 779  
 Db 2035 CGCTGTGACCGAGTGTGCTGCACACGACCCCGAAGAGCCAGGTG-----TTCCCGCTC 2088  
 Qy 780 GluLeuThrValValTyrAsnGlyHisPheAsnIleAspAsnProAlaGlnAsnLysVal 799  
 Db 2089 ASCCTCCAACTAAAGGGCGGCGCCAGCCGATCTCTGGACAGCCCTGAGCCCATGACAGTC 2148  
 Qy 800 HisLeuTyrLysCysGlyAlaMetArgGluSerCysGlyLeuCysLeu---LysAlaAsp 818  
 Db 2149 ATGGTCTATACTGTGCTGCGCAGCCCGCAGTCTTCCAGTGTGCTGGCGCGGAGAC 2208  
 Qy 819 ProAspPheAlaCysGlyTyrCysGlnGlyProGlyGlnCysThrLeuArgGlnHisCys 838  
 Db 2209 CTGGGTCACTGTGATGTGGAGTATGGC-----TGCCGCTCGCGGG----- 2253  
 Qy 839 ProAlaGlnGluSerGlnTrpLeuGluLeuSerGlyAlaLysSerLysCysThrAsnPro 858  
 Db 2254 CCTCTGCA-----CCCATGGGTGGCACC-----TGCCCGCCGCCCC 2289  
 Qy 859 ArgIleThrGluIleIleProValThrGlyProArgGluGlyGlyThrLysValThrIle 878  
 Db 2290 GAGATCCCGCGCATGAGCCCTGAGTGGCGCTGAGTGGCGGTGGACCTGCTGACCATC 2349  
 Qy 879 ArgGlyGluAsnLeuGlyLeuGluPheArgAspIleAlaSerHisValLysValAlaGly 898

Db 2350 CGAGGAAGGAACCTGGCGCGGCTCAGTGAGTGGCCACCGCGTGTGGATTGTTGTT 2409  
 Qy 899 ValGluCysSerProLeuValAspGlyTyrIleProAlaGluGln----- 913  
 Db 2410 GTGGCTGTGAGCACTGCTCAGACATACACGGTGTGGAGGAGTGGCCCGTGGGGCC 2469  
 Qy 914 -----IleValCysGluMetGlyGluAla 921  
 Db 2470 AAGGACCGCTGGCTGACACAGCACCTCCCTCAGATGCTGTGTGTACAGGGCCAGC 2529  
 Qy 922 LysProSerGlnHisAlaGlyPheValGluIleCysValAlaValCysArgProGluPhe 941  
 Db 2530 ---CCAGGACCACTCTCAGGTGTGGTACCGTG-----AACCCCTCTAAG 2571  
 Qy 942 MetAlaArgSerSerGlnLeuTyrTyrPheMetThrLeuThrLeuSerAspLeuLysPro 961  
 Db 2572 GAGGGCAAGTCCCGGACCGCTTCTCTACGCTGCTGCTCCACTCCCTCGAGCCT 2631  
 Qy 962 SerArgGlyProMetSerGlyThrGlnValThrIleThrGlyThrAsnLeuAsnAla 981  
 Db 2632 ACCATGGGCCCCAAGCGGGGCGACAGGATCACCATCCATGGGAATGATCCATCCTCA 2691  
 Qy 982 GlySerAsnValValMetPheGly---LysGlnProCysLeuPheHisArgArgSer 1000  
 Db 2692 GGCTCCAGCTCCAGTCTCTGTTGAACGACACAGACCCCTGCGAGGAGTGTGCGACA 2751  
 Qy 1001 ProSerTyrIleValCysAsnThrThrSerSerAspGluValLeuLeuMetLysValSer 1020  
 Db 2752 GATACCAAGCATCGCTGC-----ACCATGCTGAGGGGGCGCTGCGCGCTCCGCTG 2805  
 Qy 1021 ValGlnVal-----AspArgAlaLysIleHisGlnAspLeuValPheGlnTyrVal 1037  
 Db 2806 GTGTGTGGCTTCGAGCTCGGGCTGCTGCGACCGCACTCACCTCTCTGTTACATG 2865  
 Qy 1038 GluAspProThrIleValArgIleGluProGluTyrPheIleVal----- 1052  
 Db 2866 CAGAACCGGTATCATCAGGCCATCAGTCCCGCGCAGCCCTGTCAGGCTCTCTGGGCT 2925  
 Qy 1053 -----SerGlyAsnThrProIleAlaValTyr 1061  
 Db 2926 GCAGGTGCACTAGATGTTTCTGTCCTCCCGAGTGGCGGAGGACCATCAGTGGCT 2985  
 Qy 1062 GlyThrHisLeuAspLeuIleGlnAsnProGlnIleArgAlaLysHisGlyLysGlu 1081  
 Db 2986 GGTGAGCGTTCCACATGTGCAGATGTCTCATGGCGCTCCACCATGTCGCGGAG 3045  
 Qy 1082 HisIleAsnIleCysGluValLeuAsnAlaThrGluMetThrCysGlnAlaProAlaLeu 1101  
 Db 3046 CCC---ACGCTCTGCAAGTTCTCACTCCACCTCATCCTGCGCTGCTGCGGGGCC 3102  
 Qy 1102 AlaLeuGlyProAspHisGlnSerAspLeuThrGluArgProGluGluPheGlyPheIle 1121  
 Db 3103 CTGAGCAACGATCAGCGCCAGTGGACTTCTTCATCAATGGGCGGCGCTACGACAGCAG 3162  
 Qy 1122 LeuAspAsnValGlnSerLeuLeuIleLeu-----AsnLysThrAsn 1135  
 Db 3163 GTGGCTGTGGTGGAGAGTACTTGGACCCCGAGGAGGCACAGCGGGCGAGAGTTCCGC 3222  
 Qy 1136 PheThrTyrTyrProAsnProValPheGluAlaPheGlyProSerGlyIleLeuLeu 1155  
 Db 3223 CTGAGTACTCTCCCAACCCACAGTTCTCTACGGCCAAAGAGGAGAGTGGATCAAGCAC 3282  
 Qy 1156 LysProGlyThrProIleIleLeu-----LysGlyLysAsnLeuIle 1169  
 Db 3283 CACCCGGGAGGCTCTCACCTCTGTTATCCAGTGCAGCAACCAAGGG----- 3330  
 Qy 1170 ProProValAlaGly-----GlyAsnValLysLeuAsnTyrThrVal 1183  
 Db 3331 -----GCCGGGAGGAGCGAGCAGCTGGGCTCCAGATCAGAGTACCGGGTTC 3381  
 Qy 1184 LeuValGlyLysProCysThrValThrValSerAspValGlnLeuLeuCysGluSer 1203  
 Db 3382 AAGATAGGCCAAGTAAAGTGGACATCCAGATTGCTCTGACAGAGATCATCATCTGCTCG 3441

QY	1204	ProAsn-----LeuileGlyA <sup>g</sup> HisLysValMetAla <sup>g</sup> ValGlyGly	1218
Db	3442	GTCAACGAGTCCTGGCGCGCGTGGGCGAGTCCCATCACAAATCCAGGTAGGGAAC	3501
QY	1219	MetGluTy <sup>r</sup> SerProGlyMetValTy <sup>r</sup> IleAlaProAspSerProLeuSerLeuProAla	1238
Db	3502	TTCAACACGACCATCCCACTCGACTGGGGGCGAGC-----GAGACGGCCATC	3552
QY	1239	IleValSerIleAlaValAlaGlyGlyLeuLeuIleIlePheIleValAlaValLeuIle	1258
Db	3553	ATCGTGTCCATCGTCATCGCAGCGCTGCTGCTCTCCGTGGTGACC---CTGTTC	3609
QY	1259	AlaTy <sup>r</sup> ZlyArgLysSerArgGluSerAspLeuThrLeuLysArgLeuGlnMetGlnMet	1278
Db	3610	GTCTTCTGTACCAAGACCGACGTGTGACGCTACTGCGACAGAGACGCTGTGCAGATG	3669
QY	1279	AspAsnLeuGluSerArgValAlaLeuGlu-----	1288
Db	3670	GAGAGATGGAAATCTCAGATCCAGAGGAAATCCGCAAGGGGATGGGTCTCGGCGCCG	3729
QY	1289	-----CysLysGluAlaPheAlaGluLeuGlnThrAspIleHisGluLeu	1303
Db	3730	TCACGGGTGTCCTGTGTCCGCCAGGCTTCGCTGAGCTGCAGACACATGACAGATCTC	3789
QY	1304	ThrSerAspLeuAsp--GlyAlaGlyIleProPheLeuAspTy <sup>r</sup> ArgThrTy <sup>r</sup> ThrMet	1322
Db	3790	ACCAAGGAGCTGAACCGCACCGCAGGCGATCCCTTCTGTGAGTATTAAGCACTTCGTGACC	3849
QY	1323	ArgValLeuPhePro-----	1327
Db	3850	CGCACCTTCTCCCAAGTGTCTCCTTTATGAAGAGCGTTACGTGCTGCCTCCACG	3909
QY	1328	-----GlyIleGluAspHisProValLeuLeuArgAspLeu	1338
Db	3910	ACCTCAACTCCCGCGGCAGCTCCAGGCACAGAAACCCACCATCTCTGGGAGAGTGG	3969
QY	1339	GluValProGlyTy <sup>r</sup> ArgGlnGluArgValGluLysGlyLeuLysLeuPheAlaGlnLeu	1358
Db	3970	AAGATTCTGAGAGCTCCGCGCCCAACATGGAAGAGGAAATTAGTTGTTCTCTCACTA	4029
QY	1359	IleAsnAsnLysValPheLeuLeuSerPheIleArgThrLeuGluSerGlnArgSerPhe	1378
Db	4030	CTCAACAAACAGCACTTCTCATCGTCTTTGTCCACGCGTGGAGCAGCAAGAGCACTT	4089
QY	1379	SerMetArgAspArgGlyAsnValAlaSerLeuIleMetThrValLeuGlnSerLysLeu	1398
Db	4090	CGCGTGGCGACAGTGCAGCTGGCTCTGCTGTACCATCGCGTGCACGGCAGCTG	4149
QY	1399	GluTy <sup>r</sup> AlaThrAspValLeuLysGlnLeuLeuAlaAspLeuIleAspLysAsnLeuGlu	1418
Db	4150	GAGTACTACACAGCATCATGAAGAGTGTGTGTGGACCTCATTTGACGCTCTG	4203
QY	1419	SerLysAsnHisProLysLeuLeuLeuArgArgThrGluSerValAlaGluLysMetLeu	1438
Db	4204	GCCGCGAAGAACCCCAAGCTCATGCTCGGGCGCACAGAGTGTGTGTGGAGAGATGCTC	4263
QY	1439	ThrAsnTrpPheThrPheLeuLeuTy <sup>r</sup> LysPheLeuLysGluCysAlaGlyGluProLeu	1458
Db	4264	ACCAACTGGATGTCCATCTGCATGTACAGCTGTCTCGGGAGACGCTGGGGAGCCATTC	4323
QY	1459	PheSerLeuPheCysAlaIleLysGlnGlnMetGluLysGlyProIleAspAlaIleThr	1478
Db	4324	TTCTGTGCTGTGTGTCATCAACAGACGCAAAATCAACAAAGGCTCCATCGACGCATCACA	4383
QY	1479	GlyGluAlaArgTy <sup>r</sup> SerLeuSerGluAspLysLeuIleArgGlnGlnIleAspTy <sup>r</sup> Lys	1498
Db	4384	GGCAAGGCCCGCTACACTCAATGAGAGTGGTGTGTGCGGGAGAACATCGAGCCCAAG	4443
QY	1499	ThrLeuValLeuSerCysValSerProAspAsnAlaAsnSerProGluValProValLys	1518
Db	4444	CCCCGAACCTGAAAC---GTGTCTCTCCAGGCGTGTGGCATGTGACTCGCTGAGCGTCGG	4500



Db 5452 GGCCTGGAGGCAACCCACGGCCCGAGGACACAACTGCAGCACAGTTTGGACGAGTG 5511  
Qy 1887 lIeThrLeuMet 1890  
Db 5512 GTGGCTTTGATG 5523  
RESULT 13  
US-10-108-260A-802  
; Sequence 802, Application US/10108260A  
; Publication No. US20040005560A1  
; GENERAL INFORMATION:  
; APPLICANT: HELIX RESEARCH INSTITUTE  
; TITLE OF INVENTION: NO. US20040005560A1 full length cDNA  
; FILE REFERENCE: H1-A0106  
; CURRENT APPLICATION NUMBER: US/10/108,260A  
; PRED. FILING DATE: 2002-03-27  
; NUMBER OF SEQ ID NOS: 5458  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 802  
; LENGTH: 3666  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-108-260A-802  
Alignment Scores:  
Pred. No.: 1,538-209 Length: 3666  
Score: 2029.00 Matches: 385  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 20.31% Indels: 0  
DB: 16 Gaps: 0  
US-09-964-955-13 (1-1896) x US-10-108-260A-802 (1-3666)  
Qy 1510 AlaAsnSerProGluValProVallylleLeuAsnCysAspThrIleThrGlnVallys 1529  
Db 2 GCAACAGCCCGAGTCCAGTAAAGATCTCACTGTGACACCATCACTCAGGTCAAG 61  
Qy 1530 GluLysIleLeuAspAlaIlePheLysAsnValProCysSerHisArgProLysAlaIle 1549  
Db 62 GAGAAGATCTGGATGCCATCTTCAAGATGTGCTTGTCTCCACGGGCCAAAGCTGCA 121  
Qy 1550 AspMetAspLeuGluThrPargGlnGlySerGlyAlaArgMetIleLeuGlnAspGluAsp 1569  
Db 122 GATATGGATCTGGAGTGGGCAAGGAAGTGGGGCAAGGATGATCTTGCAGGATGAAGAC 181  
Qy 1570 IleThrThrLysIleGluAsnAspTrpLysArgLeuAsnThrLeuAlaHisThrGlnVal 1589  
Db 182 ATCACACCAAGATTGAGATGATTGGAAGCGACTGAACACACTGGCCCACTACCAGGTG 241  
Qy 1590 ProAspGlySerValValAlaLeuValSerLysGlnValThrAlaThrAsnAlaValAsn 1609  
Db 242 CCAGATGGTTCCTGGTGGCATTTAGTGTCCAAAGCAGGTGACAGCCCTATAACGAGTGAAC 301  
Qy 1610 AsnSerThrValSerArgThrSerAlaSerLysTrpGluAsnMetIleArgTrpThrGly 1629  
Db 302 AACTCCACCGTCTCCAGGACCTCAGCAAGTAATATGAAACATGATCCGGTACAGGGC 361  
Qy 1630 SerProAspSerLeuArgSerArgThrProMetIleThrProAspLeuGlnSerGlyVal 1649  
Db 362 AGCCCCGACAGCTCCCGTCCAGGACACCTATGATCACTCTGACCTGGAGAGTGGAGTC 421  
Qy 1650 LysMetTrpHisLeuVallylleAsnHisGluHisGlyAspGlnLysGluArgGly 1669  
Db 422 AAGATGGCACCTAGTGAAGAACCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 481  
Qy 1670 SerLysMetValSerGluIleThrLeuThrArgLeuLeuAlaThrLysGlyThrLeuGln 1689  
Db 482 AGCAAGATGGTGTCTGAAATCTACCTGACCCGACCTCTGCGCCACTAAGGGCAGCTGCAG 541  
Qy 1690 LysPheValAspAspLeuPheGluThrIlePheSerThrAlaHisArgGlySerAlaLeu 1709

Db 542 AAGTTTGTGGATGACCTCTTTGAGACCACTTTTCAGCACGGCACACCGTGGCTCTGCCCC 601  
Qy 1710 ProLeuAlaIleLysTrpMetPheAspPheLeuAspGluGlnAlaAspLysHisGlyIle 1729  
Db 602 CCCCTGGCCATCAAGTACATGTTTGTCTTCTGGATGACAGCTGATTAACATGGCAAT 661  
Qy 1730 HisAspProHisValArgHisThrTrpLysSerAsnCysLeuProLeuArgPheTrpVal 1749  
Db 662 CATGACCCGACGTCGCCCATACCTGGAAGAGCAATTGCTGCCCTGAGGTTTGGGTC 721  
Qy 1750 AsnMetIleLysAsnProGlnPheValPheAspIleHisLysAsnSerIleThrAspAla 1769  
Db 722 AACATGATCAAGAACCCGAGTTTGTGTGTGACATCCATAAGAACAGCATCACAGACGCC 781  
Qy 1770 CysLeuSerValValAlaGlnThrPheMetAspSerCysSerThrSerGluHisArgLeu 1789  
Db 782 TGCTCTCTGTGGTGGCTCAGACCTTCATGGACTCTTGTCCACGTCAGAGCACCGGCTG 841  
Qy 1790 GlyLysAspSerProSerAsnLysLeuLeuTrpAlaLysAspIleProSerTrpLysAsn 1809  
Db 842 GGCAAGGACTCGCCCTCCCAACAGCTGTGTATGCCAAGGACATCCCCAGCTACAAGAAT 901  
Qy 1810 TrpValGluArgTrpTrpSerAspIleGlyLysMetProAlaIleSerAspGlnAspMet 1829  
Db 902 TGGTGGAGAGGTATTACTCAGACATAGGAAGATGCCAGGCATCAGCGCAAGACATG 961  
Qy 1830 AsnAlaTrpLeuAlaGluGlnSerArgMetHisMetAsnGluPheAsnThrMetSerAla 1849  
Db 962 AACGCATACCTGGCTGAGCAGTCCCGGATGCACATGATGATGATCAACCATGAGTGCA 1021  
Qy 1850 LeuSerGluIlePheSerTrpValGlyLysTrpSerGluGluIleLeuGlyProLeuAsp 1869  
Db 1022 CTCTCAGAGATCTTCTCTATGTGGCAATATCAGCGAGGAGATCTTGGACCTCTGGAC 1081  
Qy 1870 HisAspAspGlnCysGlyLysGlnLysLeuAlaTrpLysLeuGluGlnValIleThrLeu 1889  
Db 1082 CACGACGACGATGTGGGAAGCAGAACTGGCCCTACAAACTAGAACAGTCAATACCCCTC 1141  
Qy 1890 MetSerLeuAspSer 1894  
Db 1142 ATGAGCTTAGACAGC 1156  
RESULT 14  
US-10-276-774-773  
; Sequence 773, Application US/10276774  
; Publication No. US20040053245A1  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc.  
; TITLE OF INVENTION: No. US20040053245A1el Nucleic Acids and Polypeptides  
; FILE REFERENCE: 21272-030  
; CURRENT APPLICATION NUMBER: US/10/276,774  
; PRED. FILING DATE: 2002-11-18  
; PRIOR APPLICATION NUMBER: 05/560,875  
; PRIOR FILING DATE: 2000-04-27  
; PRIOR APPLICATION NUMBER: 09/496,914  
; PRIOR FILING DATE: 2000-02-03  
; NUMBER OF SEQ ID NOS: 2700  
; SOFTWARE: Custom  
; SEQ ID NO 773  
; LENGTH: 1088  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-276-774-773  
Alignment Scores:  
Pred. No.: 8,618-161 Length: 1088  
Score: 1573.50 Matches: 300  
Percent Similarity: 90.70% Conservative: 22  
Best Local Similarity: 84.51% Mismatches: 32  
Query Match: 15.75% Indels: 1  
DB: 13 Gaps: 1



US-09-964-956-13 (1-1896) x US-10-276-774-773 (1-1088)

QY 1420 LysAsnHisProLysLeuLeuLeuArgThrGluSerValAlaGluLysMetLeuThr 1439  
Db 27 AGAACCACCCCAAGCTGCTACTCGCCGGAGTGGTGGCAGAGAAGATGTAAGT 86  
QY 1440 AsnTrpPheThrPheLeuLeuTyrlsPheLeuLysGluCysAlaGluProLeuPhe 1459  
Db 87 AACTGGTTCACCTTCTCTTGATTAAGTTCCTCAAGGAGAGCGCTGGGGAGCGGTGTT 146  
QY 1460 SerLeuPheCysAlaIleLysGlnMetGluLysGlyProIleAspAlaIleThrGly 1479  
Db 147 ATGCTGTACTGGCCCATCAAGCACCAGATGGAGAGGGCCCATTTGAGCCCATCGGGT 206  
QY 1480 GluAlaArgTy-SerLeuSerGluAspLysLeuIleArgGlnGlnIleAspTyrlsThr 1499  
Db 207 GAGGCACGCTACTCCTCGTGAAGTGAAGCAAGCTCATTCGCGACCTGATTGACTACAAGACA 266  
QY 1500 LeuValLeuSerCysValSerProAspAsnAlaAsnSerProGluValProValLysIle 1519  
Db 267 CTGACCTGAAGTGTGAACCTTGAGATGAATGAATGCACTGAGGTGCGCGTGAAGGG 326  
QY 1520 LeuAsnCysAspThrIleThrGlnValLysGluLysIleLeuAspAlaIlePheLysAsn 1539  
Db 327 CTGAGCTGTGACACGGGACCCAGCCAGGAGAGAGCTGCTGGACGCTGCTTACAAGGGC 386  
QY 1540 ValProCysSerHisArgProLysAlaAlaAspMetAspLeuGluTrpArgGlnLys 1559  
Db 387 GTGCCCTACTCCAGCGGCCCAAGCGCGGAGCATGAGCTGGAGTGGCGCCAGGGCGCGC 446  
QY 1560 GlyAlaArgMetIleLeuGlnAspGluAspIleThrLysIleGluAsnAspTrpLys 1579  
Db 447 ATGGCGCGATCATCTCTGAGGACGAGAGCGTCACCCCAAGATTGACCAAGATTGGAG 506  
QY 1580 ArgLeuAsnThrLeuAlaHisTrpGlnValProAspGlySerValValAlaLeuValSer 1599  
Db 507 AGGCTGAACACACTGCTCACTACCAAGTGACAGACGGGTCTCTCGGTGGCACTGGTGGCC 566  
QY 1600 LysGlnValThrAlaTrpAsnAlaValAsnAsnSerThrValSerArgThrSerAlaSer 1619  
Db 567 AAGCAGCGTCCCGCTACACATCTCCACTCTCCCTTCCCTTACCAAG---TCCCTCAGC 623  
QY 1620 LysTyrlsGluAsnMetIleArgTyrlsThrGlySerProAspSerLeuArgSerArgThrPro 1639  
Db 624 AGATACGAGAGCATGCTGGCGACGGCCAGCAGCGCCCGCAGACGCTGGCTCGCGCAGCGCC 683  
QY 1640 MetIleThrProAspLeuGluSerGlyValLysMetTrpHisLeuValLysAsnHisGlu 1659  
Db 684 ATGATCAGCGCCGACCTGGAGAGCGGCACCAAGCTGTGGCACCCTGGTGAAGAACCAACGAC 743  
QY 1660 HisGlyAspGlnLysGluGlyAspArgGlySerLysMetValSerGluIleTyrlsThr 1679  
Db 744 CACTGGACCGAGCGTGGGGTGACCGCGGAGCAAGATGCTCTCGAGATCTACTTGACA 803  
QY 1680 ArgLeuLeuAlaThrLysGlyThrLeuGlnLysPheValAspAspLeuPheGluThrIle 1699  
Db 804 CGGCTACTGGCCCAACCAAGGCGACACTGCAGAGTGTGGAGCAGCCTGTTTGAGACCATC 863  
QY 1700 PheSerThrAlaHisArgGlySerAlaLeuProLeuAlaIleLysTyrlsMetPheAspPhe 1719  
Db 864 TTGAGCAGCGACACCGGGGCTCAGCCCTGCCCTGGCCATCAAGTACATGTTTGGACTTC 923  
QY 1720 LeuAspGluGlnAlaAspLysHisGlyIleHisAspProHisValArgHisThrTrpLys 1739  
Db 924 CTGGATGAGCAGCGCGCAAGCAGACCATCCAGATGCTGACGTGGCGCCACACTGGAAG 983  
QY 1740 SerAsnCysLeuProLeuArgPheTrpValAsnMetIleLysAsnProGlnPheValPhe 1759  
Db 984 AGCAACTGCTGCCCCCTCGCGCTTCTGGGTGAACGTGATCAAGAACCCACAGTTTGTGTTTC 1043  
QY 1760 AspIleHisLysAsnSerIleThrAspAlaCysLeuSerValVal 1774  
Db 1044 GACATTACAGAAGACACATCACGACGCTGCTTGTGCGTGGTG 1088

RESULT 15

US-10-245-752-91  
; Sequence 91, Application US/10245752  
; Publication NO. US20030064473A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin  
; APPLICANT: Eaton, Dan  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stephan, Jean-Philippe  
; APPLICANT: Watanabe, Colin  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; APPLICANT: Fong, Sherman  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; TITLE OF INVENTION: ACIDS ENCODING THE SAME  
; FILE REFERENCE: P3630RIC66  
; CURRENT APPLICATION NUMBER: US/10/245,752  
; CURRENT FILING DATE: 2002-09-16  
; PRIOR APPLICATION NUMBER: 10/197942  
; PRIOR FILING DATE: 2002-07-18  
; PRIOR APPLICATION NUMBER: 60/059114  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/063046  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/065027  
; PRIOR FILING DATE: 1997-11-10  
; PRIOR APPLICATION NUMBER: 60/079689  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: 60/086478  
; PRIOR FILING DATE: 1998-05-22  
; PRIOR APPLICATION NUMBER: 60/087607  
; PRIOR FILING DATE: 1998-06-02  
; PRIOR APPLICATION NUMBER: 60/089801  
; PRIOR FILING DATE: 1998-06-18  
; PRIOR APPLICATION NUMBER: 60/090557  
; PRIOR FILING DATE: 1998-06-24  
; PRIOR APPLICATION NUMBER: 60/090689  
; PRIOR FILING DATE: 1998-06-25  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 116  
; SEQ ID NO 91  
; LENGTH: 2597  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
US-10-245-752-91  
Alignment Scores:  
Pred. No.: 3,86e-138 Length: 2597  
Score: 1372.00 Matches: 264  
Percent Similarity: 100.00% Conservative: 1  
Best Local Similarity: 99.62% Mismatches: 0  
Query Match: 13.73% Indels: 0  
DB: 13 Gaps: 0  
US-09-964-956-13 (1-1896) x US-10-245-752-91 (1-2597)  
QY 194 GluTyrlsPheProThrIleSerSerArgLysLeuThrLysAsnSerGluAlaAspGlyMet 213  
Db 2 GAGTATTTTCCACCATCTCCAGCCGGAACCTGACCAAGAACTCTGAGCGGATGGCATG 61  
QY 214 PheAlaTyrlsValPheHisAspGluPheValAlaSerMetIleLysIleProSerAspThr 233  
Db 62 TTCGGGTACGCTCTCCATGATGAGTTCGTGGCTCGATGATTAAGATCCCTTCGACACC 121  
QY 234 PheThrIleIleProAspPheAspIleTyrlsValTyrlsGlyPheSerSerGlyAsnPhe 253  
Db 122 TTCACCATCATCCCTGACTTTGATATCTATCTATGTCTATGTGTTTAGCAGTGGCAACTTT 181

QY	254	ValTyrPheLeuThrLeuGlnProGluMetValSerProProGlySerThrThrLysGlu	273
Db	182	GTCTACTTTTGGACCTTCACCTGAGATGGTGTCTCCACCAGGCTCCACCACCAAGGAG	241
QY	274	GlnValTyrThrSerLysLeuValArgLeuCysLysGluAspThrAlaPheAsnSerTyr	293
Db	242	CAGGTGTATACATCCAAAGCTCGTAGGGCTTTGCAAGGAGGACACAGCCCTTCAACTCCTAT	301
QY	294	ValGluValProIleGlyCysGluArgSerGlyValGluTyrArgLeuLeuGlnAlaAla	313
Db	302	GTAGAGGTGCCCATTTGGCTGTGAGCGCAGTGGGTGGAGTACCGCCTGCTCAGGCTGCC	361
QY	314	TyrLeuSerLysAlaGlyAlaValLeuGlyArgThrLeuGlyValHisProAspAspAsp	333
Db	362	TACCTGTCCAAAGCGGGGCGCTGCTTGGCAGGACCTTGGAGTCCATCCAGATGATGAC	421
QY	334	LeuLeuPheThrValPheSerLysGlyGlnLysArgLysMetLysSerLeuAspGluSer	353
Db	422	CTGCTCTTCACCGCTTTCTCCAAGGGCCAGAGCGGAAAAATGAATCCCTGGATGAGTCG	481
QY	354	AlaLeuCysIlePheIleLeuLysGlnIleAsnAspArgIleLysGluArgLeuGlnSer	373
Db	482	GCCCTGTGCATCTTTCATCTTGAAGCAGATAAATGACCGCATTAAAGGAGCGCTGCAGTCT	541
QY	374	CysTyrArgGlyGluGlyThrLeuAspLeuAlaTyrLeuLysValLysAspIleProCys	393
Db	542	TGTTACCGGGGGGAGGCGACGCTGGACCTGGCCTGGCTCAAGGTGAAGGACATCCCTGTC	601
QY	394	SerSerAlaLeuLeuThrIleAspAspAsnPheCysGlyLeuAspMetAsnAlaProLeu	413
Db	602	AGCAGTGGCTCTTAACCATTCACGATAACITTCGTGGCTCGACATGAATGCTCCCTG	661
QY	414	GlyValSerAspMetValArgGlyIleProValPheThrGluAspArgAspArgMetThr	433
Db	662	GGAGTGTCCGACATGGTGGTGGAAATCCCGTCTTCACGGAGGACAGGGACCGCATGACG	721
QY	434	SerValIleAlaTyrValTyrLysAsnHisSerLeuAlaPheValGlyThrLysSerGly	453
Db	722	TCTGTATCGCATATGTCTACAAAGAACCACTCTCTGGCCTTTGTGGGACCAAAAGTGGC	781
QY	454	LysLeuLysLysIle	458
Db	782	AAAGTGAAGAGGTG	796

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Job time : 1520 secs